

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
25 July 2002 (25.07.2002)

PCT

(10) International Publication Number
WO 02/057414 A2

(51) International Patent Classification⁷: **C12N**

QUERTERMOUS, Thomas [US/US]; 44 El Rey Road, Portola Valley, CA 94028 (US). **JOHNSON, Frances** [US/US]; 44 El Rey Road, Portola Valley, CA 94028 (US).

(21) International Application Number: PCT/US01/47856

(22) International Filing Date: 22 October 2001 (22.10.2001)

(74) Agents: **WARD, Michael, R.** et al.; Morrison & Foerster LLP, 425 Market Street, San Francisco, CA 94105-2482 (US).

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/241,994 20 October 2000 (20.10.2000) US
60/296,764 8 June 2001 (08.06.2001) US

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(71) Applicant (*for all designated States except US*): **BIO-CARDIA, INC.** [US/US]; 384 Oyster Point Boulevard, #4, South San Francisco, CA 94080 (US).

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **WOHLGEMUTH, Jay** [US/US]; 664 Hamilton Avenue, Palo Alto, CA 94301 (US). **FRY, Kirk** [US/US]; 2604 Ross Road, Palo Alto, CA 94303 (US). **MATCUK, George** [US/US]; 141C Escondido Village, Stanford, CA 94305 (US). **ALT-MAN, Peter** [US/US]; 717 Evelyn Avenue, Albany, CA 94706 (US). **PRENTICE, James** [US/US]; 120 Dolores Street, San Francisco, CA 94103 (US). **PHILLIPS, Julie** [US/US]; 1090 Mirador Terrace, Pacifica, CA 94044 (US). **LY, Ngoc** [US/US]; 2000 Crystal Springs Road 15-14, San Bruno, CA 94066 (US). **WOODWARD, Robert** [US/US]; 1828 Rheem Court, Pleasanton, CA 94588 (US).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: LEUKOCYTE EXPRESSION PROFILING

(57) Abstract: Leukocyte gene expression profiling is utilized to identify oligonucleotides from gene expression candidate libraries. The expression libraries are generally immobilized on an array. Diagnostic oligonucleotide sets for analysis of leukocyte-related diseases are described.

WO 02/057414 A2

LEUKOCYTE EXPRESSION PROFILING

Field of the Invention

This invention is in the field of expression profiling. In particular, this invention is in the field of leukocyte expression profiling.

Background of the Invention

Many of the current shortcomings in diagnosis, prognosis, risk stratification and treatment of disease can be approached through the identification of the molecular mechanisms underlying a disease and through the discovery of nucleotide sequences (or sets of nucleotide sequences) whose expression patterns predict the occurrence or progression of disease states, or predict a patient's response to a particular therapeutic intervention. In particular, identification of nucleotide sequences and sets of nucleotide sequences with such predictive value from cells and tissues that are readily accessible would be extremely valuable. For example, peripheral blood is attainable from all patients and can easily be obtained at multiple time points at low cost. This is a desirable contrast to most other cell and tissue types, which are less readily accessible, or accessible only through invasive and aversive procedures. In addition, the various cell types present in circulating blood are ideal for expression profiling experiments as the many cell types in the blood specimen can be easily separated if desired prior to analysis of gene expression. While blood provides a very attractive substrate for the study of diseases using expression profiling techniques, and for the development of diagnostic technologies and the identification of therapeutic targets, the value of expression profiling in blood samples rests on the degree to which changes in gene expression in these cell types are associated with a predisposition to, and pathogenesis and progression of a disease.

There is an extensive literature supporting the role of leukocytes, e.g., T-and B-lymphocytes, monocytes and granulocytes, including neutrophils, in a wide range of disease processes, including such broad classes as cardiovascular diseases, inflammatory, autoimmune and rheumatic diseases, infectious diseases, transplant rejection, cancer and malignancy, and endocrine diseases. For example, among cardiovascular diseases, such commonly occurring diseases as atherosclerosis, restenosis, transplant vasculopathy and acute coronary syndromes all demonstrate significant T cell involvement (Smith-Norowitz et al. (1999) Clin Immunol 93:168-175; Jude et al. (1994) Circulation 90:1662-8; Belch et al. (1997) Circulation

95:2027-31). These diseases are now recognized as manifestations of chronic inflammatory disorders resulting from an ongoing response to an injury process in the arterial tree (Ross et al. (1999) Ann Thorac Surg 67:1428-33). Differential expression of lymphocyte, monocyte and neutrophil genes and their products has been demonstrated clearly in the literature. Particularly interesting are examples of differential expression in circulating cells of the immune system that demonstrate specificity for a particular disease, such as arteriosclerosis, as opposed to a generalized association with other inflammatory diseases, or for example, with unstable angina rather than quiescent coronary disease.

A number of individual genes, e.g., CD11b/CD18 (Kassirer et al. (1999) Am Heart J 138:555-9); leukocyte elastase (Amaro et al. (1995) Eur Heart J 16:615-22; and CD40L (Aukrust et al. (1999) Circulation 100:614-20) demonstrate some degree of sensitivity and specificity as markers of various vascular diseases. In addition, the identification of differentially expressed target and fingerprint genes isolated from purified populations of monocytes manipulated in various in vitro paradigms has been proposed for the diagnosis and monitoring of a range of cardiovascular diseases, see, e.g., US Patents Numbers 6,048,709; 6,087,477; 6,099,823; and 6,124,433 “COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE” to Falb (*see also*, WO 97/30065). Lockhart, in US Patent Number 6,033,860 “EXPRESSION PROFILES IN ADULT AND FETAL ORGANS” proposes the use of expression profiles for a subset of identified genes in the identification of tissue samples, and the monitoring of drug effects.

The accuracy of technologies based on expression profiling for the diagnosis, prognosis, and monitoring of disease would be dramatically increased if numerous differentially expressed nucleotide sequences, each with a measure of specificity for a disease in question, could be identified and assayed in a concerted manner. In order to achieve this improved accuracy, the appropriate sets of nucleotide sequences need to be identified and validated against numerous samples in combination with relevant clinical data. The present invention addresses these and other needs, and applies to any disease or disease state for which differential regulation of genes, or other nucleotide sequences, of peripheral blood can be demonstrated.

Summary of the Invention

The present invention is thus directed to a system for detecting differential gene expression. In one format, the system has one or more isolated DNA molecules

wherein each isolated DNA molecule detects expression of a gene selected from the group of genes corresponding to the oligonucleotides depicted in the Sequence Listing. It is understood that the DNA sequences and oligonucleotides of the invention may have slightly different sequences than those identified herein. Such sequence variations are understood to those of ordinary skill in the art to be variations in the sequence which do not significantly affect the ability of the sequences to detect gene expression.

The sequences encompassed by the invention have at least 40-50, 50-60, 70-80, 80-85, 85-90, 90-95 % or 95-100% sequence identity to the sequences disclosed herein. In some embodiments, DNA molecules are less than about any of the following lengths (in bases or base pairs): 10,000; 5,000; 2500; 2000; 1500; 1250; 1000; 750; 500; 300; 250; 200; 175; 150; 125; 100; 75; 50; 25; 10. In some embodiments, DNA molecule is greater than about any of the following lengths (in bases or base pairs): 10; 15; 20; 25; 30; 40; 50; 60; 75; 100; 125; 150; 175; 200; 250; 300; 350; 400; 500; 750; 1000; 2000; 5000; 7500; 10000; 20000; 50000. Alternately, a DNA molecule can be any of a range of sizes having an upper limit of 10,000; 5,000; 2500; 2000; 1500; 1250; 1000; 750; 500; 300; 250; 200; 175; 150; 125; 100; 75; 50; 25; or 10 and an independently selected lower limit of 10; 15; 20; 25; 30; 40; 50; 60; 75; 100; 125; 150; 175; 200; 250; 300; 350; 400; 500; 750; 1000; 2000; 5000; 7500 wherein the lower limit is less than the upper limit.

The gene expression system may be a candidate library, a diagnostic agent, a diagnostic oligonucleotide set or a diagnostic probe set. The DNA molecules may be genomic DNA, protein nucleic acid (PNA), cDNA or synthetic oligonucleotides.

In one format, the gene expression system is immobilized on an array. The array may be a chip array, a plate array, a bead array, a pin array, a membrane array, a solid surface array, a liquid array, an oligonucleotide array, a polynucleotide array, a cDNA array, a microfilter plate, a membrane or a chip.

In one format, the genes detected by the gene expression system are selected from the group of genes corresponding to the oligonucleotides depicted in SEQ ID NO:2476, SEQ ID NO: 2407, SEQ ID NO:2192, SEQ ID NO: 2283, SEQ ID NO:6025, SEQ ID NO: 4481, SEQ ID NO:3761, SEQ ID NO: 3791, SEQ ID NO:4476, SEQ ID NO: 4398, SEQ ID NO:7401, SEQ ID NO: 1796, SEQ ID NO:4423, SEQ ID NO: 4429, SEQ ID NO:4430, SEQ ID NO: 4767, SEQ ID NO:4829 and SEQ ID NO: 8091.

The present invention is further directed to a diagnostic agent comprising an oligonucleotide wherein the oligonucleotide has a nucleotide sequence selected from the Sequence Listing wherein the oligonucleotide detects expression of a gene that is differentially expressed in leukocytes in an individual over time. In one format, the oligonucleotide has a nucleotide sequence selected from the group consisting of SEQ ID NO:2476, SEQ ID NO: 2407, SEQ ID NO:2192, SEQ ID NO: 2283, SEQ ID NO:6025, SEQ ID NO: 4481, SEQ ID NO:3761, SEQ ID NO: 3791, SEQ ID NO:4476, SEQ ID NO: 4398, SEQ ID NO:7401, SEQ ID NO: 1796, SEQ ID NO:4423, SEQ ID NO: 4429, SEQ ID NO:4430, SEQ ID NO: 4767, SEQ ID NO:4829 and SEQ ID NO: 8091

The present invention is further directed to a system for detecting gene expression in leukocytes comprising an isolated DNA molecule wherein the isolated DNA molecule detects expression of a gene wherein the gene is selected from the group of genes corresponding to the oligonucleotides depicted in the Sequence Listing and the gene is differentially expressed in the leukocytes in an individual with at least one disease criterion for a disease selected from Table 1 as compared to the expression of the gene in leukocytes in an individual without the at least one disease criterion.

The present invention is further directed to a gene expression candidate library comprising at least two oligonucleotides wherein the oligonucleotides have a sequence selected from those oligonucleotide sequences listed in Table 2, Table 3, and the Sequence Listing. Table 3 encompasses Tables 3A, 3B and 3C. The oligonucleotides of the candidate library may comprise deoxyribonucleic acid (DNA), ribonucleic acid (RNA), protein nucleic acid (PNA), synthetic oligonucleotides, or genomic DNA.

In one embodiment, the candidate library is immobilized on an array. The array may comprises one or more of: a chip array, a plate array, a bead array, a pin array, a membrane array, a solid surface array, a liquid array, an oligonucleotide array, a polynucleotide array or a cDNA array, a microtiter plate, a pin array, a bead array, a membrane or a chip. Individual members of the libraries are may be separately immobilized.

The present invention is further directed to a diagnostic oligonucleotide set for a disease having at least two oligonucleotides wherein the oligonucleotides have a sequence selected from those oligonucleotide sequences listed in Table 2, Table 3, or

the Sequence Listing which are differentially expressed in leukocytes genes in an individual with at least one disease criterion for at least one leukocyte-related disease as compared to the expression in leukocytes in an individual without the at least one disease criterion, wherein expression of the two or more genes of the gene expression library is correlated with at least one disease criterion.

The present invention is further directed to a diagnostic oligonucleotide set for a disease having at least one oligonucleotide wherein the oligonucleotide has a sequence selected from those sequences listed in Table 2, Table 3, or the sequence listing which is differentially expressed in leukocytes in an individual with at least one disease criterion for a disease selected from Table 1 as compared to leukocytes in an individual without at least one disease criterion, wherein expression of the at least one gene from the gene expression library is correlated with at least one disease criterion, wherein the differential expression of the at least one gene has not previously been described. In one format, two or more oligonucleotides are utilized.

In the diagnostic oligonucleotide sets of the invention the disease criterion may include data selected from patient historic, diagnostic, prognostic, risk prediction, therapeutic progress, and therapeutic outcome data. This includes lab results, radiology results, pathology results such as histology, cytology and the like, physical examination findings, and medication lists.

In the diagnostic oligonucleotide sets of the invention the leukocytes comprise peripheral blood leukocytes or leukocytes derived from a non-blood fluid. The non-blood fluid may be selected from colon, sinus, spinal fluid, saliva, lymph fluid, esophagus, small bowel, pancreatic duct, biliary tree, ureter, vagina, cervix uterus and pulmonary lavage fluid.

In the diagnostic oligonucleotide sets of the invention the leukocytes may include leukocytes derived from urine or a joint biopsy sample or biopsy of any other tissue or may be T-lymphocytes.

In the diagnostic oligonucleotide sets of the invention the disease may be selected from cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus (SLE), rheumatoid arthritis, osteoarthritis, and cytomegalovirus infection.

The diagnostic oligonucleotide sets of the invention may further include one or more cytomegalovirus (CMV) nucleotide sequences, wherein expression of the CMV nucleotide sequence is correlated with CMV infection.

The diagnostic nucleotide sets of the invention may further include one or more Epstein-Barr virus (EBV) nucleotide sequences, wherein expression of the one or more EBV nucleotide sequences is correlated with EBV infection.

In the present invention, expression may be differential expression, wherein the differential expression is one or more of a relative increase in expression, a relative decrease in expression, presence of expression or absence of expression, presence of disease or absence of disease. The differential expression may be RNA expression or protein expression. The differential expression may be between two or more samples from the same patient taken on separate occasions or between two or more separate patients or between two or more genes relative to each other.

The present invention is further directed to a diagnostic probe set for a disease where the probes correspond to at least one oligonucleotide wherein the oligonucleotides have a sequence such as those listed in Table 2, Table 3, or the Sequence Listing which is differentially expressed in leukocytes in an individual with at least one disease criterion for a disease selected from Table 1 as compared to leukocytes in an individual without the at least one disease criterion, wherein expression of the oligonucleotide is correlated with at least one disease criterion, and further wherein the differential expression of the at least one nucleotide sequence has not previously been described.

The present invention is further directed to a diagnostic probe set wherein the probes include one or more of probes useful for proteomics and probes for nucleic acids cDNA, or synthetic oligonucleotides.

The present invention is further directed to an isolated nucleic acid having a sequences such as those listed in Table 3B or Table 3C or the Sequence Listing.

The present invention is further directed to polypeptides wherein the polypeptides are encoded by the nucleic acid sequences in Tables 3B, 3C and the Sequence Listing.

The present invention is further directed to a polynucleotide expression vector containing the polynucleotide of Tables 3B-3C or the Sequence Listing in operative association with a regulatory element which controls expression of the polynucleotide in a host cell. The present invention is further directed to host cells transformed with the expression vectors of the invention. The host cell may be prokaryotic or eukaryotic.

The present invention is further directed to fusion proteins produced by the host cells of the invention. The present invention is further directed to antibodies directed to the fusion proteins of the invention. The antibodies may be monoclonal or polyclonal antibodies.

The present invention is further directed to kits comprising the diagnostic oligonucleotide sets of the invention. The kits may include instructions for use of the kit.

The present invention is further directed to a method of diagnosing a disease by obtaining a leukocyte sample from an individual, hybridizing nucleic acid derived from the leukocyte sample with a diagnostic oligonucleotide set, and comparing the expression of the diagnostic oligonucleotide set with a molecular signature indicative of the presence or absence of the disease.

The present invention is further directed to a method of detecting gene expression by a) isolating RNA and b) hybridizing the RNA to isolated DNA molecules wherein the isolated DNA molecules detect expression of a gene wherein the gene corresponds to one of the oligonucleotides depicted in the Sequence Listing.

The present invention is further directed to a method of detecting gene expression by a) isolating RNA; b) converting the RNA to nucleic acid derived from the RNA and c) hybridizing the nucleic acid derived from the RNA to isolated DNA molecules wherein the isolated DNA molecules detect expression of a gene wherein the gene corresponds to one of the oligonucleotides depicted in the Sequence Listing. In one format, the nucleic acid derived from the RNA is cDNA.

The present invention is further directed to a method of detecting gene expression by a) isolating RNA; b) converting the RNA to cRNA or aRNA and c) hybridizing the cRNA or aRNA to isolated DNA molecules wherein the isolated DNA molecules detect expression of a gene corresponding to one of the oligonucleotides depicted in the Sequence Listing.

The present invention is further directed to a method of monitoring progression of a disease by obtaining a leukocyte sample from an individual, hybridizing the nucleic acid derived from leukocyte sample with a diagnostic oligonucleotide set, and comparing the expression of the diagnostic oligonucleotide set with a molecular signature indicative of the presence or absence of disease progression.

The present invention is further directed to a method of monitoring the rate of progression of a disease by obtaining a leukocyte sample from an individual, hybridizing the nucleic acid derived from leukocyte sample with a diagnostic oligonucleotide set, and comparing the expression of the diagnostic oligonucleotide set with a molecular signature indicative of the presence or absence of disease progression.

The present invention is further directed to a method of predicting therapeutic outcome by obtaining a leukocyte sample from an individual, hybridizing the nucleic acid derived from leukocyte sample with a diagnostic oligonucleotide set, and comparing the expression of the diagnostic oligonucleotide set with a molecular signature indicative of the predicted therapeutic outcome.

The present invention is further directed to a method of determining prognosis by obtaining a leukocyte sample from an individual, hybridizing the nucleic acid derived from leukocyte sample with a diagnostic oligonucleotide set, and comparing the expression of the diagnostic oligonucleotide set with a molecular signature indicative of the prognosis.

The present invention is further directed to a method of predicting disease complications by obtaining a leukocyte sample from an individual, hybridizing nucleic acid derived from the leukocyte sample with a diagnostic oligonucleotide set, and comparing the expression of the diagnostic oligonucleotide set with a molecular signature indicative of the presence or absence of disease complications.

The present invention is further directed to a method of monitoring response to treatment, by obtaining a leukocyte sample from an individual, hybridizing the nucleic acid derived from leukocyte sample with a diagnostic oligonucleotide set, and comparing the expression of the diagnostic oligonucleotide set with a molecular signature indicative of the presence or absence of response to treatment.

In the methods of the invention the invention may further include characterizing the genotype of the individual, and comparing the genotype of the individual with a diagnostic genotype, wherein the diagnostic genotype is correlated with at least one disease criterion. The genotype may be analyzed by one or more methods selected from the group consisting of Southern analysis, RFLP analysis, PCR, single stranded conformation polymorphism and SNP analysis.

The present invention is further directed to a method of non-invasive imaging by providing an imaging probe for a nucleotide sequence that is differentially

expressed in leukocytes from an individual with at least one disease criterion for at least one leukocyte-implicated disease where leukocytes localize at the site of disease, wherein the expression of the at least one nucleotide sequence is correlated with the at least one disease criterion by (a) contacting the probe with a population of leukocytes; (b) allowing leukocytes to localize to the site of disease or injury and (c) detecting an image.

The present invention is further directed to a control RNA for use in expression profile analysis, where the RNA extracted from the buffy coat samples is from at least four individuals.

The present invention is further directed to a method of collecting expression profiles, comprising comparing the expression profile of an individual with the expression profile of buffy coat control RNA, and analyzing the profile.

The present invention is further directed to a method of RNA preparation suitable for diagnostic expression profiling by obtaining a leukocyte sample from a subject, adding actinomycin-D to a final concentration of 1 ug/ml, adding cycloheximide to a final concentration of 10 ug/ml, and extracting RNA from the leukocyte sample. In the method of RNA preparation of the invention the actinomycin-D and cycloheximide may be present in a sample tube to which the leukocyte sample is added. The method may further include centrifuging the sample at 4°C to separate mononuclear cells.

The present invention is further directed to a leukocyte oligonucleotide set including at least two oligonucleotides which are differentially expressed in leukocytes undergoing adhesion to an endothelium relative to expression in leukocytes not undergoing adhesion to an endothelium, wherein expression of the two oligonucleotides is correlated with the at least one indicator of adhesion state.

The present invention is further directed to a method of identifying at least one diagnostic probe set for assessing atherosclerosis by (a) providing a library of candidate oligonucleotides, which candidate oligonucleotides are differentially expressed in leukocytes which are undergoing adhesion to an endothelium relative to their expression in leukocytes that are not undergoing adhesion to an endothelium; (b) assessing expression of two or more oligonucleotides, which two or more oligonucleotides correspond to components of the library of candidate oligonucleotides, in a subject sample of leukocytes; (c) correlating expression of the two or more oligonucleotides with at least one criterion, which criterion includes one

or more indicators of adhesion to an endothelium; and, (d) recording the molecular signature in a database.

The present invention is further directed to a method of identifying at least one diagnostic probe set for assessing atherosclerosis by (a) providing a library of candidate oligonucleotides, which candidate oligonucleotides are differentially expressed in leukocytes which are undergoing adhesion to an endothelium relative to their expression in leukocytes that are not undergoing adhesion to an endothelium; (b) assessing expression of two or more oligonucleotides, which two or more oligonucleotides correspond to components of the library of candidate nucleotide sequences, in a subject sample of epithelial cells; (c) correlating expression of the two or more nucleotide sequences with at least one criterion, which criterion comprises one or more indicator of adhesion to an endothelium; and (d) recording the molecular signature in a database.

The present invention is further directed to methods of leukocyte expression profiling including methods of analyzing longitudinal clinical and expression data. The rate of change and/or magnitude and direction of change of gene expression can be correlated with disease states and the rate of change of clinical conditions/data and/or the magnitude and direction of changes in clinical data. Correlations may be discovered by examining these expression or clinical changes that are not found in the absence of such changes.

The present invention is further directed to methods of leukocyte profiling for analysis and/or detection of one or more viruses. The virus may be CMV, HIV, hepatitis or other viruses. Both viral and human leukocyte genes can be subjected to expression profiling for these purposes.

Brief Description of the Sequence Listing

The table below gives a description of the sequence listing. There are 8830 entries. The Sequence Listing presents 50mer oligonucleotide sequences derived from human leukocyte, plant and viral genes. These are listed as SEQ IDs 1-8143. The 50mer sequences and their sources are also displayed in Table 8. Most of these 50mers were designed from sequences of genes in Tables 2, 3A, B and C and the Sequence listing.

SEQ IDs 8144-8766 are the cDNA sequences derived from human leukocytes that were not homologous to UniGene sequences or sequences found in dbEST at the

time they were searched. Some of these sequences match human genomic sequences and are listed in Tables 3B and C. The remaining clones are putative cDNA sequences that contained less than 50% masked nucleotides when submitted to RepeatMasker, were longer than 147 nucleotides, and did not have significant similarity to the UniGene Unique database, dbEST, the NR nucleotide database of Genbank or the assembled human genome of Genbank.

SEQ IDs 8767-8770, 8828-8830 and 8832 are sequences that appear in the text and examples (primer, masked sequences, exemplary sequences, etc.).

SEQ IDs 8771-8827 are CMV PCR primers described in Example 17.

Brief Description of the Figures

Figure 1: Figure 1 is a schematic flow chart illustrating a schematic instruction set for characterization of the nucleotide sequence and/or the predicted protein sequence of novel nucleotide sequences.

Figure 2: Figure 2 depicts the components of an automated RNA preparation machine.

Figure 3: Figure 3 describes kits useful for the practice of the invention. Figure 3A describes the contents of a kit useful for the discovery of diagnostic nucleotide sets. Figure 3B describes the contents of a kit useful for the application of diagnostic nucleotide sets.

Figure 4 shows the results of six hybridizations on a mini array graphed ($n=6$ for each column). The error bars are the SEM. This experiment shows that the average signal from AP prepared RNA is 47% of the average signal from GS prepared RNA for both Cy3 and Cy5.

Figure 5 shows the average background subtracted signal for each of nine leukocyte-specific genes on a mini array. This average is for 3-6 of the above-described hybridizations for each gene. The error bars are the SEM.

Figure 6 shows the ratio of Cy3 to Cy5 signal for a number of genes. After normalization, this ratio corrects for variability among hybridizations and allows comparison between experiments done at different times. The ratio is calculated as the Cy3 background subtracted signal divided by the Cy5 background subtracted signal. Each bar is the average for 3-6 hybridizations. The error bars are SEM.

Figure 7 shows data median Cy3 background subtracted signals for control RNAs using mini arrays.

Figure 8 shows data from an array hybridization.

Figure 9 shows a comparison of gene expression in samples obtained from cardiac transplant patients with low rejection grade and high rejection grade.

Figure 10 shows differential gene expression between samples from patients with grade 0 and grade 3A rejection.

Brief Description of the Tables

Table 1: Table 1 lists diseases or conditions amenable to study by leukocyte profiling.

Table 2: Table 2 describes genes and other nucleotide sequences identified using data mining of publically available publication databases and nucleotide sequence databases. Corresponding Unigene (build 133) cluster numbers are listed with each gene or other nucleotide sequence.

Table 3A: Table 3A describes 48 clones whose sequences align to two or more non-contiguous sequences on the same assembled human contig of genomic sequence. The Accession numbers are from the March 15, 2001 build of the human genome. The file date for the downloaded data was 4/17/01. The alignments of the clone and the contig are indicated in the table. The start and stop offset of each matching region is indicated in the table. The sequence of the clones themselves is included in the sequence listing. The alignments of these clones strongly suggest that they are novel nucleotide sequences. Furthermore, no EST or mRNA aligning to the clone was found in the database. These sequences may prove useful for the prediction of clinical outcomes.

Table 3B: Table 3B describes Identified Genomic Regions that code for novel mRNAs. The table contains 591 identified genomic regions that are highly similar to the cDNA clones. Those regions that are within ~100 to 200 Kb of each other on the same contig are likely to represent exons of the same gene. The indicated clone is exemplary of the cDNA clones that match the indicated genomic region. The "number clones" column indicates how many clones were isolated from the libraries that are similar to the indicated region of the chromosome. The probability number is the likelihood that region of similarity would occur by chance on a random sequence. The Accession numbers are from the March 15, 2001 build of the human genome. The file date for the downloaded data was 4/17/01. These sequences may prove useful for the prediction of clinical outcomes.

Table 3C: Table 3C describes differentially expressed nucleotide sequences useful for the prediction of clinical outcomes. This table contains 4517 identified cDNAs and cDNA regions of genes that are members of a leukocyte candidate library, for use in measuring the expression of nucleotide sequences that could subsequently be correlated with human clinical conditions. The regions of similarity were found by searching three different databases for pair wise similarity using blastn. The three databases were UniGene Unique build 3/30/01, file Hs.seq.uniq.Z; the downloadable database at ftp.ncbi.nlm.nih.com/blast/db/est human.Z with date 4/8/01 which is a section of Genbank version 122; and the non-redundant section of Genbank ver 123. The Hs.XXXXX numbers represent UniGene accession numbers from the Hs.seq.uniq.Z file of 3/30/01. The clone sequences are not in the sequence listing.

Table 4: Table 4 describes patient groups and diagnostic gene sets

Table 5: Table 5 describes the nucleotide sequence databases used in the sequence analysis described herein.

Table 6: Table 6 describes the algorithms and software packages used for exon and polypeptide prediction used in the sequence analysis described herein.

Table 7: Table 7 describes the databases and algorithms used for the protein sequence analysis described herein.

Table 8: Table 8 describes leukocyte probes spotted on the microarrays.

Table 9: Table 9 describes Cardiac Transplant patient RNA samples and array hybridizations.

Table 10: Table 10 describes differentially expressed probes identified when comparing leukocyte expression profiles obtained from high and low grade cardiac transplant rejection patients.

Detailed Description of the Invention

Definitions

Unless defined otherwise, all scientific and technical terms are understood to have the same meaning as commonly used in the art to which they pertain. For the purpose of the present invention, the following terms are defined below.

In the context of the invention, the term "gene expression system" refers to any system, device or means to detect gene expression and includes diagnostic agents, candidate libraries, oligonucleotide sets or probe sets.

The term “diagnostic oligonucleotide set” generally refers to a set of two or more oligonucleotides that, when evaluated for differential expression of their products, collectively yields predictive data. Such predictive data typically relates to diagnosis, prognosis, monitoring of therapeutic outcomes, and the like. In general, the components of a diagnostic oligonucleotide set are distinguished from nucleotide sequences that are evaluated by analysis of the DNA to directly determine the genotype of an individual as it correlates with a specified trait or phenotype, such as a disease, in that it is the pattern of expression of the components of the diagnostic nucleotide set, rather than mutation or polymorphism of the DNA sequence that provides predictive value. It will be understood that a particular component (or member) of a diagnostic nucleotide set can, in some cases, also present one or more mutations, or polymorphisms that are amenable to direct genotyping by any of a variety of well known analysis methods, e.g., Southern blotting, RFLP, AFLP, SSCP, SNP, and the like.

A “disease specific target oligonucleotide sequence” is a gene or other oligonucleotide that encodes a polypeptide, most typically a protein, or a subunit of a multi-subunit protein, that is a therapeutic target for a disease, or group of diseases.

A “candidate library” or a “candidate oligonucleotide library” refers to a collection of oligonucleotide sequences (or gene sequences) that by one or more criteria have an increased probability of being associated with a particular disease or group of diseases. The criteria can be, for example, a differential expression pattern in a disease state or in activated or resting leukocytes in vitro as reported in the scientific or technical literature, tissue specific expression as reported in a sequence database, differential expression in a tissue or cell type of interest, or the like. Typically, a candidate library has at least 2 members or components; more typically, the library has in excess of about 10, or about 100, or about 1000, or even more, members or components.

The term “disease criterion” is used herein to designate an indicator of a disease, such as a diagnostic factor, a prognostic factor, a factor indicated by a medical or family history, a genetic factor, or a symptom, as well as an overt or confirmed diagnosis of a disease associated with several indicators such as those selected from the above list. A disease criterion includes data describing a patient’s health status, including retrospective or prospective health data, e.g. in the form of the

patient's medical history, laboratory test results, diagnostic test result, clinical events, medications, lists, response(s) to treatment and risk factors, etc.

The terms "molecular signature" or "expression profile" refers to the collection of expression values for a plurality (e.g., at least 2, but frequently about 10, about 100, about 1000, or more) of members of a candidate library. In many cases, the molecular signature represents the expression pattern for all of the nucleotide sequences in a library or array of candidate or diagnostic nucleotide sequences or genes. Alternatively, the molecular signature represents the expression pattern for one or more subsets of the candidate library. The term "oligonucleotide" refers to two or more nucleotides. Nucleotides may be DNA or RNA, naturally occurring or synthetic.

The term "healthy individual," as used herein, is relative to a specified disease or disease criterion. That is, the individual does not exhibit the specified disease criterion or is not diagnosed with the specified disease. It will be understood, that the individual in question, can, of course, exhibit symptoms, or possess various indicator factors for another disease.

Similarly, an "individual diagnosed with a disease" refers to an individual diagnosed with a specified disease (or disease criterion). Such an individual may, or may not, also exhibit a disease criterion associated with, or be diagnosed with another (related or unrelated) disease.

An "array" is a spatially or logically organized collection, e.g., of oligonucleotide sequences or nucleotide sequence products such as RNA or proteins encoded by an oligonucleotide sequence. In some embodiments, an array includes antibodies or other binding reagents specific for products of a candidate library.

When referring to a pattern of expression, a "qualitative" difference in gene expression refers to a difference that is not assigned a relative value. That is, such a difference is designated by an "all or nothing" valuation. Such an all or nothing variation can be, for example, expression above or below a threshold of detection (an on/off pattern of expression). Alternatively, a qualitative difference can refer to expression of different types of expression products, e.g., different alleles (e.g., a mutant or polymorphic allele), variants (including sequence variants as well as post-translationally modified variants), etc.

In contrast, a "quantitative" difference, when referring to a pattern of gene expression, refers to a difference in expression that can be assigned a value on a

graduated scale, (e.g., a 0-5 or 1-10 scale, a + - +++ scale, a grade 1- grade 5 scale, or the like; it will be understood that the numbers selected for illustration are entirely arbitrary and in no-way are meant to be interpreted to limit the invention).

Gene Expression Systems of the Invention

The invention is directed to a gene expression system having one or more oligonucleotides wherein the one or more oligonucleotides has a nucleotide sequence which detects expression of a gene corresponding to the oligonucleotides depicted in the Sequence Listing. In one format, the oligonucleotide detects expression of a gene that is differentially expressed in leukocytes. The gene expression system may be a candidate library, a diagnostic agent, a diagnostic oligonucleotide set or a diagnostic probe set. The DNA molecules may be genomic DNA, protein nucleic acid (PNA), cDNA or synthetic oligonucleotides. Following the procedures taught herein, one can identify sequences of interest for analyzing gene expression in leukocytes. Such sequences may be predictive of a disease state.

Diagnostic oligonucleotides of the invention

The invention relates to diagnostic nucleotide set(s) comprising members of the leukocyte candidate library listed in Table 2, Table 3 and in the Sequence Listing, for which a correlation exists between the health status of an individual, and the individual's expression of RNA or protein products corresponding to the nucleotide sequence. In some instances, only one oligonucleotide is necessary for such detection. Members of a diagnostic oligonucleotide set may be identified by any means capable of detecting expression of RNA or protein products, including but not limited to differential expression screening, PCR, RT-PCR, SAGE analysis, high-throughput sequencing, microarrays, liquid or other arrays, protein-based methods (e.g., western blotting, proteomics, and other methods described herein), and data mining methods, as further described herein.

In one embodiment, a diagnostic oligonucleotide set comprises at least two oligonucleotide sequences listed in Table 2 or Table 3 or the Sequence Listing which are differentially expressed in leukocytes in an individual with at least one disease criterion for at least one leukocyte-implicated disease relative to the expression in individual without the at least one disease criterion, wherein expression of the two or more nucleotide sequences is correlated with at least one disease criterion, as described below. In another embodiment, a diagnostic nucleotide set comprises

at least one oligonucleotide having an oligonucleotide sequence listed in Table 2 or 3 or the Sequence Listing which is differentially expressed, and further wherein the differential expression/correlation has not previously been described. In some embodiments, the diagnostic nucleotide set is immobilized on an array.

The invention also provides diagnostic probe sets. It is understood that a probe includes any reagent capable of specifically identifying a nucleotide sequence of the diagnostic nucleotide set, including but not limited to a DNA, a RNA, cDNA, synthetic oligonucleotide, partial or full-length nucleic acid sequences. In addition, the probe may identify the protein product of a diagnostic nucleotide sequence, including, for example, antibodies and other affinity reagents. It is also understood that each probe can correspond to one gene, or multiple probes can correspond to one gene, or both, or one probe can correspond to more than one gene.

Homologs and variants of the disclosed nucleic acid molecules may be used in the present invention. Homologs and variants of these nucleic acid molecules will possess a relatively high degree of sequence identity when aligned using standard methods. The sequences encompassed by the invention have at least 40-50, 50-60, 70-80, 80-85, 85-90, 90-95 or 95-100% sequence identity to the sequences disclosed herein.

It is understood that for expression profiling, variations in the disclosed sequences will still permit detection of gene expression. The degree of sequence identity required to detect gene expression varies depending on the length of the oligomer. For a 60 mer, 6-8 random mutations or 6-8 random deletions in a 60 mer do not affect gene expression detection. Hughes, TR, et al. "Expression profiling using microarrays fabricated by an ink-jet oligonucleotide synthesizer. *Nature Biotechnology*, 19:343-347(2001). As the length of the DNA sequence is increased, the number of mutations or deletions permitted while still allowing gene expression detection is increased.

As will be appreciated by those skilled in the art, the sequences of the present invention may contain sequencing errors. That is, there may be incorrect nucleotides, frameshifts, unknown nucleotides, or other types of sequencing errors in any of the sequences; however, the correct sequences will fall within the homology and stringency definitions herein.

The minimum length of an oligonucleotide probe necessary for specific hybridization in the human genome can be estimated using two approaches. The first method uses a statistical argument that the probe will be unique in the human genome by chance. Briefly, the number of independent perfect matches (Po) expected for an oligonucleotide of length L in a genome of complexity C can be calculated from the equation (Laird CD, Chromosoma 32:378 (1971):

$$Po = (1/4)^L * 2C$$

In the case of mammalian genomes, $2C = \sim 3.6 \times 10^9$, and an oligonucleotide of 14-15 nucleotides is expected to be represented only once in the genome. However, the distribution of nucleotides in the coding sequence of mammalian genomes is nonrandom (Lathe, R. J. Mol. Biol. 183:1 (1985) and longer oligonucleotides may be preferred in order to increase the specificity of hybridization. In practical terms, this works out to probes that are 19-40 nucleotides long (Sambrook J et al., *infra*). The second method for estimating the length of a specific probe is to use a probe long enough to hybridize under the chosen conditions and use a computer to search for that sequence or close matches to the sequence in the human genome and choose a unique match. Probe sequences are chosen based on the desired hybridization properties as described in Chapter 11 of Sambrook et al, *infra*. The PRIMER3 program is useful for designing these probes (S. Rozen and H. Skaletsky 1996,1997; Primer3 code available at http://www-genome.wi.mit.edu/genome_software/other/primer3.html). The sequences of these probes are then compared pair wise against a database of the human genome sequences using a program such as BLAST or MEGABLAST (Madden, T.L et al.(1996) Meth. Enzymol. 266:131-141). Since most of the human genome is now contained in the database, the number of matches will be determined. Probe sequences are chosen that are unique to the desired target sequence.

In some embodiments, a diagnostic probe set is immobilized on an array. The array is optionally comprises one or more of: a chip array, a plate array, a bead array, a pin array, a membrane array, a solid surface array, a liquid array, an oligonucleotide array, a polynucleotide array or a cDNA array, a microtiter plate, a pin array, a bead array, a membrane or a chip.

In some embodiments, the leukocyte-implicated disease is selected from the diseases listed in Table 1. In other embodiments, the disease is atherosclerosis or

cardiac allograft rejection. In other embodiments, the disease is congestive heart failure, angina, myocardial infarction, systemic lupus erythematosus (SLE) and rheumatoid arthritis.

General Molecular Biology References

In the context of the invention, nucleic acids and/or proteins are manipulated according to well known molecular biology techniques. Detailed protocols for numerous such procedures are described in, e.g., in Ausubel et al. Current Protocols in Molecular Biology (supplemented through 2000) John Wiley & Sons, New York ("Ausubel"); Sambrook et al. Molecular Cloning - A Laboratory Manual (2nd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989 ("Sambrook"), and Berger and Kimmel Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 Academic Press, Inc., San Diego, CA ("Berger").

In addition to the above references, protocols for in vitro amplification techniques, such as the polymerase chain reaction (PCR), the ligase chain reaction (LCR), Q-replicase amplification, and other RNA polymerase mediated techniques (e.g., NASBA), useful e.g., for amplifying cDNA probes of the invention, are found in Mullis et al. (1987) U.S. Patent No. 4,683,202; PCR Protocols A Guide to Methods and Applications (Innis et al. eds) Academic Press Inc. San Diego, CA (1990) ("Innis"); Arnheim and Levinson (1990) C&EN 36; The Journal Of NIH Research (1991) 3:81; Kwoh et al. (1989) Proc Natl Acad Sci USA 86, 1173; Guatelli et al. (1990) Proc Natl Acad Sci USA 87:1874; Lomell et al. (1989) J Clin Chem 35:1826; Landegren et al. (1988) Science 241:1077; Van Brunt (1990) Biotechnology 8:291; Wu and Wallace (1989) Gene 4: 560; Barringer et al. (1990) Gene 89:117, and Sooknanan and Malek (1995) Biotechnology 13:563. Additional methods, useful for cloning nucleic acids in the context of the present invention, include Wallace et al. U.S. Pat. No. 5,426,039. Improved methods of amplifying large nucleic acids by PCR are summarized in Cheng et al. (1994) Nature 369:684 and the references therein.

Certain polynucleotides of the invention, e.g., oligonucleotides can be synthesized utilizing various solid-phase strategies involving mononucleotide- and/or trinucleotide-based phosphoramidite coupling chemistry. For example, nucleic acid sequences can be synthesized by the sequential addition of activated monomers and/or

trimers to an elongating polynucleotide chain. See e.g., Caruthers, M.H. et al. (1992) Meth Enzymol 211:3.

In lieu of synthesizing the desired sequences, essentially any nucleic acid can be custom ordered from any of a variety of commercial sources, such as The Midland Certified Reagent Company (mcr@oligos.com), The Great American Gene Company (www.genco.com), ExpressGen, Inc. (www.expressgen.com), Operon Technologies, Inc. (www.operon.com), and many others.

Similarly, commercial sources for nucleic acid and protein microarrays are available, and include, e.g., Agilent Technologies, Palo Alto, CA (<http://www.agilent.com/>) Affymetrix, Santa Clara, CA (<http://www.affymetrix.com/>); and Incyte, Palo Alto, CA (<http://www.incyte.com/>) and others.

Identification of diagnostic nucleotide sets

Candidate library

Libraries of candidates that are differentially expressed in leukocytes are substrates for the identification and evaluation of diagnostic oligonucleotide sets and disease specific target nucleotide sequences.

The term leukocyte is used generically to refer to any nucleated blood cell that is not a nucleated erythrocyte. More specifically, leukocytes can be subdivided into two broad classes. The first class includes granulocytes, including, most prevalently, neutrophils, as well as eosinophils and basophils at low frequency. The second class, the non-granular or mononuclear leukocytes, includes monocytes and lymphocytes (e.g., T cells and B cells). There is an extensive literature in the art implicating leukocytes, e.g., neutrophils, monocytes and lymphocytes in a wide variety of disease processes, including inflammatory and rheumatic diseases, neurodegenerative diseases (such as Alzheimer's dementia), cardiovascular disease, endocrine diseases, transplant rejection, malignancy and infectious diseases, and other diseases listed in Table 1. Mononuclear cells are involved in the chronic immune response, while granulocytes, which make up approximately 60% of the leukocytes, have a non-specific and stereotyped response to acute inflammatory stimuli and often have a life span of only 24 hours.

In addition to their widespread involvement and/or implication in numerous disease related processes, leukocytes are particularly attractive substrates for clinical and experimental evaluation for a variety of reasons. Most importantly, they are

readily accessible at low cost from essentially every potential subject. Collection is minimally invasive and associated with little pain, disability or recovery time. Collection can be performed by minimally trained personnel (e.g., phlebotomists, medical technicians, etc.) in a variety of clinical and non-clinical settings without significant technological expenditure. Additionally, leukocytes are renewable, and thus available at multiple time points for a single subject.

Assembly of candidate libraries

At least two conceptually distinct approaches to the assembly of candidate libraries exist. Either, or both, or other, approaches can be favorably employed. The method of assembling, or identifying, candidate libraries is secondary to the criteria utilized for selecting appropriate library members. Most importantly, library members are assembled based on differential expression of RNA or protein products in leukocyte populations. More specifically, candidate nucleotide sequences are induced or suppressed, or expressed at increased or decreased levels in leukocytes from a subject with one or more disease or disease state (a disease criterion) relative to leukocytes from a subject lacking the specified disease criterion. Alternatively, or in addition, library members can be assembled from among nucleotide sequences that are differentially expressed in activated or resting leukocytes relative to other cell types.

Firstly, publication and sequence databases can be “mined” using a variety of search strategies, including, e.g., a variety of genomics and proteomics approaches. For example, currently available scientific and medical publication databases such as Medline, Current Contents, OMIM (online Mendelian inheritance in man) various Biological and Chemical Abstracts, Journal indexes, and the like can be searched using term or key-word searches, or by author, title, or other relevant search parameters. Many such databases are publicly available, and one of skill is well versed in strategies and procedures for identifying publications and their contents, e.g., genes, other nucleotide sequences, descriptions, indications, expression pattern, etc. Numerous databases are available through the internet for free or by subscription, *see*, e.g., <http://www.ncbi.nlm.nih.gov/PubMed/>; <http://www3.infotrieve.com/>; <http://www.isinet.com/>; <http://www.sciencemag.org/>. Additional or alternative publication or citation databases are also available that provide identical or similar types of information, any of which are favorably employed in the context of the invention. These databases can be searched for publications describing differential

gene expression in leukocytes between patient with and without diseases or conditions listed in Table 1. We identified the nucleotide sequences listed in Table 2 and some of the sequences listed in Table 8 (Example 20), using data mining methods.

Alternatively, a variety of publicly available and proprietary sequence databases (including GenBank, dbEST, UniGene, and TIGR and SAGE databases) including sequences corresponding to expressed nucleotide sequences, such as expressed sequence tags (ESTs) are available. For example, Genbank™ (<http://www.ncbi.nlm.nih.gov/Genbank/>) among others can be readily accessed and searched via the internet. These and other sequence and clone database resources are currently available; however, any number of additional or alternative databases comprising nucleotide sequence sequences, EST sequences, clone repositories, PCR primer sequences, and the like corresponding to individual nucleotide sequence sequences are also suitable for the purposes of the invention. Sequences from nucleotide sequences can be identified that are only found in libraries derived from leukocytes or sub-populations of leukocytes, for example see Table 2.

Alternatively, the representation, or relative frequency, of a nucleotide sequence may be determined in a leukocyte-derived nucleic acid library and compared to the representation of the sequence in non-leukocyte derived libraries. The representation of a nucleotide sequence correlates with the relative expression level of the nucleotide sequence in leukocytes and non-leukocytes. An oligonucleotide sequence which has increased or decreased representation in a leukocyte-derived nucleic acid library relative to a non-leukocyte-derived libraries is a candidate for a leukocyte-specific gene.

Nucleotide sequences identified as having specificity to activated or resting leukocytes or to leukocytes from patients or patient samples with a variety of disease types can be isolated for use in a candidate library for leukocyte expression profiling through a variety of mechanisms. These include, but are not limited to, the amplification of the nucleotide sequence from RNA or DNA using nucleotide sequence specific primers for PCR or RT-PCR, isolation of the nucleotide sequence using conventional cloning methods, the purchase of an IMAGE consortium cDNA clone (EST) with complimentary sequence or from the same expressed nucleotide sequence, design of oligonucleotides, preparation of synthetic nucleic acid sequence, or any other nucleic-acid based method. In addition, the protein product of the

nucleotide sequence can be isolated or prepared, and represented in a candidate library, using standard methods in the art, as described further below.

While the above discussion related primarily to “genomics” approaches, it is appreciated that numerous, analogous “proteomics” approaches are suitable to the present invention. For example, a differentially expressed protein product can, for example, be detected using western analysis, two-dimensional gel analysis, chromatographic separation, mass spectrometric detection, protein-fusion reporter constructs, colorimetric assays, binding to a protein array, or by characterization of polysomal mRNA. The protein is further characterized and the nucleotide sequence encoding the protein is identified using standard techniques, e.g. by screening a cDNA library using a probe based on protein sequence information.

The second approach involves the construction of a differential expression library by any of a variety of means. Any one or more of differential screening, differential display or subtractive hybridization procedures, or other techniques that preferentially identify, isolate or amplify differentially expressed nucleotide sequences can be employed to produce a library of differentially expressed candidate nucleotide sequences, a subset of such a library, a partial library, or the like. Such methods are well known in the art. For example, peripheral blood leukocytes, (i.e., a mixed population including lymphocytes, monocytes and neutrophils), from multiple donor samples are pooled to prevent bias due to a single-donor’s unique genotype. The pooled leukocytes are cultured in standard medium and stimulated with individual cytokines or growth factors e.g., with IL-2, IL-1, MCP1, TNF α , and/or IL8 according to well known procedures (*see*, e.g., Tough et al. (1999) ; Winston et al. (1999); Hansson et al. (1989)). Typically, leukocytes are recovered from Buffy coat preparations produced by centrifugation of whole blood. Alternatively, mononuclear cells (monocytes and lymphocytes) can be obtained by density gradient centrifugation of whole blood, or specific cell types (such as a T lymphocyte) can be isolated using affinity reagents to cell specific surface markers. Leukocytes may also be stimulated by incubation with ionomycin, and phorbol myristate acetate (PMA). This stimulation protocol is intended to non-specifically mimic “activation” of numerous pathways due to variety of disease conditions rather than to simulate any single disease condition or paradigm.

Using well known subtractive hybridization procedures (as described in, e.g., US Patent Numbers 5,958,738; 5,589,339; 5,827,658; 5,712,127; 5,643,761) a library

is produced that is enriched for RNA species (messages) that are differentially expressed between test and control leukocyte populations. In some embodiments, the test population of leukocytes are simply stimulated as described above to emulate non-specific activation events, while in other embodiments the test population can be selected from subjects (or patients) with a specified disease or class of diseases. Typically, the control leukocyte population lacks the defining test condition, e.g., stimulation, disease state, diagnosis, genotype, etc. Alternatively, the total RNA from control and test leukocyte populations are prepared by established techniques, treated with DNaseI, and selected for messenger RNA with an intact 3' end (i.e., polyA(+)) messenger RNA) e.g., using commercially available kits according to the manufacturer's instructions e.g. Clontech. Double stranded cDNA is synthesized utilizing reverse transcriptase. Double stranded cDNA is then cut with a first restriction enzyme (e.g., *NlaIII*, that cuts at the recognition site: CATG, and cuts the cDNA sequence at approximately 256 bp intervals) that cuts the cDNA molecules into conveniently sized fragments.

The cDNAs prepared from the test population of leukocytes are divided into (typically 2) "tester" pools, while cDNAs prepared from the control population of leukocytes are designated the "driver" pool. Typically, pooled populations of cells from multiple individual donors are utilized and in the case of stimulated versus unstimulated cells, the corresponding tester and driver pools for any single subtraction reaction are derived from the same donor pool.

A unique double-stranded adapter is ligated to each of the tester cDNA populations using unphosphorylated primers so that only the sense strand is covalently linked to the adapter. An initial hybridization is performed consisting of each of the tester pools of cDNA (each with its corresponding adapter) and an excess of the driver cDNA. Typically, an excess of about 10-100 fold driver relative to tester is employed, although significantly lower or higher ratios can be empirically determined to provide more favorable results. The initial hybridization results in an initial normalization of the cDNAs such that high and low abundance messages become more equally represented following hybridization due to a failure of driver/tester hybrids to amplify.

A second hybridization involves pooling un-hybridized sequences from initial hybridizations together with the addition of supplemental driver cDNA. In this step, the expressed sequences enriched in the two tester pools following the initial

hybridization can hybridize. Hybrids resulting from the hybridization between members of each of the two tester pools are then recovered by amplification in a polymerase chain reaction (PCR) using primers specific for the unique adapters. Again, sequences originating in a tester pool that form hybrids with components of the driver pool are not amplified. Hybrids resulting between members of the same tester pool are eliminated by the formation of “panhandles” between their common 5' and 3' ends. For additional details, see, e.g., Lukyanov et al. (1997) Biochem Biophys Res Commun 230:285-8.

Typically, the tester and driver pools are designated in the alternative, such that the hybridization is performed in both directions to ensure recovery of messenger RNAs that are differentially expressed in either a positive or negative manner (i.e., that are turned on or turned off, up-regulated or down-regulated). Accordingly, it will be understood that the designation of test and control populations is to some extent arbitrary, and that a test population can just as easily be compared to leukocytes derived from a patient with the same or another disease of interest.

If so desired, the efficacy of the process can be assessed by such techniques as semi-quantitative PCR of known (i.e., control) nucleotide sequences, of varying abundance such as β -actin. The resulting PCR products representing partial cDNAs of differentially expressed nucleotide sequences are then cloned (i.e., ligated) into an appropriate vector (e.g., a commercially available TA cloning vector, such as pGEM from Promega) and, optionally, transformed into competent bacteria for selection and screening.

Either of the above approaches, or both in combination, or indeed, any procedure, which permits the assembly of a collection of nucleotide sequences that are expressed in leukocytes, is favorably employed to produce the libraries of candidates useful for the identification of diagnostic nucleotide sets and disease specific target nucleotides of the invention. Additionally, any method that permits the assembly of a collection of nucleotides that are expressed in leukocytes and preferentially associated with one or more disease or condition, whether or not the nucleotide sequences are differentially expressed, is favorably employed in the context of the invention. Typically, libraries of about 2,000-10,000 members are produced (although libraries in excess of 10,000 are not uncommon). Following additional evaluation procedures, as described below, the proportion of unique clones in the candidate library can approximate 100%.

A candidate oligonucleotide sequence may be represented in a candidate library by a full-length or partial nucleic acid sequence, deoxyribonucleic acid (DNA) sequence, cDNA sequence, RNA sequence, synthetic oligonucleotides, etc. The nucleic acid sequence can be at least 19 nucleotides in length, at least 25 nucleotides, at least 40 nucleotides, at least 100 nucleotides, or larger. Alternatively, the protein product of a candidate nucleotide sequence may be represented in a candidate library using standard methods, as further described below.

Characterization of candidate oligonucleotide sequences

The sequence of individual members (e.g., clones, partial sequence listing in a database such as an EST, etc.) of the candidate oligonucleotide libraries is then determined by conventional sequencing methods well known in the art, e.g., by the dideoxy-chain termination method of Sanger et al. (1977) Proc Natl Acad Sci USA 74:5463-7; by chemical procedures, e.g., Maxam and Gilbert (1977) Proc Natl Acad Sci USA 74:560-4; or by polymerase chain reaction cycle sequencing methods, e.g., Olsen and Eckstein (1989) Nuc Acid Res 17:9613-20, DNA chip based sequencing techniques or variations, including automated variations (e.g., as described in Hunkapiller et al. (1991) Science 254:59-67; Pease et al. (1994) Proc Natl Acad Sci USA 91:5022-6), thereof. Numerous kits for performing the above procedures are commercially available and well known to those of skill in the art. Character strings corresponding to the resulting nucleotide sequences are then recorded (i.e., stored) in a database. Most commonly the character strings are recorded on a computer readable medium for processing by a computational device.

Generally, to facilitate subsequent analysis, a custom algorithm is employed to query existing databases in an ongoing fashion, to determine the identity, expression pattern and potential function of the particular members of a candidate library. The sequence is first processed, by removing low quality sequence. Next the vector sequences are identified and removed and sequence repeats are identified and masked. The remaining sequence is then used in a Blast algorithm against multiple publicly available, and/or proprietary databases, e.g., NCBI nucleotide, EST and protein databases, Unigene, and Human Genome Sequence. Sequences are also compared to all previously sequenced members of the candidate libraries to detect redundancy.

In some cases, sequences are of high quality, but do not match any sequence in the NCBI nr, human EST or Unigene databases. In this case the sequence is queried against the human genomic sequence. If a single chromosomal site is matched with a

high degree of confidence, that region of genomic DNA is identified and subjected to further analysis with a gene prediction program such as GRAIL. This analysis may lead to the identification of a new gene in the genomic sequence. This sequence can then be translated to identify the protein sequence that is encoded and that sequence can be further analyzed using tools such as Pfam, Blast P, or other protein structure prediction programs, as illustrated in Table 7. Typically, the above analysis is directed towards the identification of putative coding regions, e.g., previously unidentified open reading frames, confirming the presence of known coding sequences, and determining structural motifs or sequence similarities of the predicted protein (i.e., the conceptual translation product) in relation to known sequences. In addition, it has become increasingly possible to assemble "virtual cDNAs" containing large portions of coding region, simply through the assembly of available expressed sequence tags (ESTs). In turn, these extended nucleic acid and amino acid sequences allow the rapid expansion of substrate sequences for homology searches and structural and functional motif characterization. The results of these analysis permits the categorization of sequences according to structural characteristics, e.g., as structural proteins, proteins involved in signal transduction, cell surface or secreted proteins etc.

It is understood that full-length nucleotide sequences may also be identified using conventional methods, for example, library screening, RT-PCR, chromosome walking, etc., as described in *Sambrook and Ausebel, infra*.

Candidate nucleotide library of the invention

We identified members of a candidate nucleotide library that are differentially expressed in activated leukocytes and resting leukocytes. Accordingly, the invention provides the candidate leukocyte nucleotide library comprising the nucleotide sequences listed in Table 2, Table 3 and in the sequence listing. In another embodiment, the invention provides a candidate library comprising at least two nucleotide sequences listed in Table 2, Table 3, and the sequence listing. In another embodiment, the at least two nucleotide sequence are at least 19 nucleotides in length, at least 35 nucleotides, at least 40 nucleotides or at least 100 nucleotides. In some embodiments, the nucleotide sequences comprises deoxyribonucleic acid (DNA) sequence, ribonucleic acid (RNA) sequence, synthetic oligonucleotide sequence, or genomic DNA sequence. It is understood that the nucleotide sequences may each

correspond to one gene, or that several nucleotide sequences may correspond to one gene, or both.

The invention also provides probes to the candidate nucleotide library. In one embodiment of the invention, the probes comprise at least two nucleotide sequences listed in Table 2, Table 3, or the sequence listing which are differentially expressed in leukocytes in an individual with a least one disease criterion for at least one leukocyte-related disease and in leukocytes in an individual without the at least one disease criterion, wherein expression of the two or more nucleotide sequences is correlated with at least one disease criterion. It is understood that a probe may detect either the RNA expression or protein product expression of the candidate nucleotide library. Alternatively, or in addition, a probe can detect a genotype associated with a candidate nucleotide sequence, as further described below. In another embodiment, the probes for the candidate nucleotide library are immobilized on an array.

The candidate nucleotide library of the invention is useful in identifying diagnostic nucleotide sets of the invention, as described below. The candidate nucleotide sequences may be further characterized, and may be identified as a disease target nucleotide sequence and/or a novel nucleotide sequence, as described below. The candidate nucleotide sequences may also be suitable for use as imaging reagents, as described below.

Generation of Expression Patterns

RNA, DNA or protein sample procurement

Following identification or assembly of a library of differentially expressed candidate nucleotide sequences, leukocyte expression profiles corresponding to multiple members of the candidate library are obtained. Leukocyte samples from one or more subjects are obtained by standard methods. Most typically, these methods involve trans-cutaneous venous sampling of peripheral blood. While sampling of circulating leukocytes from whole blood from the peripheral vasculature is generally the simplest, least invasive, and lowest cost alternative, it will be appreciated that numerous alternative sampling procedures exist, and are favorably employed in some circumstances. No pertinent distinction exists, in fact, between leukocytes sampled from the peripheral vasculature, and those obtained, e.g., from a central line, from a central artery, or indeed from a cardiac catheter, or during a surgical procedure which accesses the central vasculature. In addition, other body fluids and tissues that are, at

least in part, composed of leukocytes are also desirable leukocyte samples. For example, fluid samples obtained from the lung during bronchoscopy may be rich in leukocytes, and amenable to expression profiling in the context of the invention, e.g., for the diagnosis, prognosis, or monitoring of lung transplant rejection, inflammatory lung diseases or infectious lung disease. Fluid samples from other tissues, e.g., obtained by endoscopy of the colon, sinuses, esophagus, stomach, small bowel, pancreatic duct, biliary tree, bladder, ureter, vagina, cervix or uterus, etc., are also suitable. Samples may also be obtained from other sources containing leukocytes, e.g., from urine, bile, cerebrospinal fluid, feces, gastric or intestinal secretions, semen, or solid organ or joint biopsies.

Most frequently, mixed populations of leukocytes, such as are found in whole blood are utilized in the methods of the present invention. A crude separation, e.g., of mixed leukocytes from red blood cells, and/or concentration, e.g., over a sucrose, percoll or ficoll gradient, or by other methods known in the art, can be employed to facilitate the recovery of RNA or protein expression products at sufficient concentrations, and to reduce non-specific background. In some instances, it can be desirable to purify sub-populations of leukocytes, and methods for doing so, such as density or affinity gradients, flow cytometry, fluorescence Activated Cell Sorting (FACS), immuno-magnetic separation, "panning," and the like, are described in the available literature and below.

Obtaining DNA, RNA and protein samples for expression profiling

Expression patterns can be evaluated at the level of DNA, or RNA or protein products. For example, a variety of techniques are available for the isolation of RNA from whole blood. Any technique that allows isolation of mRNA from cells (in the presence or absence of rRNA and tRNA) can be utilized. In brief, one method that allows reliable isolation of total RNA suitable for subsequent gene expression analysis, is described as follows. Peripheral blood (either venous or arterial) is drawn from a subject, into one or more sterile, endotoxin free, tubes containing an anticoagulant (e.g., EDTA, citrate, heparin, etc.). Typically, the sample is divided into at least two portions. One portion, e.g., of 5-8 ml of whole blood is frozen and stored for future analysis, e.g., of DNA or protein. A second portion, e.g., of approximately 8 ml whole blood is processed for isolation of total RNA by any of a

variety of techniques as described in, e.g., Sambrook, Ausubel, below, as well as U.S. Patent Numbers: 5,728,822 and 4,843,155.

Typically, a subject sample of mononuclear leukocytes obtained from about 8 ml of whole blood, a quantity readily available from an adult human subject under most circumstances, yields 5-20 μ g of total RNA. This amount is ample, e.g., for labeling and hybridization to at least two probe arrays. Labeled probes for analysis of expression patterns of nucleotides of the candidate libraries are prepared from the subject's sample of RNA using standard methods. In many cases, cDNA is synthesized from total RNA using a polyT primer and labeled, e.g., radioactive or fluorescent, nucleotides. The resulting labeled cDNA is then hybridized to probes corresponding to members of the candidate nucleotide library, and expression data is obtained for each nucleotide sequence in the library. RNA isolated from subject samples (e.g., peripheral blood leukocytes, or leukocytes obtained from other biological fluids and samples) is next used for analysis of expression patterns of nucleotides of the candidate libraries.

In some cases, however, the amount of RNA that is extracted from the leukocyte sample is limiting, and amplification of the RNA is desirable. Amplification may be accomplished by increasing the efficiency of probe labeling, or by amplifying the RNA sample prior to labeling. It is appreciated that care must be taken to select an amplification procedure that does not introduce any bias (with respect to gene expression levels) during the amplification process.

Several methods are available that increase the signal from limiting amounts of RNA, e.g. use of the Clontech (Glass Fluorescent Labeling Kit) or Stratagene (Fairplay Microarray Labeling Kit), or the Micromax kit (New England Nuclear, Inc.). Alternatively, cDNA is synthesized from RNA using a T7- polyT primer, in the absence of label, and DNA dendrimers from Genisphere (3DNA Submicro) are hybridized to the poly T sequence on the primer, or to a different "capture sequence" which is complementary to a fluorescently labeled sequence. Each 3DNA molecule has 250 fluorescent molecules and therefore can strongly label each cDNA.

Alternatively, the RNA sample is amplified prior to labeling. For example, linear amplification may be performed, as described in U.S. Patent No. 6,132,997. A T7-polyT primer is used to generate the cDNA copy of the RNA. A second DNA strand is then made to complete the substrate for amplification. The T7 promoter

incorporated into the primer is used by a T7 polymerase to produce numerous antisense copies of the original RNA. Fluorescent dye labeled nucleotides are directly incorporated into the RNA. Alternatively, amino allyl labeled nucleotides are incorporated into the RNA, and then fluorescent dyes are chemically coupled to the amino allyl groups, as described in Hughes. Other exemplary methods for amplification are described below.

It is appreciated that the RNA isolated must contain RNA derived from leukocytes, but may also contain RNA from other cell types to a variable degree. Additionally, the isolated RNA may come from subsets of leukocytes, e.g. monocytes and/or T-lymphocytes, as described above. Such consideration of cell type used for the derivation of RNA depend on the method of expression profiling used.

DNA samples may be obtained for analysis of the presence of DNA mutations, single nucleotide polymorphisms (SNPs), or other polymorphisms. DNA is isolated using standard techniques, e.g. *Maniatus, supra*.

Expression of products of candidate nucleotides may also be assessed using proteomics. Protein(s) are detected in samples of patient serum or from leukocyte cellular protein. Serum is prepared by centrifugation of whole blood, using standard methods. Proteins present in the serum may have been produced from any of a variety of leukocytes and non-leukocyte cells, and include secreted proteins from leukocytes. Alternatively, leukocytes or a desired sub-population of leukocytes are prepared as described above. Cellular protein is prepared from leukocyte samples using methods well known in the art, e.g., Trizol (Invitrogen Life Technologies, cat # 15596108; Chomczynski, P. and Sacchi, N. (1987) *Anal. Biochem.* 162, 156; Simms, D., Cizdziel, P.E., and Chomczynski, P. (1993) *Focus®* 15, 99; Chomczynski, P., Bowers-Finn, R., and Sabatini, L. (1987) *J. of NIH Res.* 6, 83; Chomczynski, P. (1993) *Bio/Techniques* 15, 532; Bracete, A.M., Fox, D.K., and Simms, D. (1998) *Focus* 20, 82; Sewall, A. and McRae, S. (1998) *Focus* 20, 36; *Anal Biochem* 1984 Apr;138(1):141-3, A method for the quantitative recovery of protein in dilute solution in the presence of detergents and lipids; Wessel D, Flugge UI. (1984) *Anal Biochem.* 1984 Apr;138(1):141-143.

Obtaining expression patterns

Expression patterns, or profiles, of a plurality of nucleotides corresponding to members of the candidate library are then evaluated in one or more samples of leukocytes. Typically, the leukocytes are derived from patient peripheral blood

samples, although, as indicated above, many other sample sources are also suitable. These expression patterns constitute a set of relative or absolute expression values for a some number of RNAs or protein products corresponding to the plurality of nucleotide sequences evaluated, which is referred to herein as the subject's "expression profile" for those nucleotide sequences. While expression patterns for as few as one independent member of the candidate library can be obtained, it is generally preferable to obtain expression patterns corresponding to a larger number of nucleotide sequences, e.g., about 2, about 5, about 10, about 20, about 50, about 100, about 200, about 500, or about 1000, or more. The expression pattern for each differentially expressed component member of the library provides a finite specificity and sensitivity with respect to predictive value, e.g., for diagnosis, prognosis, monitoring, and the like.

Clinical Studies, Data and Patient Groups

For the purpose of discussion, the term subject, or subject sample of leukocytes, refers to an individual regardless of health and/or disease status. A subject can be a patient, a study participant, a control subject, a screening subject, or any other class of individual from whom a leukocyte sample is obtained and assessed in the context of the invention. Accordingly, a subject can be diagnosed with a disease, can present with one or more symptom of a disease, or a predisposing factor, such as a family (genetic) or medical history (medical) factor, for a disease, or the like. Alternatively, a subject can be healthy with respect to any of the aforementioned factors or criteria. It will be appreciated that the term "healthy" as used herein, is relative to a specified disease, or disease factor, or disease criterion, as the term "healthy" cannot be defined to correspond to any absolute evaluation or status. Thus, an individual defined as healthy with reference to any specified disease or disease criterion, can in fact be diagnosed with any other one or more disease, or exhibit any other one or more disease criterion.

Furthermore, while the discussion of the invention focuses, and is exemplified using human sequences and samples, the invention is equally applicable, through construction or selection of appropriate candidate libraries, to non-human animals, such as laboratory animals, e.g., mice, rats, guinea pigs, rabbits; domesticated livestock, e.g., cows, horses, goats, sheep, chicken, etc.; and companion animals, e.g., dogs, cats, etc.

Methods for obtaining expression data

Numerous methods for obtaining expression data are known, and any one or more of these techniques, singly or in combination, are suitable for determining expression profiles in the context of the present invention. For example, expression patterns can be evaluated by northern analysis, PCR, RT-PCR, Taq Man analysis, FRET detection, monitoring one or more molecular beacon, hybridization to an oligonucleotide array, hybridization to a cDNA array, hybridization to a polynucleotide array, hybridization to a liquid microarray, hybridization to a microelectric array, molecular beacons, cDNA sequencing, clone hybridization, cDNA fragment fingerprinting, serial analysis of gene expression (SAGE), subtractive hybridization, differential display and/or differential screening (*see*, e.g., Lockhart and Winzler (2000) Nature 405:827-836, and references cited therein).

For example, specific PCR primers are designed to a member(s) of a candidate nucleotide library. cDNA is prepared from subject sample RNA by reverse transcription from a poly-dT oligonucleotide primer, and subjected to PCR. Double stranded cDNA may be prepared using primers suitable for reverse transcription of the PCR product, followed by amplification of the cDNA using in vitro transcription. The product of in vitro transcription is a sense-RNA corresponding to the original member(s) of the candidate library. PCR product may be also be evaluated in a number of ways known in the art, including real-time assessment using detection of labeled primers, e.g. TaqMan or molecular beacon probes. Technology platforms suitable for analysis of PCR products include the ABI 7700, 5700, or 7000 Sequence Detection Systems (Applied Biosystems, Foster City, CA), the MJ Research Opticon (MJ Research, Waltham, MA), the Roche Light Cycler (Roche Diagnostics, Indianapolis, IN), the Stratagene MX4000 (Stratagene, La Jolla, CA), and the Bio-Rad iCycler (Bio-Rad Laboratories, Hercules, CA). Alternatively, molecular beacons are used to detect presence of a nucleic acid sequence in an unamplified RNA or cDNA sample, or following amplification of the sequence using any method, e.g. IVT (In Vitro transcription) or NASBA (nucleic acid sequence based amplification). Molecular beacons are designed with sequences complementary to member(s) of a candidate nucleotide library, and are linked to fluorescent labels. Each probe has a different fluorescent label with non-overlapping emission wavelengths. For example,

expression of ten genes may be assessed using ten different sequence-specific molecular beacons.

Alternatively, or in addition, molecular beacons are used to assess expression of multiple nucleotide sequences at once. Molecular beacons with sequence complimentary to the members of a diagnostic nucleotide set are designed and linked to fluorescent labels. Each fluorescent label used must have a non-overlapping emission wavelength. For example, 10 nucleotide sequences can be assessed by hybridizing 10 sequence specific molecular beacons (each labeled with a different fluorescent molecule) to an amplified or un-amplified RNA or cDNA sample. Such an assay bypasses the need for sample labeling procedures.

Alternatively, or in addition bead arrays can be used to assess expression of multiple sequences at once. See, e.g, LabMAP 100, Luminex Corp, Austin, Texas). Alternatively, or in addition electric arrays are used to assess expression of multiple sequences, as exemplified by the e-Sensor technology of Motorola (Chicago, Ill.) or Nanochip technology of Nanogen (San Diego, CA.)

Of course, the particular method elected will be dependent on such factors as quantity of RNA recovered, practitioner preference, available reagents and equipment, detectors, and the like. Typically, however, the elected method(s) will be appropriate for processing the number of samples and probes of interest. Methods for high-throughput expression analysis are discussed below.

Alternatively, expression at the level of protein products of gene expression is performed. For example, protein expression, in a sample of leukocytes, can be evaluated by one or more method selected from among: western analysis, two-dimensional gel analysis, chromatographic separation, mass spectrometric detection, protein-fusion reporter constructs, colorimetric assays, binding to a protein array and characterization of polysomal mRNA. One particularly favorable approach involves binding of labeled protein expression products to an array of antibodies specific for members of the candidate library. Methods for producing and evaluating antibodies are widespread in the art, *see*, e.g., Coligan, *supra*; and Harlow and Lane (1989) Antibodies: A Laboratory Manual, Cold Spring Harbor Press, NY (“Harlow and Lane”). Additional details regarding a variety of immunological and immunoassay procedures adaptable to the present invention by selection of antibody reagents specific for the products of candidate nucleotide sequences can be found in, e.g., Stites and Terr (eds.)(1991) Basic and Clinical Immunology, 7th ed., and Paul, *supra*.

Another approach uses systems for performing desorption spectrometry. Commercially available systems, e.g., from Ciphergen Biosystems, Inc. (Fremont, CA) are particularly well suited to quantitative analysis of protein expression. Indeed, Protein Chip® arrays (*see*, e.g., <http://www.ciphergen.com/>) used in desorption spectrometry approaches provide arrays for detection of protein expression. Alternatively, affinity reagents, e.g., antibodies, small molecules, etc.) are developed that recognize epitopes of the protein product. Affinity assays are used in protein array assays, e.g. to detect the presence or absence of particular proteins. Alternatively, affinity reagents are used to detect expression using the methods described above. In the case of a protein that is expressed on the cell surface of leukocytes, labeled affinity reagents are bound to populations of leukocytes, and leukocytes expressing the protein are identified and counted using fluorescent activated cell sorting (FACS).

It is appreciated that the methods of expression evaluation discussed herein, although discussed in the context of discovery of diagnostic nucleotide sets, are equally applicable for expression evaluation when using diagnostic nucleotide sets for, e.g. diagnosis of diseases, as further discussed below.

High Throughput Expression Assays

A number of suitable high throughput formats exist for evaluating gene expression. Typically, the term high throughput refers to a format that performs at least about 100 assays, or at least about 500 assays, or at least about 1000 assays, or at least about 5000 assays, or at least about 10,000 assays, or more per day. When enumerating assays, either the number of samples or the number of candidate nucleotide sequences evaluated can be considered. For example, a northern analysis of, e.g., about 100 samples performed in a gridded array, e.g., a dot blot, using a single probe corresponding to a candidate nucleotide sequence can be considered a high throughput assay. More typically, however, such an assay is performed as a series of duplicate blots, each evaluated with a distinct probe corresponding to a different member of the candidate library. Alternatively, methods that simultaneously evaluate expression of about 100 or more candidate nucleotide sequences in one or more samples, or in multiple samples, are considered high throughput.

Numerous technological platforms for performing high throughput expression analysis are known. Generally, such methods involve a logical or physical array of

either the subject samples, or the candidate library, or both. Common array formats include both liquid and solid phase arrays. For example, assays employing liquid phase arrays, e.g., for hybridization of nucleic acids, binding of antibodies or other receptors to ligand, etc., can be performed in multiwell, or microtiter, plates. Microtiter plates with 96, 384 or 1536 wells are widely available, and even higher numbers of wells, e.g, 3456 and 9600 can be used. In general, the choice of microtiter plates is determined by the methods and equipment, e.g., robotic handling and loading systems, used for sample preparation and analysis. Exemplary systems include, e.g., the ORCA™ system from Beckman-Coulter, Inc. (Fullerton, CA) and the Zymate systems from Zymark Corporation (Hopkinton, MA).

Alternatively, a variety of solid phase arrays can favorably be employed in to determine expression patterns in the context of the invention. Exemplary formats include membrane or filter arrays (e.g, nitrocellulose, nylon), pin arrays, and bead arrays (e.g., in a liquid “slurry”). Typically, probes corresponding to nucleic acid or protein reagents that specifically interact with (e.g., hybridize to or bind to) an expression product corresponding to a member of the candidate library are immobilized, for example by direct or indirect cross-linking, to the solid support. Essentially any solid support capable of withstanding the reagents and conditions necessary for performing the particular expression assay can be utilized. For example, functionalized glass, silicon, silicon dioxide, modified silicon, any of a variety of polymers, such as (poly)tetrafluoroethylene, (poly)vinylidenedifluoride, polystyrene, polycarbonate, or combinations thereof can all serve as the substrate for a solid phase array.

In a preferred embodiment, the array is a “chip” composed, e.g., of one of the above specified materials. Polynucleotide probes, e.g., RNA or DNA, such as cDNA, synthetic oligonucleotides, and the like, or binding proteins such as antibodies, that specifically interact with expression products of individual components of the candidate library are affixed to the chip in a logically ordered manner, i.e., in an array. In addition, any molecule with a specific affinity for either the sense or anti-sense sequence of the marker nucleotide sequence (depending on the design of the sample labeling), can be fixed to the array surface without loss of specific affinity for the marker and can be obtained and produced for array production, for example, proteins that specifically recognize the specific nucleic acid sequence of the marker,

ribozymes, peptide nucleic acids (PNA), or other chemicals or molecules with specific affinity.

Detailed discussion of methods for linking nucleic acids and proteins to a chip substrate, are found in, e.g., US Patent No. 5,143,854 "LARGE SCALE PHOTOLITHOGRAPHIC SOLID PHASE SYNTHESIS OF POLYPEPTIDES AND RECEPTOR BINDING SCREENING THEREOF" to Pirrung et al., issued, September 1, 1992; US Patent No. 5,837,832 "ARRAYS OF NUCLEIC ACID PROBES ON BIOLOGICAL CHIPS" to Chee et al., issued November 17, 1998; US Patent No. 6,087,112 "ARRAYS WITH MODIFIED OLIGONUCLEOTIDE AND POLYNUCLEOTIDE COMPOSITIONS" to Dale, issued July 11, 2000; US Patent No. 5,215,882 "METHOD OF IMMOBILIZING NUCLEIC ACID ON A SOLID SUBSTRATE FOR USE IN NUCLEIC ACID HYBRIDIZATION ASSAYS" to Bahl et al., issued June 1, 1993; US Patent No. 5,707,807 "MOLECULAR INDEXING FOR EXPRESSED GENE ANALYSIS" to Kato, issued January 13, 1998; US Patent No. 5,807,522 "METHODS FOR FABRICATING MICROARRAYS OF BIOLOGICAL SAMPLES" to Brown et al., issued September 15, 1998; US Patent No. 5,958,342 "JET DROPLET DEVICE" to Gamble et al., issued Sept. 28, 1999; US Patent 5,994,076 "METHODS OF ASSAYING DIFFERENTIAL EXPRESSION" to Chenchik et al., issued Nov. 30, 1999; US Patent No. 6,004,755 "QUANTITATIVE MICROARRAY HYBRIDIZATION ASSAYS" to Wang, issued Dec. 21, 1999; US Patent No. 6,048,695 "CHEMICALLY MODIFIED NUCLEIC ACIDS AND METHOD FOR COUPLING NUCLEIC ACIDS TO SOLID SUPPORT" to Bradley et al., issued April 11, 2000; US Patent No. 6,060,240 "METHODS FOR MEASURING RELATIVE AMOUNTS OF NUCLEIC ACIDS IN A COMPLEX MIXTURE AND RETRIEVAL OF SPECIFIC SEQUENCES THEREFROM" to Kamb et al., issued May 9, 2000; US Patent No. 6,090,556 "METHOD FOR QUANTITATIVELY DETERMINING THE EXPRESSION OF A GENE" to Kato, issued July 18, 2000; and US Patent 6,040,138 "EXPRESSION MONITORING BY HYBRIDIZATION TO HIGH DENSITY OLIGONUCLEOTIDE ARRAYS" to Lockhart et al., issued March 21, 2000.

For example, cDNA inserts corresponding to candidate nucleotide sequences, in a standard TA cloning vector are amplified by a polymerase chain reaction for approximately 30-40 cycles. The amplified PCR products are then arrayed onto a glass support by any of a variety of well known techniques, e.g., the VSLIPS™

technology described in US Patent No. 5,143,854. RNA, or cDNA corresponding to RNA, isolated from a subject sample of leukocytes is labeled, e.g., with a fluorescent tag, and a solution containing the RNA (or cDNA) is incubated under conditions favorable for hybridization, with the “probe” chip. Following incubation, and washing to eliminate non-specific hybridization, the labeled nucleic acid bound to the chip is detected qualitatively or quantitatively, and the resulting expression profile for the corresponding candidate nucleotide sequences is recorded. It is appreciated that the probe used for diagnostic purposes may be identical to the probe used during diagnostic nucleotide sequence discovery and validation. Alternatively, the probe sequence may be different than the sequence used in diagnostic nucleotide sequence discovery and validation. Multiple cDNAs from a nucleotide sequence that are non-overlapping or partially overlapping may also be used.

In another approach, oligonucleotides corresponding to members of a candidate nucleotide library are synthesized and spotted onto an array. Alternatively, oligonucleotides are synthesized onto the array using methods known in the art, e.g. Hughes, et al. *supra*. The oligonucleotide is designed to be complementary to any portion of the candidate nucleotide sequence. In addition, in the context of expression analysis for, e.g. diagnostic use of diagnostic nucleotide sets, an oligonucleotide can be designed to exhibit particular hybridization characteristics, or to exhibit a particular specificity and/or sensitivity, as further described below.

Hybridization signal may be amplified using methods known in the art, and as described herein, for example use of the Clontech kit (Glass Fluorescent Labeling Kit), Stratagene kit (Fairplay Microarray Labeling Kit), the Micromax kit (New England Nuclear, Inc.), the Genisphere kit (3DNA Submicro), linear amplification, e.g. as described in U.S. Patent No. 6,132,997 or described in Hughes, TR, et al., *Nature Biotechnology*, 19:343-347 (2001) and/or Westin et al. *Nat Biotech.* 18:199-204.

Alternatively, fluorescently labeled cDNA are hybridized directly to the microarray using methods known in the art. For example, labeled cDNA are generated by reverse transcription using Cy3- and Cy5-conjugated deoxynucleotides, and the reaction products purified using standard methods. It is appreciated that the methods for signal amplification of expression data useful for identifying diagnostic nucleotide sets are also useful for amplification of expression data for diagnostic purposes.

Microarray expression may be detected by scanning the microarray with a variety of laser or CCD-based scanners, and extracting features with numerous software packages, for example, Imagen (Biodiscovery), Feature Extraction (Agilent), Scanalyze (Eisen, M. 1999. SCANALYZE User Manual; Stanford Univ., Stanford, CA. Ver 2.32.), GenePix (Axon Instruments).

In another approach, hybridization to microelectric arrays is performed, e.g. as described in Umek et al (2001) J Mol Diagn. 3:74-84. An affinity probe, e.g. DNA, is deposited on a metal surface. The metal surface underlying each probe is connected to a metal wire and electrical signal detection system. Unlabelled RNA or cDNA is hybridized to the array, or alternatively, RNA or cDNA sample is amplified before hybridization, e.g. by PCR. Specific hybridization of sample RNA or cDNA results in generation of an electrical signal, which is transmitted to a detector. See Westin (2000) Nat Biotech. 18:199-204 (describing anchored multiplex amplification of a microelectronic chip array); Edman (1997) NAR 25:4907-14; Vignali (2000) J Immunol Methods 243:243-55.

In another approach, a microfluidics chip is used for RNA sample preparation and analysis. This approach increases efficiency because sample preparation and analysis are streamlined. Briefly, microfluidics may be used to sort specific leukocyte sub-populations prior to RNA preparation and analysis. Microfluidics chips are also useful for, e.g., RNA preparation, and reactions involving RNA (reverse transcription, RT-PCR). Briefly, a small volume of whole, anti-coagulated blood is loaded onto a microfluidics chip, for example chips available from Caliper (Mountain View, CA) or Nanogen (San Diego, CA.) A microfluidics chip may contain channels and reservoirs in which cells are moved and reactions are performed. Mechanical, electrical, magnetic, gravitational, centrifugal or other forces are used to move the cells and to expose them to reagents. For example, cells of whole blood are moved into a chamber containing hypotonic saline, which results in selective lysis of red blood cells after a 20-minute incubation. Next, the remaining cells (leukocytes) are moved into a wash chamber and finally, moved into a chamber containing a lysis buffer such as guanidine isothiocyanate. The leukocyte cell lysate is further processed for RNA isolation in the chip, or is then removed for further processing, for example, RNA extraction by standard methods. Alternatively, the microfluidics chip is a circular disk containing ficoll or another density reagent. The blood sample is injected into the center of the disc, the disc is rotated at a speed that generates a

centrifugal force appropriate for density gradient separation of mononuclear cells, and the separated mononuclear cells are then harvested for further analysis or processing.

It is understood that the methods of expression evaluation, above, although discussed in the context of discovery of diagnostic nucleotide sets, are also applicable for expression evaluation when using diagnostic nucleotide sets for, e.g. diagnosis of diseases, as further discussed below.

Evaluation of expression patterns

Expression patterns can be evaluated by qualitative and/or quantitative measures. Certain of the above described techniques for evaluating gene expression (as RNA or protein products) yield data that are predominantly qualitative in nature. That is, the methods detect differences in expression that classify expression into distinct modes without providing significant information regarding quantitative aspects of expression. For example, a technique can be described as a qualitative technique if it detects the presence or absence of expression of a candidate nucleotide sequence, i.e., an on/off pattern of expression. Alternatively, a qualitative technique measures the presence (and/or absence) of different alleles, or variants, of a gene product.

In contrast, some methods provide data that characterizes expression in a quantitative manner. That is, the methods relate expression on a numerical scale, e.g., a scale of 0-5, a scale of 1-10, a scale of + - +++, from grade 1 to grade 5, a grade from a to z, or the like. It will be understood that the numerical, and symbolic examples provided are arbitrary, and that any graduated scale (or any symbolic representation of a graduated scale) can be employed in the context of the present invention to describe quantitative differences in nucleotide sequence expression. Typically, such methods yield information corresponding to a relative increase or decrease in expression.

Any method that yields either quantitative or qualitative expression data is suitable for evaluating expression of candidate nucleotide sequence in a subject sample of leukocytes. In some cases, e.g., when multiple methods are employed to determine expression patterns for a plurality of candidate nucleotide sequences, the recovered data, e.g., the expression profile, for the nucleotide sequences is a combination of quantitative and qualitative data.

In some applications, expression of the plurality of candidate nucleotide sequences is evaluated sequentially. This is typically the case for methods that can be characterized as low- to moderate-throughput. In contrast, as the throughput of the elected assay increases, expression for the plurality of candidate nucleotide sequences in a sample or multiple samples of leukocytes, is assayed simultaneously. Again, the methods (and throughput) are largely determined by the individual practitioner, although, typically, it is preferable to employ methods that permit rapid, e.g. automated or partially automated, preparation and detection, on a scale that is time-efficient and cost-effective.

It is understood that the preceding discussion, while directed at the assessment of expression of the members of candidate libraries, is also applies to the assessment of the expression of members of diagnostic nucleotide sets, as further discussed below.

Genotyping

In addition to, or in conjunction with the correlation of expression profiles and clinical data, it is often desirable to correlate expression patterns with the subject's genotype at one or more genetic loci. The selected loci can be, for example, chromosomal loci corresponding to one or more member of the candidate library, polymorphic alleles for marker loci, or alternative disease related loci (not contributing to the candidate library) known to be, or putatively associated with, a disease (or disease criterion). Indeed, it will be appreciated, that where a (polymorphic) allele at a locus is linked to a disease (or to a predisposition to a disease), the presence of the allele can itself be a disease criterion.

Numerous well known methods exist for evaluating the genotype of an individual, including southern analysis, restriction fragment length polymorphism (RFLP) analysis, polymerase chain reaction (PCR), amplification length polymorphism (AFLP) analysis, single stranded conformation polymorphism (SSCP) analysis, single nucleotide polymorphism (SNP) analysis (e.g., via PCR, Taqman or molecular beacons), among many other useful methods. Many such procedures are readily adaptable to high throughput and/or automated (or semi-automated) sample preparation and analysis methods. Most, can be performed on nucleic acid samples recovered via simple procedures from the same sample of leukocytes as yielded the

material for expression profiling. Exemplary techniques are described in, e.g., Sambrook, and Ausubel, *supra*.

Identification of the diagnostic nucleotide sets of the invention

Identification of diagnostic nucleotide sets and disease specific target nucleotide sequence proceeds by correlating the leukocyte expression profiles with data regarding the subject's health status to produce a data set designated a "molecular signature." Examples of data regarding a patient's health status, also termed "disease criteria(ion)", is described below and in the Section titled "selected diseases," below. Methods useful for correlation analysis are further described elsewhere in the specification.

Generally, relevant data regarding the subject's health status includes retrospective or prospective health data, e.g., in the form of the subject's medical history, as provided by the subject, physician or third party, such as, medical diagnoses, laboratory test results, diagnostic test results, clinical events, or medication lists, as further described below. Such data may include information regarding a patient's response to treatment and/or a particular medication and data regarding the presence of previously characterized "risk factors." For example, cigarette smoking and obesity are previously identified risk factors for heart disease. Further examples of health status information, including diseases and disease criteria, is described in the section titled Selected diseases, below.

Typically, the data describes prior events and evaluations (i.e., retrospective data). However, it is envisioned that data collected subsequent to the sampling (i.e., prospective data) can also be correlated with the expression profile. The tissue sampled, e.g., peripheral blood, bronchial lavage, etc., can be obtained at one or more multiple time points and subject data is considered retrospective or prospective with respect to the time of sample procurement.

Data collected at multiple time points, called "longitudinal data", is often useful, and thus, the invention encompasses the analysis of patient data collected from the same patient at different time points. Analysis of paired samples, such as samples from a patient at different time, allows identification of differences that are specifically related to the disease state since the genetic variability specific to the patient is controlled for by the comparison. Additionally, other variables that exist between patients may be controlled for in this way, for example, the presence or

absence of inflammatory diseases (e.g., rheumatoid arthritis) the use of medications that may effect leukocyte gene expression, the presence or absence of co-morbid conditions, etc. Methods for analysis of paired samples are further described below. Moreover, the analysis of a pattern of expression profiles (generated by collecting multiple expression profiles) provides information relating to changes in expression level over time, and may permit the determination of a rate of change, a trajectory, or an expression curve. Two longitudinal samples may provide information on the change in expression of a gene over time, while three longitudinal samples may be necessary to determine the “trajectory” of expression of a gene. Such information may be relevant to the diagnosis of a disease. For example, the expression of a gene may vary from individual to individual, but a clinical event, for example , a heart attack, may cause the level of expression to double in each patient. In this example, clinically interesting information is gleaned from the change in expression level, as opposed to the absolute level of expression in each individual.

Generally, small sample sizes of 10-40 samples from 10-20 individuals are used to identify a diagnostic nucleotide set. Larger sample sizes are generally necessary to validate the diagnostic nucleotide set for use in large and varied patient populations, as further described below. For example, extension of gene expression correlations to varied ethnic groups, demographic groups, nations, peoples or races may require expression correlation experiments on the population of interest.

Expression Reference Standards

Expression profiles derived from a patient (i.e., subjects diagnosed with, or exhibiting symptoms of, or exhibiting a disease criterion, or under a doctor’s care for a disease) sample are compared to a control or standard expression RNA to facilitate comparison of expression profiles (e.g. of a set of candidate nucleotide sequences) from a group of patients relative to each other (i.e., from one patient in the group to other patients in the group, or to patients in another group).

For example, in one approach to identifying diagnostic nucleotide sets, expression profiles derived from patient samples are compared to a expression reference “standard.” Standard expression reference can be, for example, RNA derived from resting cultured leukocytes or commercially available reference RNA, such as Universal reference RNA from Stratagene. *See Nature*, V406, 8-17-00, p. 747-752. Use of an expression reference standard is particularly useful when the expression of large numbers of nucleotide sequences is assayed, e.g. in an array, and

in certain other applications, e.g. qualitative PCR, RT-PCR, etc., where it is desirable to compare a sample profile to a standard profile, and/or when large numbers of expression profiles, e.g. a patient population, are to be compared. Generally, an expression reference standard should be available in large quantities, should be a good substrate for amplification and labeling reactions, and should be capable of detecting a large percentage of candidate nucleic acids using suitable expression profiling technology.

Alternatively, or in addition, the expression profile derived from a patient sample is compared with the expression of an internal reference control gene, for example, β -actin or CD4. The relative expression of the profiled genes and the internal reference control gene (from the same individual) is obtained. An internal reference control may also be used with a reference RNA. For example, an expression profile for "gene 1" and the gene encoding CD4 can be determined in a patient sample and in a reference RNA. The expression of each gene can be expressed as the "relative" ratio of expression the gene in the patient sample compared with expression of the gene in the reference RNA. The expression ratio (sample/reference) for gene 1 may be divided by the expression ratio for CD4 (sample/reference) and thus the relative expression of gene 1 to CD4 is obtained.

The invention also provides a buffy coat control RNA useful for expression profiling, and a method of using control RNA produced from a population of buffy coat cells, the white blood cell layer derived from the centrifugation of whole blood. Buffy coat contains all white blood cells, including granulocytes, mononuclear cells and platelets. The invention also provides a method of preparing control RNA from buffy coat cells for use in expression profile analysis of leukocytes. Buffy coat fractions are obtained, e.g. from a blood bank or directly from individuals, preferably from a large number of individuals such that bias from individual samples is avoided and so that the RNA sample represents an average expression of a healthy population. Buffy coat fractions from about 50 or about 100, or more individuals are preferred. 10 ml buffy coat from each individual is used. Buffy coat samples are treated with an erythrocyte lysis buffer, so that erythrocytes are selectively removed. The leukocytes of the buffy coat layer are collected by centrifugation. Alternatively, the buffy cell sample can be further enriched for a particular leukocyte sub-populations, e.g. mononuclear cells, T-lymphocytes, etc. To enrich for mononuclear cells, the

buffy cell pellet, above, is diluted in PBS (phosphate buffered saline) and loaded onto a non-polystyrene tube containing a polysucrose and sodium diatrizoate solution adjusted to a density of 1.077 \pm 0.001 g/ml. To enrich for T-lymphocytes, 45 ml of whole blood is treated with RosetteSep (Stem Cell Technologies), and incubated at room temperature for 20 minutes. The mixture is diluted with an equal volume of PBS plus 2% FBS and mixed by inversion. 30 ml of diluted mixture is layered on top of 15 ml DML medium (Stem Cell Technologies). The tube is centrifuged at 1200 x g, and the enriched cell layer at the plasma : medium interface is removed, washed with PBS + 2% FBS, and cells collected by centrifugation at 1200 x g. The cell pellet is treated with 5 ml of erythrocyte lysis buffer (EL buffer, Qiagen) for 10 minutes on ice, and enriched T-lymphocytes are collected by centrifugation.

In addition or alternatively, the buffy cells (whole buffy coat or sub-population, e.g. mononuclear fraction) can be cultured *in vitro* and subjected to stimulation with cytokines or activating chemicals such as phorbol esters or ionomycin. Such stimuli may increase expression of nucleotide sequences that are expressed in activated immune cells and might be of interest for leukocyte expression profiling experiments.

Following sub-population selection and/or further treatment, e.g. stimulation as described above, RNA is prepared using standard methods. For example, cells are pelleted and lysed with a phenol/guanidinium thiocyanate and RNA is prepared. RNA can also be isolated using a silica gel-based purification column or the column method can be used on RNA isolated by the phenol/guanidinium thiocyanate method. RNA from individual buffy coat samples can be pooled during this process, so that the resulting reference RNA represents the RNA of many individuals and individual bias is minimized or eliminated. In addition, a new batch of buffy coat reference RNA can be directly compared to the last batch to ensure similar expression pattern from one batch to another, using methods of collecting and comparing expression profiles described above/below. One or more expression reference controls are used in an experiment. For example, RNA derived from one or more of the following sources can be used as controls for an experiment: stimulated or unstimulated whole buffy coat, stimulated or unstimulated peripheral mononuclear cells, or stimulated or unstimulated T-lymphocytes.

Alternatively, the expression reference standard can be derived from any subject or class of subjects including healthy subjects or subjects diagnosed with the

same or a different disease or disease criterion. Expression profiles from subjects in two distinct classes are compared to determine which subset of nucleotide sequences in the candidate library best distinguish between the two subject classes, as further discussed below. It will be appreciated that in the present context, the term “distinct classes” is relevant to at least one distinguishable criterion relevant to a disease of interest, a “disease criterion.” The classes can, of course, demonstrate significant overlap (or identity) with respect to other disease criteria, or with respect to disease diagnoses, prognoses, or the like. The mode of discovery involves, e.g., comparing the molecular signature of different subject classes to each other (such as patient to control, patients with a first diagnosis to patients with a second diagnosis, etc.) or by comparing the molecular signatures of a single individual taken at different time points. The invention can be applied to a broad range of diseases, disease criteria, conditions and other clinical and/or epidemiological questions, as further discussed above/below.

It is appreciated that while the present discussion pertains to the use of expression reference controls while identifying diagnostic nucleotide sets, expression reference controls are also useful during use of diagnostic nucleotide sets, e.g. use of a diagnostic nucleotide set for diagnosis of a disease, as further described below.

Analysis of expression profiles

In order to facilitate ready access, e.g., for comparison, review, recovery, and/or modification, the molecular signatures/expression profiles are typically recorded in a database. Most typically, the database is a relational database accessible by a computational device, although other formats, e.g., manually accessible indexed files of expression profiles as photographs, analogue or digital imaging readouts, spreadsheets, etc. can be used. Further details regarding preferred embodiments are provided below. Regardless of whether the expression patterns initially recorded are analog or digital in nature and/or whether they represent quantitative or qualitative differences in expression, the expression patterns, expression profiles (collective expression patterns), and molecular signatures (correlated expression patterns) are stored digitally and accessed via a database. Typically, the database is compiled and maintained at a central facility, with access being available locally and/or remotely.

As additional samples are obtained, and their expression profiles determined and correlated with relevant subject data, the ensuing molecular signatures are likewise recorded in the database. However, rather than each subsequent addition

being added in an essentially passive manner in which the data from one sample has little relation to data from a second (prior or subsequent) sample, the algorithms optionally additionally query additional samples against the existing database to further refine the association between a molecular signature and disease criterion. Furthermore, the data set comprising the one (or more) molecular signatures is optionally queried against an expanding set of additional or other disease criteria. The use of the database in integrated systems and web embodiments is further described below.

Analysis of expression profile data from arrays

Expression data is analyzed using methods well known in the art, including the software packages Imagene (Biodiscovery, Marina del Rey, CA), Feature Extraction (Agilent, Palo Alto, CA), and Scanalyze (Stanford University). In the discussion that follows, a “feature” refers to an individual spot of DNA on an array. Each gene may have more than one feature. For example, hybridized microarrays are scanned and analyzed on an Axon Instruments scanner using GenePix 3.0 software (Axon Instruments, Union City, CA). The data extracted by GenePix is used for all downstream quality control and expression evaluation. The data is derived as follows. The data for all features flagged as “not found” by the software is removed from the dataset for individual hybridizations. The “not found” flag by GenePix indicates that the software was unable to discriminate the feature from the background. Each feature is examined to determine the value of its signal. The median pixel intensity of the background (B_n) is subtracted from the median pixel intensity of the feature (F_n) to produce the background-subtracted signal (hereinafter, “BGSS”). The BGSS is divided by the standard deviation of the background pixels to provide the signal-to-noise ratio (hereinafter, “S/N”). Features with a S/N of three or greater in both the Cy3 channel (corresponding to the sample RNA) and Cy5 channel (corresponding to the reference RNA) are used for further analysis (hereinafter denoted “useable features”). Alternatively, different S/Ns are used for selecting expression data for an analysis. For example, only expression data with signal to noise ratios > 3 might be used in an analysis.

For each usable feature (i), the expression level (e) is expressed as the logarithm of the ratio (R) of the Background Subtracted Signal (hereinafter “BGSS”) for the Cy3 (sample RNA) channel divided by the BGSS for the Cy5 channel (reference RNA). This “log ratio” value is used for comparison to other experiments.

$$R_i = \frac{BGSS_{sample}}{BGSS_{reference}} \quad (0.1)$$

$$e_i = \log r_i \quad (0.2)$$

Variation in signal across hybridizations may be caused by a number of factors affecting hybridization, DNA spotting, wash conditions, and labeling efficiency.

A single reference RNA may be used with all of the experimental RNAs, permitting multiple comparisons in addition to individual comparisons. By comparing sample RNAs to the same reference, the gene expression levels from each sample are compared across arrays, permitting the use of a consistent denominator for our experimental ratios.

Scaling

The data may be scaled (normalized) to control for labeling and hybridization variability within the experiment, using methods known in the art. Scaling is desirable because it facilitates the comparison of data between different experiments, patients, etc. Generally the BGSS are scaled to a factor such as the median, the mean, the trimmed mean, and percentile. Additional methods of scaling include: to scale between 0 and 1, to subtract the mean, or to subtract the median.

Scaling is also performed by comparison to expression patterns obtained using a common reference RNA, as described in greater detail above. As with other scaling methods, the reference RNA facilitates multiple comparisons of the expression data, e.g., between patients, between samples, etc. Use of a reference RNA provides a consistent denominator for experimental ratios.

In addition to the use of a reference RNA, individual expression levels may be adjusted to correct for differences in labeling efficiency between different hybridization experiments, allowing direct comparison between experiments with different overall signal intensities, for example. A scaling factor (α) may be used to adjust individual expression levels as follows. The median of the scaling factor (α), for example, BGSS, is determined for the set of all features with a S/N greater than three. Next, the BGSS_i (the BGSS for each feature "i") is divided by the median for

all features (a), generating a scaled ratio. The scaled ratio is used to determine the expression value for the feature (e_i), or the log ratio.

$$S_i = \frac{BGSS_i}{a} \quad (0.3)$$

$$e_i = \log \left(\frac{Cy3S_i}{Cy5S_i} \right) \quad (0.4)$$

In addition, or alternatively, control features are used to normalize the data for labeling and hybridization variability within the experiment. Control feature may be cDNA for genes from the plant, *Arabidopsis thaliana*, that are included when spotting the mini-array. Equal amounts of RNA complementary to control cDNAs are added to each of the samples before they were labeled. Using the signal from these control genes, a normalization constant (L) is determined according to the following formula:

$$L_j = \frac{\frac{\sum_{i=1}^N BGSS_{j,i}}{N}}{\frac{\sum_{j=1}^K \frac{\sum_{i=1}^N BGSS_{j,i}}{N}}{K}}$$

where $BGSS_i$ is the signal for a specific feature, N is the number of *A. thaliana* control features, K is the number of hybridizations, and L_j is the normalization constant for each individual hybridization.

Using the formula above, the mean for all control features of a particular hybridization and dye (e.g., Cy3) is calculated. The control feature means for all Cy3 hybridizations are averaged, and the control feature mean in one hybridization divided by the average of all hybridizations to generate a normalization constant for that particular Cy3 hybridization (L_j), which is used as a in equation (0.3). The same normalization steps may be performed for Cy3 and Cy5 values.

Many additional methods for normalization exist and can be applied to the data. In one method, the average ratio of Cy3 BGSS / Cy5 BGSS is determined for all features on an array. This ratio is then scaled to some arbitrary number, such as 1 or some other number. The ratio for each probe is then multiplied by the scaling

factor required to bring the average ratio to the chosen level. This is performed for each array in an analysis. Alternatively, the ratios are normalized to the average ratio across all arrays in an analysis.

Correlation analysis

Correlation analysis is performed to determine which array probes have expression behavior that best distinguishes or serves as markers for relevant groups of samples representing a particular clinical condition. Correlation analysis, or comparison among samples representing different disease criteria (e.g., clinical conditions), is performed using standard statistical methods. Numerous algorithms are useful for correlation analysis of expression data, and the selection of algorithms depends in part on the data analysis to be performed. For example, algorithms can be used to identify the single most informative gene with expression behavior that reliably classifies samples, or to identify all the genes useful to classify samples. Alternatively, algorithms can be applied that determine which set of 2 or more genes have collective expression behavior that accurately classifies samples. The use of multiple expression markers for diagnostics may overcome the variability in expression of a gene between individuals, or overcome the variability intrinsic to the assay. Multiple expression markers may include redundant markers, in that two or more genes or probes may provide the same information with respect to diagnosis. This may occur, for example, when two or more genes or gene probes are coordinately expressed. It will be appreciated that while the discussion above pertains to the analysis of RNA expression profiles the discussion is equally applicable to the analysis of profiles of proteins or other molecular markers.

Prior to analysis, expression profile data may be formatted or prepared for analysis using methods known in the art. For example, often the log ratio of scaled expression data for every array probe is calculated using the following formula:

$\log (\text{Cy } 3 \text{ BGSS} / \text{Cy}5 \text{ BGSS})$, where Cy 3 signal corresponds to the expression of the gene in the clinical sample, and Cy5 signal corresponds to expression of the gene in the reference RNA.

Data may be further filtered depending on the specific analysis to be done as noted below. For example, filtering may be aimed at selecting only samples with expression above a certain level, or probes with variability above a certain level between sample sets.

The following non-limiting discussion consider several statistical methods known in the art. Briefly, the t-test and ANOVA are used to identify single genes with expression differences between or among populations, respectively. Multivariate methods are used to identify a set of two or more genes for which expression discriminates between two disease states more specifically than expression of any single gene.

t-test

The simplest measure of a difference between two groups is the Student's t test. See, e.g., Welsh et al. (2001) Proc Natl Acad Sci USA 98:1176-81 (demonstrating the use of an unpaired Student's t-test for the discovery of differential gene expression in ovarian cancer samples and control tissue samples). The t- test assumes equal variance and normally distributed data. This test identifies the probability that there is a difference in expression of a single gene between two groups of samples. The number of samples within each group that is required to achieve statistical significance is dependent upon the variation among the samples within each group. The standard formula for a t-test is:

$$t(e_i) = \frac{\bar{e}_{i,c} - \bar{e}_{i,t}}{\sqrt{(s_{i,c}^2/n_c) + (s_{i,t}^2/n_t)}}, \quad (0.5)$$

where \bar{e}_i is the difference between the mean expression level of gene i in groups c and t, $s_{i,c}$ is the variance of gene x in group c and $s_{i,t}$ is the variance of gene x in group t. n_c and n_t are the numbers of samples in groups c and t.

The combination of the t statistic and the degrees of freedom $[\min(n_t, n_c)-1]$ provides a p value, the probability of rejecting the null hypothesis. A p-value of ≤ 0.01 , signifying a 99 percent probability the mean expression levels are different between the two groups (a 1% chance that the mean expression levels are in fact not different and that the observed difference occurred by statistical chance), is often considered acceptable.

When performing tests on a large scale, for example, on a large dataset of about 8000 genes, a correction factor must be included to adjust for the number of individual tests being performed. The most common and simplest correction is the

Bonferroni correction for multiple tests, which divides the p-value by the number of tests run. Using this test on an 8000 member dataset indicates that a p value of ≤ 0.00000125 is required to identify genes that are likely to be truly different between the two test conditions.

Wilcoxon's signed ranks test

This method is non-parametric and is utilized for paired comparisons. See e.g., Sokal and Rohlf (1987) Introduction to Biostatistics 2nd edition, WH Freeman, New York. At least 6 pairs are necessary to apply this statistic. This test is useful for analysis of paired expression data (for example, a set of patients who have cardiac transplant biopsy on 2 occasions and have a grade 0 on one occasion and a grade 3A on another).

ANOVA

Differences in gene expression across multiple related groups may be assessed using an Analysis of Variance (ANOVA), a method well known in the art (Michelson and Schofield, 1996).

Multivariate analysis

Many algorithms suitable for multivariate analysis are known in the art. Generally, a set of two or more genes for which expression discriminates between two disease states more specifically than expression of any single gene is identified by searching through the possible combinations of genes using a criterion for discrimination, for example the expression of gene X must increase from normal 300 percent, while the expression of genes Y and Z must decrease from normal by 75 percent. Ordinarily, the search starts with a single gene, then adds the next best fit at each step of the search. Alternatively, the search starts with all of the genes and genes that do not aid in the discrimination are eliminated step-wise.

Paired samples

Paired samples, or samples collected at different time-points from the same patient, are often useful, as described above. For example, use of paired samples permits the reduction of variation due to genetic variation among individuals. In addition, the use of paired samples has a statistical significance, in that data derived from paired samples can be calculated in a different manner that recognizes the reduced variability. For example, the formula for a t-test for paired samples is:

$$t(e_x) = \frac{\overline{D}_{\bar{e}_x}}{\sqrt{\frac{\sum D^2 - (\sum D)^2 / b}{b-1}}}, \quad (0.5)$$

where D is the difference between each set of paired samples and b is the number of sample pairs. \overline{D} is the mean of the differences between the members of the pairs. In this test, only the differences between the paired samples are considered, then grouped together (as opposed to taking all possible differences between groups, as would be the case with an ordinary t-test). Additional statistical tests useful with paired data, e.g., ANOVA and Wilcoxon's signed rank test, are discussed above.

Diagnostic classification

Once a discriminating set of genes is identified, the diagnostic classifier (a mathematical function that assigns samples to diagnostic categories based on expression data) is applied to unknown sample expression levels.

Methods that can be used for this analysis include the following non-limiting list:

CLEAVER is an algorithm used for classification of useful expression profile data. See Raychaudhuri et al. (2001) Trends Biotechnol 19:189-193. CLEAVER uses positive training samples (e.g., expression profiles from samples known to be derived from a particular patient or sample diagnostic category, disease or disease criteria), negative training samples (e.g., expression profiles from samples known not to be derived from a particular patient or sample diagnostic category, disease or disease criteria) and test samples (e.g., expression profiles obtained from a patient), and determines whether the test sample correlates with the particular disease or disease criteria, or does not correlate with a particular disease or disease criteria. CLEAVER also generates a list of the 20 most predictive genes for classification.

Artificial neural networks (hereinafter, "ANN") can be used to recognize patterns in complex data sets and can discover expression criteria that classify samples into more than 2 groups. The use of artificial neural networks for discovery of gene expression diagnostics for cancers using expression data generated by oligonucleotide expression microarrays is demonstrated by Khan et al. (2001) Nature Med. 7:673-9. Khan found that 96 genes provided 0% error rate in classification of the tumors. The most important of these genes for classification was then determined

by measuring the sensitivity of the classification to a change in expression of each gene. Hierarchical clustering using the 96 genes results in correct grouping of the cancers into diagnostic categories.

Golub uses cDNA microarrays and a distinction calculation to identify genes with expression behavior that distinguishes myeloid and lymphoid leukemias. See Golub et al. (1999) Science 286:531-7. Self organizing maps were used for new class discovery. Cross validation was done with a “leave one out” analysis. 50 genes were identified as useful markers. This was reduced to as few as 10 genes with equivalent diagnostic accuracy.

Hierarchical and non-hierarchical clustering methods are also useful for identifying groups of genes that correlate with a subset of clinical samples such as with transplant rejection grade. Alizadeh used hierarchical clustering as the primary tool to distinguish different types of diffuse B-cell lymphomas based on gene expression profile data. See Alizadeh et al. (2000) Nature 403:503-11. Alizadeh used hierarchical clustering as the primary tool to distinguish different types of diffuse B-cell lymphomas based on gene expression profile data. A cDNA array carrying 17856 probes was used for these experiments, 96 samples were assessed on 128 arrays, and a set of 380 genes was identified as being useful for sample classification.

Perou demonstrates the use of hierarchical clustering for the molecular classification of breast tumor samples based on expression profile data. See Perou et al. (2000) Nature 406:747-52. In this work, a cDNA array carrying 8102 gene probes was used. 1753 of these genes were found to have high variation between breast tumors and were used for the analysis.

Hastie describes the use of gene shaving for discovery of expression markers. Hastie et al. (2000) Genome Biol. 1(2):RESEARCH 0003.1-0003.21. The gene shaving algorithm identifies sets of genes with similar or coherent expression patterns, but large variation across conditions (RNA samples, sample classes, patient classes). In this manner, genes with a tight expression pattern within a transplant rejection grade, but also with high variability across rejection grades are grouped together. The algorithm takes advantage of both characteristics in one grouping step. For example, gene shaving can identify useful marker genes with co-regulated expression. Sets of useful marker genes can be reduced to a smaller set, with each gene providing some non-redundant value in classification. This algorithm was used on the data set

described in Alizadeh et al., supra, and the set of 380 informative gene markers was reduced to 234.

Selected Diseases

In principle, diagnostic nucleotide sets of the invention may be developed and applied to essentially any disease, or disease criterion, as long as at least one subset of nucleotide sequences is differentially expressed in samples derived from one or more individuals with a disease criteria or disease and one or more individuals without the disease criteria or disease, wherein the individual may be the same individual sampled at different points in time, or the individuals may be different individuals (or populations of individuals). For example, the subset of nucleotide sequences may be differentially expressed in the sampled tissues of subjects with the disease or disease criterion (e.g., a patient with a disease or disease criteria) as compared to subjects without the disease or disease criterion (e.g., patients without a disease (control patients)). Alternatively, or in addition, the subset of nucleotide sequence(s) may be differentially expressed in different samples taken from the same patient, e.g. at different points in time, at different disease stages, before and after a treatment, in the presence or absence of a risk factor, etc.

Expression profiles corresponding to sets of nucleotide sequences that correlate not with a diagnosis, but rather with a particular aspect of a disease can also be used to identify the diagnostic nucleotide sets and disease specific target nucleotide sequences of the invention. For example, such an aspect, or disease criterion, can relate to a subject's medical or family history, e.g., childhood illness, cause of death of a parent or other relative, prior surgery or other intervention, medications, symptoms (including onset and/or duration of symptoms), etc. Alternatively, the disease criterion can relate to a diagnosis, e.g., hypertension, diabetes, atherosclerosis, or prognosis (e.g., prediction of future diagnoses, events or complications), e.g., acute myocardial infarction, restenosis following angioplasty, reperfusion injury, allograft rejection, rheumatoid arthritis or systemic lupus erythematosus disease activity or the like. In other cases, the disease criterion corresponds to a therapeutic outcome, e.g., transplant rejection, bypass surgery or response to a medication, restenosis after stent implantation, collateral vessel growth due to therapeutic angiogenesis therapy, decreased angina due to revascularization, resolution of symptoms associated with a myriad of therapies, and the like. Alternatively, the disease criteria corresponds with

previously identified or classic risk factors and may correspond to prognosis or future disease diagnosis. As indicated above, a disease criterion can also correspond to genotype for one or more loci. Disease criteria (including patient data) may be collected (and compared) from the same patient at different points in time, from different patients, between patients with a disease (criterion) and patients representing a control population, etc. Longitudinal data, i.e., data collected at different time points from an individual (or group of individuals) may be used for comparisons of samples obtained from an individual (group of individuals) at different points in time, to permit identification of differences specifically related to the disease state, and to obtain information relating to the change in expression over time, including a rate of change or trajectory of expression over time. The usefulness of longitudinal data is further discussed in the section titled "Identification of diagnostic nucleotide sets of the invention".

It is further understood that diagnostic nucleotide sets may be developed for use in diagnosing conditions for which there is no present means of diagnosis. For example, in rheumatoid arthritis, joint destruction is often well under way before a patient experience symptoms of the condition. A diagnostic nucleotide set may be developed that diagnoses rheumatic joint destruction at an earlier stage than would be possible using present means of diagnosis, which rely in part on the presentation of symptoms by a patient. Diagnostic nucleotide sets may also be developed to replace or augment current diagnostic procedures. For example, the use of a diagnostic nucleotide set to diagnose cardiac allograft rejection may replace the current diagnostic test, a graft biopsy.

It is understood that the following discussion of diseases is exemplary and non-limiting, and further that the general criteria discussed above, e.g. use of family medical history, are generally applicable to the specific diseases discussed below.

In addition to leukocytes, as described throughout, the general method is applicable to nucleotide sequences that are differentially expressed in any subject tissue or cell type, by the collection and assessment of samples of that tissue or cell type. However, in many cases, collection of such samples presents significant technical or medical problems given the current state of the art.

Organ transplant rejection and success

A frequent complication of organ transplantation is recognition of the transplanted organ as foreign by the immune system resulting in rejection. Diagnostic

nucleotide sets can be identified and validated for monitoring organ transplant success, rejection and treatment. Medications currently exist that suppress the immune system, and thereby decrease the rate of and severity of rejection. However, these drugs also suppress the physiologic immune responses, leaving the patient susceptible to a wide variety of opportunistic infections. At present there is no easy, reliable way to diagnose transplant rejection. Organ biopsy is the preferred method, but this is expensive, painful and associated with significant risk and has inadequate sensitivity for focal rejection.

Diagnostic nucleotide sets of the present invention can be developed and validated for use as diagnostic tests for transplant rejection and success. It is appreciated that the methods of identifying diagnostic nucleotide sets are applicable to any organ transplant population. For example, diagnostic nucleotide sets are developed for cardiac allograft rejection and success. In some cases, disease criteria correspond to acute stage rejection diagnosis based on organ biopsy and graded using the International Society for Heart and Lung Transplantation (“ISHLT”) criteria. Other disease criteria correspond to information from the patient’s medical history and information regarding the organ donor. Alternatively, disease criteria include the presence or absence of cytomegalovirus (CMV) infection, Epstein-Barr virus (EBV) infection, allograft dysfunction measured by physiological tests of cardiac function (e.g., hemodynamic measurements from catheterization or echocardiograph data), and symptoms of other infections. Alternatively, disease criteria corresponds to therapeutic outcome, e.g. graft failure, re-transplantation, transplant vasculopathy, response to immunosuppressive medications, etc. Disease criteria may further correspond to a rejection episode of at least moderate histologic grade, which results in treatment of the patient with additional corticosteroids, anti-T cell antibodies, or total lymphoid irradiation; a rejection with histologic grade 2 or higher; a rejection with histologic grade <2; the absence of histologic rejection and normal or unchanged allograft function (based on hemodynamic measurements from catheterization or on echocardiographic data); the presence of severe allograft dysfunction or worsening allograft dysfunction during the study period (based on hemodynamic measurements from catheterization or on echocardiographic data).; documented CMV infection by culture, histology, or PCR, and at least one clinical sign or symptom of infection; specific graft biopsy rejection grades; rejection of mild to moderate histologic severity prompting augmentation of the patient’s chronic immunosuppressive regimen;

rejection of mild to moderate severity with allograft dysfunction prompting plasmaphoresis or a diagnosis of “humoral” rejection; infections other than CMV, especially infection with Epstein Barr virus (EBV); lymphoproliferative disorder (also called post-transplant lymphoma); transplant vasculopathy diagnosed by increased intimal thickness on intravascular ultrasound (IVUS), angiography, or acute myocardial infarction; graft failure or retransplantation; and all cause mortality. Further specific examples of clinical data useful as disease criteria are provided in Example 11.

In another example, diagnostic nucleotide sets are developed and validated for use in treatment of kidney allograft rejection. Disease criteria correspond to, e.g., results of biopsy analysis for kidney allograft rejection, serum creatine level, and urinalysis results. Another disease criteria corresponds to the need for hemodialysis or other renal replacement therapy. Diagnostic nucleotide sets are developed and validated for use in diagnosis and treatment of bone marrow transplant rejection and liver transplant rejection, respectively. Disease criteria for bone marrow transplant rejection correspond to the diagnosis and monitoring of graft rejection and/or graft versus host disease. Disease criteria for liver transplant rejection include levels of serum markers for liver damage and liver function such as AST (aspartate aminotransferase), ALT (alanine aminotransferase), Alkaline phosphatase, GGT, (gamma-glutamyl transpeptidase) Bilirubin, Albumin and Prothrombin time. Further disease criteria correspond to hepatic encephalopathy, medication usage, ascites, and histological rejection on graft biopsy. In addition, urine can be utilized for at the target tissue for profiling in renal transplant, while biliary and intestinal and feces may be used favorably for hepatic or intestinal organ allograft rejection.

Atherosclerosis and Stable Angina Pectoris

Over 50 million patients in the U.S. have atherosclerotic coronary artery disease (hereinafter, “CAD”), and it is of great importance to identify patients who will suffer complications from the disease. Atherosclerosis leads to progressive narrowing of the coronary arteries, which may lead to myocardial ischemia, which manifests as stable angina pectoris, or chest pain with exertion. In addition to chest pain, patients may also have shortness of breath (dyspnea), fatigue, nausea or other symptoms with exertion. Myocardial infarction (heart attack) and unstable angina are acute events associated with atherosclerosis. There is currently no way to accurately predict the occurrence of acute events in patients with atherosclerosis, however.

Although the presence of classic risk factors and arterial wall calcification (as assessed by CT scanning) is weakly correlated with the occurrence of acute coronary syndrome, the degree of artery stenosis (i.e. vessel occlusion as a result of atherosclerosis) correlates poorly with the occurrence of future acute events, as acute events occur more commonly in coronary arteries with 40-50% blockage than arteries that are 80-90% blocked. Coronary angiography can provide information about degree of coronary blockage, but is a poor tool for the measurement of disease activity and the prediction of the likelihood of acute events and other poor outcomes.

Diagnostic nucleotide sets are developed and validated for use in diagnosis and monitoring of atherosclerosis, and in predicting the likelihood of complications, e.g. angina and myocardial infarction. Alternatively, or in addition, disease criteria correspond to symptoms or diagnosis of disease progression, e.g. clinical results of angiography indicating progressive narrowing of vessel lumens. In another aspect, diagnostic nucleotide sets are developed for use in predicting the likelihood of future acute events in patients suffering from atherosclerosis. Disease criteria correspond to retrospective data, for example a recent history of unstable angina or myocardial infarction. Disease criteria also correspond to prospective data, for example, the occurrence of unstable angina or myocardial infarction. In another case, disease criteria correspond to standard medical indicators of occurrence of an acute event, e.g. serum enzyme levels, electrocardiographic testing, chest pain, nuclear magnetic imaging, etc.

Congestive Heart Failure

Congestive heart failure (hereinafter, "CHF") is a disease that affects increasing numbers of individuals. Without being bound by theory, it is believed that CHF is associated with systemic inflammation. Markers of systemic inflammation and serum cytokine levels such as erythrocyte sedimentation rate (ESR) and C-reactive protein (CRP) and serum cytokine levels are elevated (or altered) in patients with CHF, and elevation correlates with the severity and progression of the disease. Furthermore, serum catecholamine levels (epinephrine and norepinephrine) are also elevated in proportion to the severity of CHF, and may directly alter leukocyte expression patterns. Currently, echocardiography is the test primarily used to assess the severity of CHF and monitor progression of the disease. There are a number of drugs that are efficacious in treating CHF, such as beta-blockers and ACE inhibitors.

A leukocyte test with the ability to determine the rate of progression and the adequacy of therapy is of great interest.

Diagnostic nucleotide sets are developed and validated for use in diagnosis and monitoring of progression and rate of progression (activity) of CHF. Disease criteria correspond to the results of echocardiography testing, which may indicate diagnosis of CHF or increasing severity of CHF as evidenced by worsening parameters for ventricular function, such as the ejection fraction, fractional shortening, wall motion or ventricular pressures. Alternatively, or in addition, disease criteria correspond to hospitalization for CHF, death, pulmonary edema, increased cardiac chamber dimensions on echocardiography or another imaging test, exercise testing of hemodynamic measurements, serial CRP, other serum markers, NYHA functional classes, quality of life measures, renal function, transplant listing, pulmonary edema, left ventricular assist device use, medication use and changes, and worsening of Ejection Fraction by echocardiography, angiography, MRI, CT or nuclear imaging.. In another aspect, disease criteria correspond to response to drug therapy, e.g. beta-blockers or ACE inhibitors.

Risk factors for coronary artery disease

The established and classic risks for the occurrence of coronary artery disease and complications of that disease are: cigarette smoking, diabetes, hypertension, hyperlipidemia and a family history of early atherosclerosis. Obesity, sedentary lifestyle, syndrome X, cocaine use, chronic hemodialysis and renal disease, radiation exposure, endothelial dysfunction, elevated plasma homocysteine, elevated plasma lipoprotein a, elevated CRP, infection with CMV and chlamydia infection are less well established, controversial, or putative risk factors for the disease. Risk factors are known to be associated with patient prognosis and outcome, but the contribution of each risk factor to the future clinical state of a patient is difficult to measure. The effect of risk factor modification (e.g., smoking cessation, treatment of hypercholesterolemia) on overall risk and future outcome is also difficult to quantify.

Diagnostic nucleotide sets may be developed that correlate with these risk factors, or the sum of the risk factors for use in predicting occurrence of coronary artery disease. Disease criteria correspond to risk factors, as exemplified above, as well as to occurrence of coronary artery disease. Alternatively, or in addition, disease criteria corresponding to risk factors may contribute to a numerical weighted average, which itself may be treated as a disease criteria and may be used for correlation to

gene expression. In another aspect, risk factors may be modified in a patient, e.g. by behavioral change, or decrease cholesterol through chemotherapy in patients with hypocholesteremia. Disease criteria may further correspond to diagnosis of coronary disease.

Restenosis

Angioplasty can re-open a narrowed artery. However, the long-term success rate of these procedures is limited by restenosis, the re-narrowing of a coronary artery after an angioplasty. Currently, about 50% of treated arteries re-narrow after angioplasty and about 30% re-narrow after standard stent placement. Restenosis usually becomes apparent within 3 months of the angioplasty procedure. Presently, there is no reliable method for predicting which arteries will succumb to restenosis, though small vessels tend to be more likely to re-narrow, as do vessels of diabetics, renal patients and vessels exposed to high-pressure balloon inflation during balloon angioplasty.

Diagnostic nucleotide sets are developed and validated to predict restenosis in patients before undergoing angioplasty or shortly thereafter. Disease criteria correspond to angiogram testing (diagnosis of restenosis), as well as clinical symptoms of restenosis, e.g. chest pain due to re-narrowing of the artery, as confirmed by angiogram. Anti-restenotic drug therapy is also identified for each patient. The diagnostic nucleotide set are useful to identify patients about to undergo angioplasty who would benefit from stents, radiation-emitting stents, and anti-restenotic drug delivering stents. Patients that would benefit from post-angioplasty anti-restenotic drug therapy may also be identified.

Rheumatoid Arthritis

Rheumatoid arthritis (RA) affects about two million patients in the US and is a chronic and debilitating inflammatory arthritis, particularly involving pain and destruction of the joints. RA often goes undiagnosed because patients may have no pain, but the disease is actively destroying the joint. Other patients are known to have RA, and are treated to alleviate symptoms, but the rate of progression of joint destruction can't easily be monitored. Drug therapy is available, but the most effective medicines are toxic (e.g., steroids, methotrexate) and thus need to be used with caution. A new class of medications (TNF blockers) is very effective, but the drugs are expensive, have side effects, and not all patients respond. Side-effects are

common and include immune suppression, toxicity to organ systems, allergy and metabolic disturbances.

Diagnostic nucleotide sets of the invention are developed and validated for use in diagnosis and treatment of RA. Disease criteria correspond to disease symptoms (e.g., joint pain, joint swelling and joint stiffness and any of the American College for Rheumatology criteria for the diagnosis of RA, see Arnett et al (1988) Arthr. Rheum. 31:315-24), progression of joint destruction (e.g. as measured by serial hand radiographs, assessment of joint function and mobility), surgery, need for medication, additional diagnoses of inflammatory and non-inflammatory conditions, and clinical laboratory measurements including complete blood counts with differentials, CRP, ESR, ANA, Serum IL6, Soluble CD40 ligand, LDL, HDL, Anti-DNA antibodies, rheumatoid factor, C3, C4, serum creatinine. In addition, or alternatively, disease criteria correspond to response to drug therapy and presence or absence of side-effects or measures of improvement exemplified by the American College of Rheumatology "20%" and "50%" response/improvement rates. See Felson et al (1995) Arthr Rheum 38:531-37. Diagnostic nucleotide sets are identified that monitor and predict disease progression including flaring (acute worsening of disease accompanied by joint pain or other symptoms), response to drug treatment and likelihood of side-effects.

In addition to peripheral leukocytes, surgical specimens of rheumatoid joints can be used for leukocyte expression profiling experiments. Members of diagnostic nucleotide sets are candidates for leukocyte target nucleotide sequences, e.g. as a candidate drug target for rheumatoid arthritis.

Systemic Lupus Erythematosus (SLE)

SLE is a chronic, systemic inflammatory disease characterized by dysregulation of the immune system, which effects up to 2 million patients in the US. Symptoms of SLE include rashes, joint pain, abnormal blood counts, renal dysfunction and damage, infections, CNS disorders, arthralgias and autoimmunity. Patients may also have early onset atherosclerosis.

Diagnostic nucleotide sets are identified and validated for use in diagnosis and monitoring of SLE activity and progression. Disease criteria correspond to clinical data, e.g. symptom rash, joint pain, malaise, rashes, blood counts (white and red), tests of renal function e.g. creatinine, blood urea nitrogen (hereinafter, "bun") creative clearance, data obtained from laboratory tests including complete blood counts with differentials, CRP, ESR, ANA, Serum IL6, Soluble CD40 ligand, LDL, HDL, Anti-

DNA antibodies, rheumatoid factor, C3, C4, serum creatinine and any medication levels, the need for pain medications, cumulative doses or immunosuppressive therapy, symptoms or any manifestation of carotid atherosclerosis (e.g. ultrasound diagnosis or any other manifestations of the disease), data from surgical procedures such as gross operative findings and pathological evaluation of resected tissues and biopsies (e.g., renal, CNS), information on pharmacological therapy and treatment changes, clinical diagnoses of disease “flare”, hospitalizations, death, quantitative joint exams, results from health assessment questionnaires (HAQs), and other clinical measures of patient symptoms and disability. In addition, disease criteria correspond to the clinical score known as SLEDAI (Bombadier C, Gladman DD, Urowitz MB, Caron D, Chang CH and the Committee on Prognosis Studies in SLE: Derivation of the SLEDAI for Lupus Patients. Arthritis Rheum 35:630-640, 1992.). Diagnostic nucleotide sets may be useful for diagnosis of SLE, monitoring disease progression including progressive renal dysfunction, carotid atherosclerosis and CNS dysfunction, and predicting occurrence of side-effects, for example.

Dermatomyositis/Polymyositis

Dermatomyositis/Polymyositis is an autoimmune/inflammatory disease of muscle and skin. Disease criteria correspond to clinical markers of muscle damage (e.g. creatine kinase or myoglobin), muscle strength, symptoms, skin rash or muscle biopsy results.

Diabetes

Insulin dependent (type I) diabetes is caused by an autoimmune attack of insulin producing cells in the pancreas. The disease does not manifest until greater than 90% of the insulin producing cells are destroyed. Diagnostic nucleotide sets are developed and validated for use in detecting diabetes before it is clinically evident. Disease criteria correspond to future occurrence of diabetes, glucose tolerance, serum glucose level, and levels of hemoglobin A1c or other markers.

Inflammatory Bowel Disease (Crohn's and Ulcerative Colitis)

Inflammatory Bowel Disease, e.g., Crohn's Disease and Ulcerative Colitis, are chronic inflammatory diseases of the intestine. Together they effect at least 1 million in the US. Currently, diagnosis and monitoring is accomplished by intestinal endoscopy with or without a biopsy. Steroids and other immune suppressing drugs are useful in treating these diseases, but these drugs cause toxicity and severe side-effects. Diagnostic nucleotide sets are developed for use in diagnosis and monitoring

of disease progression. Disease criteria correspond to clinical criteria, e.g. symptoms of abdominal or pelvic pain, diarrhea, fever and rectal bleeding. Alternatively, or in addition, disease criteria correspond to endoscopy results or bowel biopsy results.

Osteoarthritis

20-40 million patients in the US have osteoarthritis. Patient groups are heterogeneous, with a subset of patients having earlier onset, more aggressive joint damage, involving more inflammation (leukocyte infiltration) leukocyte diagnostics can be used to distinguish osteoarthritis from rheumatoid arthritis, define likelihood and degree of response to NSAID therapy (non-steroidal anti-inflammatory drugs). Rate of progression of joint damage can also be assessed. Diagnostic nucleotide sets may be developed for use in selection and titration of treatment therapies. Disease criteria correspond to response to therapy, and disease progression using certain therapies, need for joint surgery, joint pain and disability.

Asthma

Asthma is a chronic inflammatory disease of the lungs. Clinical symptoms include chronic or acute airflow obstruction. Patients are treated with inhaled steroids or bronchodilators or systemic steroids and other medication, and disease progression is monitored clinically using a peak air flow meter or formal pulmonary function tests. Even with these tests, it is difficult to predict which patients are at highest risk for acute worsening of airway obstruction (an “asthma attack”). Diagnostic nucleotide sets are developed for use in predicting likelihood of acute asthma attacks, and for use in choosing and titrating drug therapy. Disease criteria correspond to pulmonary function testing, peak flow meter measurements, ER visits, inhaler use, subjective patient assessment of response to therapy, hospitalization and need for steroids.

Other inflammatory diseases:

Other inflammatory disease suitable for development and use of diagnostic nucleotide sets are polymyalgia rheumatica, temporal arteritis, polyarteritis nodosa, Wegener's granulomatosis, Whipple's disease, heterotopic ossification, Periprosthetic Osteolysis, Sepsis/ARDS, scleroderma, Grave's disease, Hashimoto's thyroiditis, psoriasis numerous others (See Table 1).

Viral diseases

Diagnostic leukocyte nucleotide sets may be developed and validated for use in diagnosing viral disease. In another aspect, viral nucleotide sequences may be

added to a leukocyte nucleotide set for use in diagnosis of viral diseases.

Alternatively, viral nucleotide sets and leukocyte nucleotides sets may be used sequentially.

Epstein-Barr virus (EBV)

EBV causes a variety of diseases such as mononucleosis, B-cell lymphoma, and pharyngeal carcinoma. It infects mononuclear cells and circulating atypical lymphocytes are a common manifestation of infection. Peripheral leukocyte gene expression is altered by infection. Transplant recipients and patients who are immunosuppressed are at increased risk for EBV-associated lymphoma.

Diagnostic nucleotide sets may be developed and validated for use in diagnosis and monitoring of EBV. In one aspect, the diagnostic nucleotide set is a leukocyte nucleotide set. Alternatively, EBV nucleotide sequences are added to a leukocyte nucleotide set, for use in diagnosing EBV. Disease criteria correspond with diagnosis of EBV, and, in patients who are EBV-sero-positive, presence (or prospective occurrence) of EBV-related illnesses such as mononucleosis, and EBV-associated lymphoma. Diagnostic nucleotide sets are useful for diagnosis of EBV, and prediction of occurrence of EBV-related illnesses.

Cytomegalovirus (CMV)

Cytomegalovirus cause inflammation and disease in almost any tissue, particularly the colon, lung, bone marrow and retina, and is a very important cause of disease in immunosuppressed patients, e.g. transplant, cancer, AIDS. Many patients are infected with or have been exposed to CMV, but not all patients develop clinical disease from the virus. Also, CMV negative recipients of allografts that come from CMV positive donors are at high risk for CMV infection. As immunosuppressive drugs are developed and used, it is increasingly important to identify patients with current or impending clinical CMV disease, because the potential benefit of immunosuppressive therapy must be balanced with the increased rate of clinical CMV infection and disease that may result from the use of immunosuppression therapy. CMV may also play a role in the occurrence of atherosclerosis or restenosis after angioplasty.

Diagnostic nucleotide sets are developed for use in diagnosis and monitoring of CMV infection or re-activation of CMV infection. In one aspect, the diagnostic nucleotide set is a leukocyte nucleotide set. In another aspect, CMV nucleotide sequences are added to a leukocyte nucleotide set, for use in diagnosing CMV.

Disease criteria correspond to diagnosis of CMV (e.g., sero-positive state) and presence of clinically active CMV. Disease criteria may also correspond to prospective data, e.g. the likelihood that CMV will become clinically active or impending clinical CMV infection. Antiviral medications are available and diagnostic nucleotide sets can be used to select patients for early treatment, chronic suppression or prophylaxis of CMV activity.

Hepatitis B and C

These chronic viral infections affect about 1.25 and 2.7 million patients in the US, respectively. Many patients are infected, but suffer no clinical manifestations. Some patients with infection go on to suffer from chronic liver failure, cirrhosis and hepatic carcinoma.

Diagnostic nucleotide sets are developed for use in diagnosis and monitoring of HBV or HCV infection. In one aspect, the diagnostic nucleotide set is a leukocyte nucleotide set. In another aspect, viral nucleotide sequences are added to a leukocyte nucleotide set, for use in diagnosing the virus and monitoring progression of liver disease. Disease criteria correspond to diagnosis of the virus (e.g., sero-positive state or other disease symptoms). Alternatively, disease criteria correspond to liver damage, e.g., elevated alkaline phosphatase, ALT, AST or evidence of ongoing hepatic damage on liver biopsy. Alternatively, disease criteria correspond to serum liver tests (AST, ALT, Alkaline Phosphatase, GGT, PT, bilirubin), liver biopsy, liver ultrasound, viral load by serum PCR, cirrhosis, hepatic cancer, need for hospitalization or listing for liver transplant. Diagnostic nucleotide sets are used to diagnose HBV and HCV, and to predict likelihood of disease progression. Antiviral therapeutic usage, such as Interferon gamma and Ribavirin, can also be disease criteria.

HIV

HIV infects T cells and certainly causes alterations in leukocyte expression. Diagnostic nucleotide sets are developed for diagnosis and monitoring of HIV. In one aspect, the diagnostic nucleotide set is a leukocyte nucleotide set. In another aspect, viral nucleotide sequences are added to a leukocyte nucleotide set, for use in diagnosing the virus. Disease criteria correspond to diagnosis of the virus (e.g., sero-positive state). In addition, disease criteria correspond to viral load, CD4 T cell counts, opportunistic infection, response to antiretroviral therapy, progression to AIDS, rate of progression and the occurrence of other HIV related outcomes (e.g.,

malignancy, CNS disturbance). Response to antiretrovirals may also be disease criteria.

Pharmacogenomics

Pharmacogenomics is the study of the individual propensity to respond to a particular drug therapy (combination of therapies). In this context, response can mean whether a particular drug will work on a particular patient, e.g. some patients respond to one drug but not to another drug. Response can also refer to the likelihood of successful treatment or the assessment of progress in treatment. Titration of drug therapy to a particular patient is also included in this description, e.g. different patients can respond to different doses of a given medication. This aspect may be important when drugs with side-effects or interactions with other drug therapies are contemplated.

Diagnostic nucleotide sets are developed and validated for use in assessing whether a patient will respond to a particular therapy and/or monitoring response of a patient to drug therapy(therapies). Disease criteria correspond to presence or absence of clinical symptoms or clinical endpoints, presence of side-effects or interaction with other drug(s). The diagnostic nucleotide set may further comprise nucleotide sequences that are targets of drug treatment or markers of active disease.

Validation and accuracy of diagnostic nucleotide set using correlation analysis

Prior to widespread application of the diagnostic probe sets of the invention, the predictive value of the probe set is validated.

Typically, the oligonucleotide sequence of each probe is confirmed, e.g. by DNA sequencing using an oligonucleotide-specific primer. Partial sequence obtained is generally sufficient to confirm the identity of the oligonucleotide probe. Alternatively, a complementary polynucleotide is fluorescently labeled and hybridized to the array, or to a different array containing a resynthesized version of the oligo nucleotide probe, and detection of the correct probe is confirmed.

Typically, validation is performed by statistically evaluating the accuracy of the correspondence between the molecular signature for a diagnostic probe set and a selected indicator. For example, the expression differential for a nucleotide sequence between two subject classes can be expressed as a simple ratio of relative expression. The expression of the nucleotide sequence in subjects with selected indicator can be

compared to the expression of that nucleotide sequence in subjects without the indicator, as described in the following equations.

$\sum E_x a_i / N = E_x A$ the average expression of nucleotide sequence x in the members of group A;

$\sum E_x b_i / M = E_x B$ the average expression of nucleotide sequence x in the members of group B;

$E_x A / E_x B = \Delta E_x AB$ the average differential expression of nucleotide sequence x between groups A

and B:

where \sum indicates a sum; E_x is the expression of nucleotide sequence x relative to a standard; a_i are the individual members of group A, group A has N members; b_i are the individual members of group B, group B has M members.

The expression of at least two nucleotide sequences, e.g., nucleotide sequence X and nucleotide sequence Y are measured relative to a standard in at least one subject of group A (e.g., with a disease) and group B (e.g., without the disease). Ideally, for purposes of validation the indicator is independent from (i.e., not assigned based upon) the expression pattern. Alternatively, a minimum threshold of gene expression for nucleotide sequences X and Y, relative to the standard, are designated for assignment to group A. For nucleotide sequence x, this threshold is designated ΔE_x , and for nucleotide sequence y, the threshold is designated ΔE_y .

The following formulas are used in the calculations below:

Sensitivity = (true positives/true positives + false negatives)

Specificity = (true negatives/true negatives + false positives)

If, for example, expression of nucleotide sequence x above a threshold: $x > \Delta E_x$, is observed for 80/100 subjects in group A and for 10/100 subjects in group B, the sensitivity of nucleotide sequence x for the assignment to group A, at the given expression threshold ΔE_x , is 80%, and the specificity is 90%.

If the expression of nucleotide sequence y is $> \Delta E_y$ in 80/100 subjects in group A, and in 10/100 subjects in group B, then, similarly the sensitivity of nucleotide sequence y for the assignment to group A at the given threshold ΔE_y is 80% and the specificity is 90%. If in addition, 60 of the 80 subjects in group A that meet the expression threshold for nucleotide sequence y also meet the expression threshold ΔE_x and that 5 of the 10 subjects in group B that meet the expression

threshold for nucleotide sequence y also meet the expression threshold ΔEx , the sensitivity of the test ($x > \Delta Ex$ and $y > \Delta Ey$) for assignment of subjects to group A is 60% and the specificity is 95%.

Alternatively, if the criteria for assignment to group A are change to: Expression of $x > \Delta Ex$ or expression of $y > \Delta Ey$, the sensitivity approaches 100% and the specificity is 85%.

Clearly, the predictive accuracy of any diagnostic probe set is dependent on the minimum expression threshold selected. The expression of nucleotide sequence X (relative to a standard) is measured in subjects of groups A (with disease) and B (without disease). The minimum threshold of nucleotide sequence expression for x , required for assignment to group A is designated $\Delta Ex 1$.

If 90/100 patients in group A have expression of nucleotide sequence $x > \Delta Ex 1$ and 20/100 patients in group B have expression of nucleotide sequence $x > \Delta Ex 1$, then the sensitivity of the expression of nucleotide sequence x (using $\Delta Ex 1$ as a minimum expression threshold) for assignment of patients to group A will be 90% and the specificity will be 80%.

Altering the minimum expression threshold results in an alteration in the specificity and sensitivity of the nucleotide sequences in question. For example, if the minimum expression threshold of nucleotide sequence x for assignment of subjects to group A is lowered to $\Delta Ex 2$, such that 100/100 subjects in group A and 40/100 subjects in group B meet the threshold, then the sensitivity of the test for assignment of subjects to group A will be 100% and the specificity will be 60%.

Thus, for 2 nucleotide sequences X and Y: the expression of nucleotide sequence x and nucleotide sequence y (relative to a standard) are measured in subjects belonging to groups A (with disease) and B (without disease). Minimum thresholds of nucleotide sequence expression for nucleotide sequences X and Y (relative to common standards) are designated for assignment to group A. For nucleotide sequence x , this threshold is designated $\Delta Ex 1$ and for nucleotide sequence y , this threshold is designated $\Delta Ey 1$.

If in group A, 90/100 patients meet the minimum requirements of expression $\Delta Ex 1$ and $\Delta Ey 1$, and in group B, 10/100 subjects meet the minimum requirements of expression $\Delta Ex 1$ and $\Delta Ey 1$, then the sensitivity of the test for assignment of subjects to group A is 90% and the specificity is 90%.

Increasing the minimum expression thresholds for X and Y to $\Delta Ex2$ and $\Delta Ey2$, such that in group A, 70/100 subjects meet the minimum requirements of expression $\Delta Ex2$ and $\Delta Ey2$, and in group B, 3/100 subjects meet the minimum requirements of expression $\Delta Ex2$ and $\Delta Ey2$. Now the sensitivity of the test for assignment of subjects to group A is 70% and the specificity is 97%.

If the criteria for assignment to group A is that the subject in question meets either threshold, $\Delta Ex2$ or $\Delta Ey2$, and it is found that 100/100 subjects in group A meet the criteria and 20/100 subjects in group B meet the criteria, then the sensitivity of the test for assignment to group A is 100% and the specificity is 80%.

Individual components of a diagnostic probe set each have a defined sensitivity and specificity for distinguishing between subject groups. Such individual nucleotide sequences can be employed in concert as a diagnostic probe set to increase the sensitivity and specificity of the evaluation. The database of molecular signatures is queried by algorithms to identify the set of nucleotide sequences (i.e., corresponding to members of the probe set) with the highest average differential expression between subject groups. Typically, as the number of nucleotide sequences in the diagnostic probe set increases, so does the predictive value, that is, the sensitivity and specificity of the probe set. When the probe sets are defined they may be used for diagnosis and patient monitoring as discussed below. The diagnostic sensitivity and specificity of the probe sets for the defined use can be determined for a given probe set with specified expression levels as demonstrated above. By altering the expression threshold required for the use of each nucleotide sequence as a diagnostic, the sensitivity and specificity of the probe set can be altered by the practitioner. For example, by lowering the magnitude of the expression differential threshold for each nucleotide sequence in the set, the sensitivity of the test will increase, but the specificity will decrease. As is apparent from the foregoing discussion, sensitivity and specificity are inversely related and the predictive accuracy of the probe set is continuous and dependent on the expression threshold set for each nucleotide sequence. Although sensitivity and specificity tend to have an inverse relationship when expression thresholds are altered, both parameters can be increased as nucleotide sequences with predictive value are added to the diagnostic nucleotide set. In addition a single or a few markers may not be reliable expression markers across a population of patients. This is because of the variability in expression and measurement of expression that exists between measurements, individuals and

individuals over time. Inclusion of a large number of candidate nucleotide sequences or large numbers of nucleotide sequences in a diagnostic nucleotide set allows for this variability as not all nucleotide sequences need to meet a threshold for diagnosis. Generally, more markers are better than a single marker. If many markers are used to make a diagnosis, the likelihood that all expression markers will not meet some thresholds based upon random variability is low and thus the test will give fewer false negatives.

It is appreciated that the desired diagnostic sensitivity and specificity of the diagnostic nucleotide set may vary depending on the intended use of the set. For example, in certain uses, high specificity and high sensitivity are desired. For example, a diagnostic nucleotide set for predicting which patient population may experience side effects may require high sensitivity so as to avoid treating such patients. In other settings, high sensitivity is desired, while reduced specificity may be tolerated. For example, in the case of a beneficial treatment with few side effects, it may be important to identify as many patients as possible (high sensitivity) who will respond to the drug, and treatment of some patients who will not respond is tolerated. In other settings, high specificity is desired and reduced sensitivity may be tolerated. For example, when identifying patients for an early-phase clinical trial, it is important to identify patients who may respond to the particular treatment. Lower sensitivity is tolerated in this setting as it merely results in reduced patients who enroll in the study or requires that more patients are screened for enrollment.

Methods of using diagnostic nucleotide sets.

The invention also provide methods of using the diagnostic nucleotide sets to: diagnose disease; assess severity of disease; predict future occurrence of disease; predict future complications of disease; determine disease prognosis; evaluate the patient's risk, or "stratify" a group of patients; assess response to current drug therapy; assess response to current non-pharmacological therapy; determine the most appropriate medication or treatment for the patient; predict whether a patient is likely to respond to a particular drug; and determine most appropriate additional diagnostic testing for the patient, among other clinically and epidemiologically relevant applications.

The nucleotide sets of the invention can be utilized for a variety of purposes by physicians, healthcare workers, hospitals, laboratories, patients, companies and

other institutions. As indicated previously, essentially any disease, condition, or status for which at least one nucleotide sequence is differentially expressed in leukocyte populations (or sub-populations) can be evaluated, e.g., diagnosed, monitored, etc. using the diagnostic nucleotide sets and methods of the invention. In addition to assessing health status at an individual level, the diagnostic nucleotide sets of the present invention are suitable for evaluating subjects at a “population level,” e.g., for epidemiological studies, or for population screening for a condition or disease.

Collection and preparation of sample

RNA, protein and/or DNA is prepared using methods well-known in the art, as further described herein. It is appreciated that subject samples collected for use in the methods of the invention are generally collected in a clinical setting, where delays may be introduced before RNA samples are prepared from the subject samples of whole blood, e.g. the blood sample may not be promptly delivered to the clinical lab for further processing. Further delay may be introduced in the clinical lab setting where multiple samples are generally being processed at any given time. For this reason, methods which feature lengthy incubations of intact leukocytes at room temperature are not preferred, because the expression profile of the leukocytes may change during this extended time period. For example, RNA can be isolated from whole blood using a phenol/guanidine isothiocyanate reagent or another direct whole-blood lysis method, as described in, e.g., U.S. Patent Nos. 5,346,994 and 4,843,155. This method may be less preferred under certain circumstances because the large majority of the RNA recovered from whole blood RNA extraction comes from erythrocytes since these cells outnumber leukocytes 1000:1. Care must be taken to ensure that the presence of erythrocyte RNA and protein does not introduce bias in the RNA expression profile data or lead to inadequate sensitivity or specificity of probes.

Alternatively, intact leukocytes may be collected from whole blood using a lysis buffer that selectively lyses erythrocytes, but not leukocytes, as described, e.g., in (U.S. Patent Nos. 5,973,137, and 6,020,186). Intact leukocytes are then collected by centrifugation, and leukocyte RNA is isolated using standard protocols, as described herein. However, this method does not allow isolation of sub-populations of leukocytes, e.g. mononuclear cells, which may be desired. In addition, the expression profile may change during the lengthy incubation in lysis buffer, especially

in a busy clinical lab where large numbers of samples are being prepared at any given time.

Alternatively, specific leukocyte cell types can be separated using density gradient reagents (Boyum, A, 1968.). For example, mononuclear cells may be separated from whole blood using density gradient centrifugation, as described, e.g., in U.S. Patents Nos. 4190535, 4350593, 4751001, 4818418, and 5053134. Blood is drawn directly into a tube containing an anticoagulant and a density reagent (such as Ficoll or Percoll). Centrifugation of this tube results in separation of blood into an erythrocyte and granulocyte layer, a mononuclear cell suspension, and a plasma layer. The mononuclear cell layer is easily removed and the cells can be collected by centrifugation, lysed, and frozen. Frozen samples are stable until RNA can be isolated. Density centrifugation, however, must be conducted at room temperature, and if processing is unduly lengthy, such as in a busy clinical lab, the expression profile may change.

The quality and quantity of each clinical RNA sample is desirably checked before amplification and labeling for array hybridization, using methods known in the art. For example, one microliter of each sample may be analyzed on a Bioanalyzer (Agilent 2100 Palo Alto, CA. USA) using an RNA 6000 nano LabChip (Caliper, Mountain View, CA. USA). Degraded RNA is identified by the reduction of the 28S to 18S ribosomal RNA ratio and/or the presence of large quantities of RNA in the 25-100 nucleotide range.

It is appreciated that the RNA sample for use with a diagnostic nucleotide set may be produced from the same or a different cell population, sub-population and/or cell type as used to identify the diagnostic nucleotide set. For example, a diagnostic nucleotide set identified using RNA extracted from mononuclear cells may be suitable for analysis of RNA extracted from whole blood or mononuclear cells, depending on the particular characteristics of the members of the diagnostic nucleotide set. Generally, diagnostic nucleotide sets must be tested and validated when used with RNA derived from a different cell population, sub-population or cell type than that used when obtaining the diagnostic gene set. Factors such as the cell-specific gene expression of diagnostic nucleotide set members, redundancy of the information provided by members of the diagnostic nucleotide set, expression level of the member of the diagnostic nucleotide set, and cell-specific alteration of expression of a member of the diagnostic nucleotide set will contribute to the usefulness of using a different

RNA source than that used when identifying the members of the diagnostic nucleotide set. It is appreciated that it may be desirable to assay RNA derived from whole blood, obviating the need to isolate particular cell types from the blood.

Rapid method of RNA extraction suitable for production in a clinical setting of high quality RNA for expression profiling

In a clinical setting, obtaining high quality RNA preparations suitable for expression profiling, from a desired population of leukocytes poses certain technical challenges, including: the lack of capacity for rapid, high-throughput sample processing in the clinical setting, and the possibility that delay in processing (in a busy lab or in the clinical setting) may adversely affect RNA quality, e.g. by a permitting the expression profile of certain nucleotide sequences to shift. Also, use of toxic and expensive reagents, such as phenol, may be disfavored in the clinical setting due to the added expense associated with shipping and handling such reagents.

A useful method for RNA isolation for leukocyte expression profiling would allow the isolation of monocyte and lymphocyte RNA in a timely manner, while preserving the expression profiles of the cells, and allowing inexpensive production of reproducible high-quality RNA samples. Accordingly, the invention provides a method of adding inhibitor(s) of RNA transcription and/or inhibitor(s) of protein synthesis, such that the expression profile is “frozen” and RNA degradation is reduced. A desired leukocyte population or sub-population is then isolated, and the sample may be frozen or lysed before further processing to extract the RNA. Blood is drawn from subject population and exposed to ActinomycinD (to a final concentration of 10 ug/ml) to inhibit transcription, and cycloheximide (to a final concentration of 10 ug/ml) to inhibit protein synthesis. The inhibitor(s) can be injected into the blood collection tube in liquid form as soon as the blood is drawn, or the tube can be manufactured to contain either lyophilized inhibitors or inhibitors that are in solution with the anticoagulant. At this point, the blood sample can be stored at room temperature until the desired leukocyte population or sub-population is isolated, as described elsewhere. RNA is isolated using standard methods, e.g., as described above, or a cell pellet or extract can be frozen until further processing of RNA is convenient.

The invention also provides a method of using a low-temperature density gradient for separation of a desired leukocyte sample. In another embodiment, the invention provides the combination of use of a low-temperature density gradient and the use of transcriptional and/or protein synthesis inhibitor(s). A desired leukocyte population is separated using a density gradient solution for cell separation that maintains the required density and viscosity for cell separation at 0-4°C. Blood is drawn into a tube containing this solution and may be refrigerated before and during processing as the low temperatures slow cellular processes and minimize expression profile changes. Leukocytes are separated, and RNA is isolated using standard methods. Alternately, a cell pellet or extract is frozen until further processing of RNA is convenient. Care must be taken to avoid rewarming the sample during further processing steps.

Alternatively, the invention provides a method of using low-temperature density gradient separation, combined with the use of actinomycin A and cyclohexamide, as described above.

Assessing expression for diagnostics

Expression profiles for the set of diagnostic nucleotide sequences in a subject sample can be evaluated by any technique that determines the expression of each component nucleotide sequence. Methods suitable for expression analysis are known in the art, and numerous examples are discussed in the Sections titled “Methods of obtaining expression data” and “high throughput expression Assays”, above.

In many cases, evaluation of expression profiles is most efficiently, and cost effectively, performed by analyzing RNA expression. Alternatively, the proteins encoded by each component of the diagnostic nucleotide set are detected for diagnostic purposes by any technique capable of determining protein expression, e.g., as described above. Expression profiles can be assessed in subject leukocyte sample using the same or different techniques as those used to identify and validate the diagnostic nucleotide set. For example, a diagnostic nucleotide set identified as a subset of sequences on a cDNA microarray can be utilized for diagnostic (or prognostic, or monitoring, etc.) purposes on the same array from which they were identified. Alternatively, the diagnostic nucleotide sets for a given disease or condition can be organized onto a dedicated sub-array for the indicated purpose. It is important to note that if diagnostic nucleotide sets are discovered using one

technology, e.g. RNA expression profiling, but applied as a diagnostic using another technology, e.g. protein expression profiling, the nucleotide sets must generally be validated for diagnostic purposes with the new technology. In addition, it is appreciated that diagnostic nucleotide sets that are developed for one use, e.g. to diagnose a particular disease, may later be found to be useful for a different application, e.g. to predict the likelihood that the particular disease will occur. Generally, the diagnostic nucleotide set will need to be validated for use in the second circumstance. As discussed herein, the sequence of diagnostic nucleotide set members may be amplified from RNA or cDNA using methods known in the art providing specific amplification of the nucleotide sequences.

Identification of novel nucleotide sequences that are differentially expressed in leukocytes

Novel nucleotide sequences that are differentially expressed in leukocytes are also part of the invention. Previously unidentified open reading frames may be identified in a library of differentially expressed candidate nucleotide sequences, as described above, and the DNA and predicted protein sequence may be identified and characterized as noted above. We identified unnamed (not previously described as corresponding to a gene, or an expressed gene) nucleotide sequences in the our candidate nucleotide library, depicted in Table 3A, 3B and the sequence listing. Accordingly, further embodiments of the invention are the isolated nucleic acids described in Tables 3A and 3B, and in the sequence listing. The novel differentially expressed nucleotide sequences of the invention are useful in the diagnostic nucleotide set of the invention described above, and are further useful as members of a diagnostic nucleotide set immobilized on an array. The novel partial nucleotide sequences may be further characterized using sequence tools and publically or privately accessible sequence databases, as is well known in the art: Novel differentially expressed nucleotide sequences may be identified as disease target nucleotide sequences, described below. Novel nucleotide sequences may also be used as imaging reagent, as further described below.

As used herein, “novel nucleotide sequence” refers to (a) a nucleotide sequence containing at least one of the DNA sequences disclosed herein (as shown in FIGS. Table 3A, 3B and the sequence listing); (b) any DNA sequence that encodes the amino acid sequence encoded by the DNA sequences disclosed herein; (c) any

DNA sequence that hybridizes to the complement of the coding sequences disclosed herein, contained within the coding region of the nucleotide sequence to which the DNA sequences disclosed herein (as shown in Table 3A, 3B and the sequence listing) belong, under highly stringent conditions, e.g., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65° C, and washing in 0.1XSSC/0.1% SDS at 68° C. (Ausubel F. M. et al., eds., 1989, Current Protocols in Molecular Biology, Vol. I, Green Publishing Associates, Inc., and John Wiley & sons, Inc., New York, at p. 2.10.3), (d) any DNA sequence that hybridizes to the complement of the coding sequences disclosed herein, (as shown in Table 3A, 3B and the sequence listing) contained within the coding region of the nucleotide sequence to which DNA sequences disclosed herein (as shown in TABLES 3A, 3B and the sequence listing) belong, under less stringent conditions, such as moderately stringent conditions, e.g., washing in 0.2XSSC/0.1% SDS at 42°C. (Ausubel et al., 1989, supra), yet which still encodes a functionally equivalent gene product; and/or (e) any DNA sequence that is at least 90% identical, at least 80% identical or at least 70% identical to the coding sequences disclosed herein (as shown in TABLES 3A, 3B and the sequence listing), wherein % identity is determined using standard algorithms known in the art.

The invention also includes nucleic acid molecules, preferably DNA molecules, that hybridize to, and are therefore the complements of, the DNA sequences (a) through (c), in the preceding paragraph. Such hybridization conditions may be highly stringent or less highly stringent, as described above. In instances wherein the nucleic acid molecules are deoxyoligonucleotides ("oligos"), highly stringent conditions may refer, e.g., to washing in 6xSSC/0.05% sodium pyrophosphate at 37°C. (for 14-base oligos), 48°C. (for 17-base oligos), 55°C. (for 20-base oligos), and 60°C. (for 23-base oligos). These nucleic acid molecules may act as target nucleotide sequence antisense molecules, useful, for example, in target nucleotide sequence regulation and/or as antisense primers in amplification reactions of target nucleotide sequence nucleic acid sequences. Further, such sequences may be used as part of ribozyme and/or triple helix sequences, also useful for target nucleotide sequence regulation. Still further, such molecules may be used as components of diagnostic methods whereby the presence of a disease-causing allele, may be detected.

The invention also encompasses (a) DNA vectors that contain any of the foregoing coding sequences and/or their complements (i.e., antisense); (b) DNA expression vectors that contain any of the foregoing coding sequences operatively associated with a regulatory element that directs the expression of the coding sequences; and (c) genetically engineered host cells that contain any of the foregoing coding sequences operatively associated with a regulatory element that directs the expression of the coding sequences in the host cell. As used herein, regulatory elements include but are not limited to inducible and non-inducible promoters, enhancers, operators and other elements known to those skilled in the art that drive and regulate expression. The invention includes fragments of any of the DNA sequences disclosed herein. Fragments of the DNA sequences may be at least 5, at least 10, at least 15, at least 19 nucleotides, at least 25 nucleotides, at least 50 nucleotides, at least 100 nucleotides, at least 200, at least 500, or larger.

In addition to the nucleotide sequences described above, homologues of such sequences, as may, for example be present in other species, may be identified and may be readily isolated, without undue experimentation, by molecular biological techniques well known in the art, as well as use of gene analysis tools described above, and e.g., in Example 4. Further, there may exist nucleotide sequences at other genetic loci within the genome that encode proteins which have extensive homology to one or more domains of such gene products. These nucleotide sequences may also be identified via similar techniques.

For example, the isolated differentially expressed nucleotide sequence may be labeled and used to screen a cDNA library constructed from mRNA obtained from the organism of interest. Hybridization conditions will be of a lower stringency when the cDNA library was derived from an organism different from the type of organism from which the labeled sequence was derived. Alternatively, the labeled fragment may be used to screen a genomic library derived from the organism of interest, again, using appropriately stringent conditions. Such low stringency conditions will be well known to those of skill in the art, and will vary predictably depending on the specific organisms from which the library and the labeled sequences are derived. For guidance regarding such conditions see, for example, Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, Cold Springs Harbor Press, N.Y.; and Ausubel et al., 1989, *Current Protocols in Molecular Biology*, Green Publishing Associates and Wiley Interscience, N.Y.

Novel nucleotide products include those proteins encoded by the novel nucleotide sequences described, above. Specifically, novel gene products may include polypeptides encoded by the novel nucleotide sequences contained in the coding regions of the nucleotide sequences to which DNA sequences disclosed herein (in TABLES 3A, 3B and the sequence listing).

In addition, novel protein products of novel nucleotide sequences may include proteins that represent functionally equivalent gene products. Such an equivalent novel gene product may contain deletions, additions or substitutions of amino acid residues within the amino acid sequence encoded by the novel nucleotide sequences described, above, but which result in a silent change, thus producing a functionally equivalent novel nucleotide sequence product. Amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved.

For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Functionally equivalent", as utilized herein, refers to a protein capable of exhibiting a substantially similar *in vivo* activity as the endogenous novel gene products encoded by the novel nucleotide described, above.

The novel gene products (protein products of the novel nucleotide sequences) may be produced by recombinant DNA technology using techniques well known in the art. Thus, methods for preparing the novel gene polypeptides and peptides of the invention by expressing nucleic acid encoding novel nucleotide sequences are described herein. Methods which are well known to those skilled in the art can be used to construct expression vectors containing novel nucleotide sequence protein coding sequences and appropriate transcriptional/translational control signals. These methods include, for example, *in vitro* recombinant DNA techniques, synthetic techniques and *in vivo* recombination/genetic recombination. See, for example, the techniques described in Sambrook et al., 1989, *supra*, and Ausubel et al., 1989, *supra*. Alternatively, RNA capable of encoding novel nucleotide sequence protein sequences may be chemically synthesized using, for example, synthesizers. See, for example,

the techniques described in "Oligonucleotide Synthesis", 1984, Gait, M. J. ed., IRL Press, Oxford.

A variety of host-expression vector systems may be utilized to express the novel nucleotide sequence coding sequences of the invention. Such host-expression systems represent vehicles by which the coding sequences of interest may be produced and subsequently purified, but also represent cells which may, when transformed or transfected with the appropriate nucleotide coding sequences, exhibit the novel protein encoded by the novel nucleotide sequence of the invention in situ. These include but are not limited to microorganisms such as bacteria (e.g., *E. coli*, *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing novel nucleotide sequence protein coding sequences; yeast (e.g. *Saccharomyces*, *Pichia*) transformed with recombinant yeast expression vectors containing the novel nucleotide sequence protein coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing the novel nucleotide sequence protein coding sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing novel nucleotide sequence protein coding sequences; or mammalian cell systems (e.g. COS, CHO, BHK, 293, 3T3) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5 K promoter).

In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the novel nucleotide sequence protein being expressed. For example, when a large quantity of such a protein is to be produced, for the generation of antibodies or to screen peptide libraries, for example, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited, to the *E. coli* expression vector pUR278 (Ruther et al., 1983, EMBO J. 2:1791), in which the novel nucleotide sequence protein coding sequence may be ligated individually into the vector in frame with the lac Z coding region so that a fusion protein is produced; pIN vectors (Inouye & Inouye, 1985, Nucleic Acids Res. 13:3101-3109; Van Heeke & Schuster, 1989, J. Biol. Chem. 264:5503-5509); and the likes of pGEX vectors may

also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target nucleotide sequence protein can be released from the GST moiety. Other systems useful in the invention include use of the FLAG epitope or the 6-HIS systems.

In an insect system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign nucleotide sequences. The virus grows in *Spodoptera frugiperda* cells. The novel nucleotide sequence coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter). Successful insertion of novel nucleotide sequence coding sequence will result in inactivation of the polyhedrin gene and production of non-occluded recombinant virus (i.e., virus lacking the proteinaceous coat coded for by the polyhedrin gene). These recombinant viruses are then used to infect *Spodoptera frugiperda* cells in which the inserted nucleotide sequence is expressed. (E.g., see Smith et al., 1983, J. Virol. 46: 584; Smith, U.S. Pat. No. 4,215,051).

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the novel nucleotide sequence coding sequence of interest may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric nucleotide sequence may then be inserted in the adenovirus genome by in vitro or in vivo recombination. Insertion in a non-essential region of the viral genome (e.g., region E1 or E3) will result in a recombinant virus that is viable and capable of expressing novel nucleotide sequence encoded protein in infected hosts. (E.g., See Logan & Shenk, 1984, Proc. Natl. Acad. Sci. USA 81:3655-3659). Specific initiation signals may also be required for efficient translation of inserted novel nucleotide sequence coding sequences. These signals include the ATG initiation codon and adjacent sequences. In cases where an entire novel nucleotide sequence, including its own initiation codon and adjacent sequences, is inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only a portion of the novel nucleotide sequence coding sequence is inserted, exogenous translational control signals, including,

perhaps, the ATG initiation codon, must be provided. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see Bittner et al., 1987, *Methods in Enzymol.* 153:516-544).

In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the product of the nucleotide sequence in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be used. Such mammalian host cells include but are not limited to CHO, VERO, BHK, HeLa, COS, MDCK, 293, 3T3, WI38, etc.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express the novel nucleotide sequence encoded protein may be engineered. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of the foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines which express novel nucleotide sequence encoded protein. Such engineered cell lines may be particularly useful in screening and evaluation of compounds that affect the endogenous activity of the novel nucleotide sequence encoded protein.

A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler, et al., 1977, Cell 11:223), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, 1962, Proc. Natl. Acad. Sci. USA 48:2026), and adenine phosphoribosyltransferase (Lowy, et al., 1980, Cell 22:817) genes can be employed in tk-, hgp^rt- or ap^rt- cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for dhfr, which confers resistance to methotrexate (Wigler, et al., 1980, Natl. Acad. Sci. USA 77:3567; O'Hare, et al., 1981, Proc. Natl. Acad. Sci. USA 78:1527); gpt, which confers resistance to mycophenolic acid (Mulligan & Berg, 1981, Proc. Natl. Acad. Sci. USA 78:2072); neo, which confers resistance to the aminoglycoside G-418 (Colberre-Garapin, et al., 1981, J. Mol. Biol. 150:1); and hyg^r, which confers resistance to hygromycin (Santerre, et al., 1984, Gene 30:147) genes.

An alternative fusion protein system allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht, et al., 1991, Proc. Natl. Acad. Sci. USA 88: 8972-8976). In this system, the nucleotide sequence of interest is subcloned into a vaccinia recombination plasmid such that the nucleotide sequence's open reading frame is translationally fused to an amino-terminal tag consisting of six histidine residues. Extracts from cells infected with recombinant vaccinia virus are loaded onto Ni²⁺-nitriloacetic acid-agarose columns and histidine-tagged proteins are selectively eluted with imidazole-containing buffers.

Where recombinant DNA technology is used to produce the protein encoded by the novel nucleotide sequence for such assay systems, it may be advantageous to engineer fusion proteins that can facilitate labeling, immobilization and/or detection.

Indirect labeling involves the use of a protein, such as a labeled antibody, which specifically binds to the protein encoded by the novel nucleotide sequence. Such antibodies include but are not limited to polyclonal, monoclonal, chimeric, single chain, Fab fragments and fragments produced by an Fab expression library.

The invention also provides for antibodies to the protein encoded by the novel nucleotide sequences. Described herein are methods for the production of antibodies capable of specifically recognizing one or more novel nucleotide sequence epitopes. Such antibodies may include, but are not limited to polyclonal antibodies, monoclonal antibodies (mAbs), humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab')₂ fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies, and epitope-binding fragments of any of the above.

Such antibodies may be used, for example, in the detection of a novel nucleotide sequence in a biological sample, or, alternatively, as a method for the inhibition of abnormal gene activity, for example, the inhibition of a disease target nucleotide sequence, as further described below. Thus, such antibodies may be utilized as part of cardiovascular or other disease treatment method, and/or may be used as part of diagnostic techniques whereby patients may be tested for abnormal levels of novel nucleotide sequence encoded proteins, or for the presence of abnormal forms of the such proteins.

For the production of antibodies to a novel nucleotide sequence, various host animals may be immunized by injection with a novel protein encoded by the novel nucleotide sequence, or a portion thereof. Such host animals may include but are not limited to rabbits, mice, and rats, to name but a few. Various adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and *Corynebacterium parvum*.

Polyclonal antibodies are heterogeneous populations of antibody molecules derived from the sera of animals immunized with an antigen, such as novel gene product, or an antigenic functional derivative thereof. For the production of polyclonal antibodies, host animals such as those described above, may be immunized by injection with novel gene product supplemented with adjuvants as also described above.

Monoclonal antibodies, which are homogeneous populations of antibodies to a particular antigen, may be obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to the hybridoma technique of Kohler and Milstein, (1975, *Nature* 256:495-497; and U.S. Pat. No. 4,376,110), the human B-cell hybridoma technique (Kosbor et al., 1983, *Immunology Today* 4:72; Cole et al., 1983, *Proc. Natl. Acad. Sci. USA* 80:2026-2030), and the EBV-hybridoma technique (Cole et al., 1985, *Monoclonal Antibodies And Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96). Such antibodies may be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD

and any subclass thereof. The hybridoma producing the mAb of this invention may be cultivated in vitro or in vivo.

In addition, techniques developed for the production of "chimeric antibodies" (Morrison et al., 1984, Proc. Natl. Acad. Sci., 81:6851-6855; Neuberger et al., 1984, Nature, 312:604-608; Takeda et al., 1985, Nature, 314:452-454) by splicing the genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity can be used. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region.

Alternatively, techniques described for the production of single chain antibodies (U.S. Pat. No. 4,946,778; Bird, 1988, Science 242:423-426; Huston et al., 1988, Proc. Natl. Acad. Sci. USA 85:5879-5883; and Ward et al., 1989, Nature 334:544-546) can be adapted to produce novel nucleotide sequence-single chain antibodies. Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide.

Antibody fragments which recognize specific epitopes may be generated by known techniques. For example, such fragments include but are not limited to: the F(ab')₂ fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed (Huse et al., 1989, Science, 246:1275-1281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity.

Disease specific target nucleotide sequences

The invention also provides disease specific target nucleotide sequences, and sets of disease specific target nucleotide sequences. The diagnostic nucleotide sets, subsets thereof, novel nucleotide sequences, and individual members of the diagnostic nucleotide sets identified as described above are also disease specific target nucleotide sequences. In particular, individual nucleotide sequences that are differentially regulated or have predictive value that is strongly correlated with a disease or disease criterion are especially favorable as disease specific target nucleotide sequences. Sets of genes that are co-regulated may also be identified as disease specific target

nucleotide sets. Such nucleotide sequences and/or nucleotide sequence products are targets for modulation by a variety of agents and techniques. For example, disease specific target nucleotide sequences (or the products of such nucleotide sequences, or sets of disease specific target nucleotide sequences) can be inhibited or activated by, e.g., target specific monoclonal antibodies or small molecule inhibitors, or delivery of the nucleotide sequence or gene product of the nucleotide sequence to patients. Also, sets of genes can be inhibited or activated by a variety of agents and techniques. The specific usefulness of the target nucleotide sequence(s) depends on the subject groups from which they were discovered, and the disease or disease criterion with which they correlate.

Imaging

The invention also provides for imaging reagents. The differentially expressed leukocyte nucleotide sequences, diagnostic nucleotide sets, or portions thereof, and novel nucleotide sequences of the invention are nucleotide sequences expressed in cells with or without disease. Leukocytes expressing a nucleotide sequence(s) that is differentially expressed in a disease condition may localize within the body to sites that are of interest for imaging purposes. For example, a leukocyte expressing a nucleotide sequence(s) that are differentially expressed in an individual having atherosclerosis may localize or accumulate at the site of an atherosclerotic plaque. Such leukocytes, when labeled, may provide a detection reagent for use in imaging regions of the body where labeled leukocyte accumulate or localize, for example, at the atherosclerotic plaque in the case of atherosclerosis. For example, leukocytes are collected from a subject, labeled in vitro, and reintroduced into a subject. Alternatively, the labeled reagent is introduced into the subject individual, and leukocyte labeling occurs within the patient.

Imaging agents that detect the imaging targets of the invention are produced by well-known molecular and immunological methods (for exemplary protocols, *see*, e.g., Ausubel, Berger, and Sambrook, as well as Harlow and Lane, *supra*).

For example, a full-length nucleic acid sequence, or alternatively, a gene fragment encoding an immunogenic peptide or polypeptide fragments, is cloned into a convenient expression vector, for example, a vector including an in-frame epitope or substrate binding tag to facilitate subsequent purification. Protein is then expressed from the cloned cDNA sequence and used to generate antibodies, or other specific

binding molecules, to one or more antigens of the imaging target protein.

Alternatively, a natural or synthetic polypeptide (or peptide) or small molecule that specifically binds (or is specifically bound to) the expressed imaging target can be identified through well established techniques (*see, e.g., Mendel et al. (2000) Anticancer Drug Des 15:29-41; Wilson (2000) Curr Med Chem 7:73-98; Hamby and Showalter (1999) Pharmacol Ther 82:169-93; and Shimazawa et al. (1998) Curr Opin Struct Biol 8:451-8*). The binding molecule, e.g., antibody, small molecule ligand, etc., is labeled with a contrast agent or other detectable label, e.g., gadolinium, iodine, or a gamma-emitting source. For in-vivo imaging of a disease process that involved leukocytes, the labeled antibody is infused into a subject, e.g., a human patient or animal subject, and a sufficient period of time is passed to permit binding of the antibody to target cells. The subject is then imaged with appropriate technology such as MRI (when the label is gadolinium) or with a gamma counter (when the label is a gamma emitter).

Identification of nucleotide sequence involved in leukocyte adhesion

The invention also encompasses a method of identifying nucleotide sequences involved in leukocyte adhesion. The interaction between the endothelial cell and leukocyte is a fundamental mechanism of all inflammatory disorders, including the diseases listed in Table 1. For example, the first visible abnormality in atherosclerosis is the adhesion to the endothelium and diapedesis of mononuclear cells (e.g., T-cell and monocyte). Insults to the endothelium (for example, cytokines, tobacco, diabetes, hypertension and many more) lead to endothelial cell activation. The endothelium then expresses adhesion molecules, which have counter receptors on mononuclear cells. Once the leukocyte receptors have bound the endothelial adhesion molecules, they stick to the endothelium, roll a short distance, stop and transmigrate across the endothelium. A similar set of events occurs in both acute and chronic inflammation.

Human endothelial cells, e.g. derived from human coronary arteries, human aorta, human pulmonary artery, human umbilical vein or microvascular endothelial cells, are cultured as a confluent monolayer, using standard methods. Some of the endothelial cells are then exposed to cytokines or another activating stimuli such as oxidized LDL, hyperglycemia, shear stress, or hypoxia (Moser et al. 1992). Some endothelial cells are not exposed to such stimuli and serve as controls. For example, the endothelial cell monolayer is incubated with culture medium containing 5 U/ml of human recombinant IL-1alpha or 10 ng/ml TNF (tumor necrosis factor), for a period of minutes to overnight. The culture medium composition is changed or the flask is sealed to induce hypoxia. In addition, tissue culture plate is rotated to induce sheer stress.

Human T-cells and/or monocytes are cultured in tissue culture flasks or plates, with LGM-3 media from Clonetics. Cells are incubated at 37 degree C, 5% CO₂ and 95% humidity. These leukocytes are exposed to the activated or control endothelial layer by adding a suspension of leukocytes on to the endothelial cell monolayer. The endothelial cell monolayer is cultured on a tissue culture treated plate/ flask or on a microporous membrane. After a variable duration of exposures, the endothelial cells and leukocytes are harvested separately by treating all cells with trypsin and then sorting the endothelial cells from the leukocytes by magnetic affinity reagents to an endothelial cell specific marker such as PECAM-1 (Stem Cell Technologies). RNA is extracted from the isolated cells by standard techniques. Leukocyte RNA is labeled as described above, and hybridized to leukocyte candidate nucleotide library. Epithelial cell RNA is also labeled and hybridized to the leukocyte candidate nucleotide library. Alternatively, the epithelial cell RNA is hybridized to a epithelial cell candidate nucleotide library, prepared according to the methods described for leukocyte candidate libraries, above.

Hybridization to candidate nucleotide libraries will reveal nucleotide sequences that are up-regulated or down-regulated in leukocyte and/or epithelial cells undergoing adhesion. The differentially regulated nucleotide sequences are further characterized, e.g. by isolating and sequencing the full-length sequence, analysis of the DNA and predicted protein sequence, and functional characterization of the protein product of the nucleotide sequence, as described above. Further characterization may result in the identification of leukocyte adhesion specific target nucleotide sequences, which may be candidate targets for regulation of the

inflammatory process. Small molecule or antibody inhibitors can be developed to inhibit the target nucleotide sequence function. Such inhibitors are tested for their ability to inhibit leukocyte adhesion in the in vitro test described above.

Integrated systems

Integrated systems for the collection and analysis of expression profiles, and molecular signatures, as well as for the compilation, storage and access of the databases of the invention, typically include a digital computer with software including an instruction set for sequence searching and analysis, and, optionally, high-throughput liquid control software, image analysis software, data interpretation software, a robotic control armature for transferring solutions from a source to a destination (such as a detection device) operably linked to the digital computer, an input device (e.g., a computer keyboard) for entering subject data to the digital computer, or to control analysis operations or high throughput sample transfer by the robotic control armature. Optionally, the integrated system further comprises an image scanner for digitizing label signals from labeled assay components, e.g., labeled nucleic acid hybridized to a candidate library microarray. The image scanner can interface with image analysis software to provide a measurement of the presence or intensity of the hybridized label, i.e., indicative of an on/off expression pattern or an increase or decrease in expression.

Readily available computational hardware resources using standard operating systems are fully adequate, e.g., a PC (Intel x86 or Pentium chip- compatible DOS,TM OS2,TM WINDOWS,TM WINDOWS NT,TM WINDOWS95,TM WINDOWS98,TM LINUX, or even Macintosh, Sun or PCs will suffice) for use in the integrated systems of the invention. Current art in software technology is similarly adequate (i.e., there are a multitude of mature programming languages and source code suppliers) for design, e.g., of an upgradeable open-architecture object-oriented heuristic algorithm, or instruction set for expression analysis, as described herein. For example, software for aligning or otherwise manipulating ,molecular signatures can be constructed by one of skill using a standard programming language such as Visual basic, Fortran, Basic, Java, or the like, according to the methods herein.

Various methods and algorithms, including genetic algorithms and neural networks, can be used to perform the data collection, correlation, and storage functions, as well as other desirable functions, as described herein. In addition, digital

or analog systems such as digital or analog computer systems can control a variety of other functions such as the display and/or control of input and output files.

For example, standard desktop applications such as word processing software (e.g., Corel WordPerfect™ or Microsoft Word™) and database software (e.g., spreadsheet software such as Corel Quattro Pro™, Microsoft Excel™, or database programs such as Microsoft Access™ or Paradox™) can be adapted to the present invention by inputting one or more character string corresponding, e.g., to an expression pattern or profile, subject medical or historical data, molecular signature, or the like, into the software which is loaded into the memory of a digital system, and carrying out the operations indicated in an instruction set, e.g., as exemplified in Figure 2. For example, systems can include the foregoing software having the appropriate character string information, e.g., used in conjunction with a user interface in conjunction with a standard operating system such as a Windows, Macintosh or LINUX system. For example, an instruction set for manipulating strings of characters, either by programming the required operations into the applications or with the required operations performed manually by a user (or both). For example, specialized sequence alignment programs such as PILEUP or BLAST can also be incorporated into the systems of the invention, e.g., for alignment of nucleic acids or proteins (or corresponding character strings).

Software for performing the statistical methods required for the invention, e.g., to determine correlations between expression profiles and subsets of members of the diagnostic nucleotide libraries, such as programmed embodiments of the statistical methods described above, are also included in the computer systems of the invention. Alternatively, programming elements for performing such methods as principle component analysis (PCA) or least squares analysis can also be included in the digital system to identify relationships between data. Exemplary software for such methods is provided by Partek, Inc., St. Peter, Mo; <http://www.partek.com>.

Any controller or computer optionally includes a monitor which can include, e.g., a flat panel display (e.g., active matrix liquid crystal display, liquid crystal display), a cathode ray tube ("CRT") display, or another display system which serves as a user interface, e.g., to output predictive data. Computer circuitry, including numerous integrated circuit chips, such as a microprocessor, memory, interface circuits, and the like, is often placed in a casing or box which optionally also includes

a hard disk drive, a floppy disk drive, a high capacity removable drive such as a writeable CD-ROM, and other common peripheral elements.

Inputting devices such as a keyboard, mouse, or touch sensitive screen, optionally provide for input from a user and for user selection, e.g., of sequences or data sets to be compared or otherwise manipulated in the relevant computer system. The computer typically includes appropriate software for receiving user instructions, either in the form of user input into a set parameter or data fields (e.g., to input relevant subject data), or in the form of preprogrammed instructions, e.g., preprogrammed for a variety of different specific operations. The software then converts these instructions to appropriate language for instructing the system to carry out any desired operation.

The integrated system may also be embodied within the circuitry of an application specific integrated circuit (ASIC) or programmable logic device (PLD). In such a case, the invention is embodied in a computer readable descriptor language that can be used to create an ASIC or PLD. The integrated system can also be embodied within the circuitry or logic processors of a variety of other digital apparatus, such as PDAs, laptop computer systems, displays, image editing equipment, etc.

The digital system can comprise a learning component where expression profiles, and relevant subject data are compiled and monitored in conjunction with physical assays, and where correlations, e.g., molecular signatures with predictive value for a disease, are established or refined. Successful and unsuccessful combinations are optionally documented in a database to provide justification/preferences for user-base or digital system based selection of diagnostic nucleotide sets with high predictive accuracy for a specified disease or condition.

The integrated systems can also include an automated workstation. For example, such a workstation can prepare and analyze leukocyte RNA samples by performing a sequence of events including: preparing RNA from a human blood sample; labeling the RNA with an isotopic or non-isotopic label; hybridizing the labeled RNA to at least one array comprising all or part of the candidate library; and detecting the hybridization pattern. The hybridization pattern is digitized and recorded in the appropriate database.

Automated RNA preparation tool

The invention also includes an automated RNA preparation tool for the preparation of mononuclear cells from whole blood samples, and preparation of RNA from the mononuclear cells. In a preferred embodiment, the use of the RNA preparation tool is fully automated, so that the cell separation and RNA isolation would require no human manipulations. Full automation is advantageous because it minimizes delay, and standardizes sample preparation across different laboratories. This standardization increases the reproducibility of the results.

Figure 2 depicts the processes performed by the RNA preparation tool of the invention. A primary component of the device is a centrifuge (A). Tubes of whole blood containing a density gradient solution, transcription/translation inhibitors, and a gel barrier that separates erythrocytes from mononuclear cells and serum after centrifugation are placed in the centrifuge (B). The barrier is permeable to erythrocytes and granulocytes during centrifugation, but does not allow mononuclear cells to pass through (or the barrier substance has a density such that mononuclear cells remain above the level of the barrier during the centrifugation). After centrifugation, the erythrocytes and granulocytes are trapped beneath the barrier, facilitating isolation of the mononuclear cell and serum layers. A mechanical arm removes the tube and inverts it to mix the mononuclear cell layer and the serum (C). The arm next pours the supernatant into a fresh tube (D), while the erythrocytes and granulocytes remained below the barrier. Alternatively, a needle is used to aspirate the supernatant and transfer it to a fresh tube. The mechanical arms of the device opens and closes lids, dispenses PBS to aid in the collection of the mononuclear cells by centrifugation, and moves the tubes in and out of the centrifuge. Following centrifugation, the supernatant is poured off or removed by a vacuum device (E), leaving an isolated mononuclear cell pellet. Purification of the RNA from the cells is performed automatically, with lysis buffer and other purification solutions (F) automatically dispensed and removed before and after centrifugation steps. The result is a purified RNA solution. In another embodiment, RNA isolation is performed using a column or filter method. In yet another embodiment, the invention includes an on-board homogenizer for use in cell lysis.

Other automated systems

Automated and/or semi-automated methods for solid and liquid phase high-throughput sample preparation and evaluation are available, and supported by commercially available devices. For example, robotic devices for preparation of nucleic acids from bacterial colonies, e.g., to facilitate production and characterization of the candidate library include, for example, an automated colony picker (e.g., the Q-bot, Genetix, U.K.) capable of identifying, sampling, and inoculating up to 10,000/4 hrs different clones into 96 well microtiter dishes. Alternatively, or in addition, robotic systems for liquid handling are available from a variety of sources, e.g., automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Beckman Coulter, Inc. (Fullerton, CA)) which mimic the manual operations performed by a scientist. Any of the above devices are suitable for use with the present invention, e.g., for high-throughput analysis of library components or subject leukocyte samples. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art.

High throughput screening systems that automate entire procedures, e.g., sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the relevant assay are commercially available. (*see, e.g.,* Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, *etc.*). These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. Similarly, arrays and array readers are available, e.g., from Affymetrix, PE Biosystems, and others.

The manufacturers of such systems provide detailed protocols the various high throughput. Thus, for example, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

A variety of commercially available peripheral equipment, including, e.g., optical and fluorescent detectors, optical and fluorescent microscopes, plate readers, CCD arrays, phosphorimagers, scintillation counters, phototubes, photodiodes, and the like, and software is available for digitizing, storing and analyzing a digitized video or digitized optical or other assay results, e.g., using PC (Intel x86 or pentium

chip- compatible DOS™, OS2™ WINDOWS™, WINDOWS NT™ or WINDOWS95™ based machines), MACINTOSH™, or UNIX based (e.g., SUN™ work station) computers.

Embodiment in a web site.

The methods described above can be implemented in a localized or distributed computing environment. For example, if a localized computing environment is used, an array comprising a candidate nucleotide library, or diagnostic nucleotide set, is configured in proximity to a detector, which is, in turn, linked to a computational device equipped with user input and output features.

In a distributed environment, the methods can be implemented on a single computer with multiple processors or, alternatively, on multiple computers. The computers can be linked, e.g. through a shared bus, but more commonly, the computer(s) are nodes on a network. The network can be generalized or dedicated, at a local level or distributed over a wide geographic area. In certain embodiments, the computers are components of an intra-net or an internet.

The predictive data corresponding to subject molecular signatures (e.g., expression profiles, and related diagnostic, prognostic, or monitoring results) can be shared by a variety of parties. In particular, such information can be utilized by the subject, the subject's health care practitioner or provider, a company or other institution, or a scientist. An individual subject's data, a subset of the database or the entire database recorded in a computer readable medium can be accessed directly by a user by any method of communication, including, but not limited to, the internet. With appropriate computational devices, integrated systems, communications networks, users at remote locations, as well as users located in proximity to, e.g., at the same physical facility, the database can access the recorded information. Optionally, access to the database can be controlled using unique alphanumeric passwords that provide access to a subset of the data. Such provisions can be used, e.g., to ensure privacy, anonymity, etc.

Typically, a client (e.g., a patient, practitioner, provider, scientist, or the like) executes a Web browser and is linked to a server computer executing a Web server. The Web browser is, for example, a program such as IBM's Web Explorer, Internet explorer, NetScape or Mosaic, or the like. The Web server is typically, but not necessarily, a program such as IBM's HTTP Daemon or other WWW daemon (e.g.,

LINUX-based forms of the program). The client computer is bi-directionally coupled with the server computer over a line or via a wireless system. In turn, the server computer is bi-directionally coupled with a website (server hosting the website) providing access to software implementing the methods of this invention.

A user of a client connected to the Intranet or Internet may cause the client to request resources that are part of the web site(s) hosting the application(s) providing an implementation of the methods described herein. Server program(s) then process the request to return the specified resources (assuming they are currently available). A standard naming convention has been adopted, known as a Uniform Resource Locator ("URL"). This convention encompasses several types of location names, presently including subclasses such as Hypertext Transport Protocol ("http"), File Transport Protocol ("ftp"), gopher, and Wide Area Information Service ("WAIS"). When a resource is downloaded, it may include the URLs of additional resources. Thus, the user of the client can easily learn of the existence of new resources that he or she had not specifically requested.

Methods of implementing Intranet and/or Intranet embodiments of computational and/or data access processes are well known to those of skill in the art and are documented, e.g., in ACM Press, pp. 383-392; ISO-ANSI, Working Draft, "Information Technology-Database Language SQL", Jim Melton, Editor, International Organization for Standardization and American National Standards Institute, Jul. 1992; ISO Working Draft, "Database Language SQL-Part 2:Foundation (SQL/Foundation)", CD9075-2:199.chi.SQL, Sep. 11, 1997; and Cluer et al. (1992) A General Framework for the Optimization of Object-Oriented Queries, Proc SIGMOD International Conference on Management of Data, San Diego, California, Jun. 2-5, 1992, SIGMOD Record, vol. 21, Issue 2, Jun., 1992; Stonebraker, M., Editor;. Other resources are available, e.g., from Microsoft, IBM, Sun and other software development companies.

Using the tools described above, users of the reagents, methods and database as discovery or diagnostic tools can query a centrally located database with expression and subject data. Each submission of data adds to the sum of expression and subject information in the database. As data is added, a new correlation statistical analysis is automatically run that incorporates the added clinical and expression data. Accordingly, the predictive accuracy and the types of correlations of the recorded molecular signatures increases as the database grows.

For example, subjects, such as patients, can access the results of the expression analysis of their leukocyte samples and any accrued knowledge regarding the likelihood of the patient's belonging to any specified diagnostic (or prognostic, or monitoring, or risk group), i.e., their expression profiles, and/or molecular signatures. Optionally, subjects can add to the predictive accuracy of the database by providing additional information to the database regarding diagnoses, test results, clinical or other related events that have occurred since the time of the expression profiling. Such information can be provided to the database via any form of communication, including, but not limited to, the internet. Such data can be used to continually define (and redefine) diagnostic groups. For example, if 1000 patients submit data regarding the occurrence of myocardial infarction over the 5 years since their expression profiling, and 300 of these patients report that they have experienced a myocardial infarction and 700 report that they have not, then the 300 patients define a new "group A." As the algorithm is used to continually query and revise the database, a new diagnostic nucleotide set that differentiates groups A and B (i.e., with and without myocardial infarction within a five year period) is identified. This newly defined nucleotide set is then be used (in the manner described above) as a test that predicts the occurrence of myocardial infarction over a five-year period. While submission directly by the patient is exemplified above, any individual with access and authority to submit the relevant data e.g., the patient's physician, a laboratory technician, a health care or study administrator, or the like, can do so.

As will be apparent from the above examples, transmission of information via the internet (or via an intranet) is optionally bi-directional. That is, for example, data regarding expression profiles, subject data, and the like are transmitted via a communication system to the database, while information regarding molecular signatures, predictive analysis, and the like, are transmitted from the database to the user. For example, using appropriate configurations of an integrated system including a microarray comprising a diagnostic nucleotide set, a detector linked to a computational device can directly transmit (locally or from a remote workstation at great distance, e.g., hundreds or thousands of miles distant from the database) expression profiles and a corresponding individual identifier to a central database for analysis according to the methods of the invention. According to, e.g., the algorithms described above, the individual identifier is assigned to one or more diagnostic (or prognostic, or monitoring, etc.) categories. The results of this classification are then

relayed back, via, e.g., the same mode of communication, to a recipient at the same or different internet (or intranet) address.

Kits

The present invention is optionally provided to a user as a kit. Typically, a kit contains one or more diagnostic nucleotide sets of the invention. Alternatively, the kit contains the candidate nucleotide library of the invention. Most often, the kit contains a diagnostic nucleotide probe set, or other subset of a candidate library, e.g., as a cDNA or antibody microarray packaged in a suitable container. The kit may further comprise, one or more additional reagents, e.g., substrates, labels, primers, for labeling expression products, tubes and/or other accessories, reagents for collecting blood samples, buffers, e.g., erythrocyte lysis buffer, leukocyte lysis buffer, hybridization chambers, cover slips, etc., as well as a software package, e.g., including the statistical methods of the invention, e.g., as described above, and a password and/or account number for accessing the compiled database. The kit optionally further comprises an instruction set or user manual detailing preferred methods of using the diagnostic nucleotide sets in the methods of the invention. Exemplary kits are described in Figure 3.

This invention will be better understood by reference to the following non-limiting Examples:

EXAMPLES

List of Example titles

Example 1: Generation of subtracted leukocyte candidate nucleotide library

Example 2: Identification of nucleotide sequences for candidate library using data mining techniques

Example 3: DNA Sequencing and Processing of raw sequence data.

Example 4: Further sequence analysis of novel nucleotide sequences identified by subtractive hybridization screening

Example 5: Further sequence analysis of novel Clone 596H6

Example 6: Further sequence analysis of novel Clone 486E11

Example 7: Preparation of a leukocyte cDNA array comprising a candidate gene library

Example 8: Preparation of RNA from mononuclear cells for expression profiling

Example 9: Preparation of Buffy Coat Control RNA for use in leukocyte expression profiling

Example 10. RNA Labeling and hybridization to a leukocyte cDNA array of candidate nucleotide sequences.

Example 11: Identification of diagnostic gene sets useful in diagnosis and treatment of Cardiac allograft rejection

Example 12: Identification of diagnostic nucleotide sets for kidney and liver allograft rejection

Example 13: Identification of diagnostic nucleotide sequences sets for use in the diagnosis and treatment of Atherosclerosis, Stable Angina Pectoris, and acute coronary syndrome.

Example 14: Identification of diagnostic nucleotide sets for use in diagnosing and treating Restenosis

Example 15: Identification of diagnostic nucleotide sets for use in monitoring treatment and/or progression of Congestive Heart Failure

Example 16: Identification of diagnostic nucleotide sets for use in diagnosis of rheumatoid arthritis.

Example 17: Identification of diagnostic nucleotide sets for diagnosis of cytomegalovirus

Example 18: Identification of diagnostic nucleotide sets for diagnosis of Epstein Barr Virus

Example 19: Identification of diagnostic nucleotides sets for monitoring response to statin drugs.

Example 20: Probe selection for a 24,000 feature Array.

Example 21: Design of oligonucleotide probes.

Example 22: Production of an array of 8,000 spotted 50 mer oligonucleotides.

Example 23: Amplification, labeling and hybridization of total RNA to an oligonucleotide microarray.

Example 24: Analysis of Human Transplant Patient Mononuclear cell RNA Hybridized to a 24,000 Feature Microarray.

Examples

Example 1: Generation of subtracted leukocyte candidate nucleotide library

To produce a candidate nucleotide library with representatives from the spectrum of nucleotide sequences that are differentially expressed in leukocytes, subtracted hybridization libraries were produced from the following cell types and conditions:

1. Buffy Coat leukocyte fractions - stimulated with ionomycin and PMA
2. Buffy Coat leukocyte fractions – un-stimulated
3. Peripheral blood mononuclear cells – stimulated with ionomycin and PMA
4. Peripheral blood mononuclear cells – un-stimulated
5. T lymphocytes – stimulated with PMA and ionomycin
6. T lymphocytes – resting

Cells were obtained from multiple individuals to avoid introduction of bias by using only one person as a cell source.

Buffy coats (platelets and leukocytes that are isolated from whole blood) were purchased from Stanford Medical School Blood Center. Four buffy coats were used, each of which was derived from about 350 ml of whole blood from one donor individual. 10 ml of buffy coat sample was drawn from the sample bag using a needle and syringe. 40 ml of Buffer EL (Qiagen) was added per 10 ml of buffy coat to lyse red blood cells. The sample was placed on ice for 15 minutes, and cells were collected by centrifugation at 2000 rpm for 10 minutes. The supernatant was decanted and the cell pellet was re-suspended in leukocyte growth media supplemented with DNase (LGM-3 from Clonetics supplemented with Dnase at a final concentration of 30 U/ml). Cell density was determined using a hemocytometer. Cells were plated in media at a density of 1×10^6 cells/ml in a total volume of 30 ml in a T-75 flask (Corning). Half of the cells were stimulated with ionomycin and phorbol myristate acetate (PMA) at a final concentration of 1 μ g/ml and 62 ng/ml, respectively. Cells were incubated at 37°C and at 5% CO₂ for 3 hours, then cells were scraped off the flask and collected into 50 ml tubes. Stimulated and resting cell populations were kept separate. Cells were centrifuged at 2000 rpm for 10 minutes and the supernatant was removed. Cells were lysed in 6 ml of phenol/guanidine isothiocyanate (Trizol reagent, GibcoBRL), homogenized using a rotary

homogenizer, and frozen at 80°. Total RNA and mRNA were isolated as described below.

Two frozen vials of 5×10^6 human peripheral blood mononuclear cells (PBMCs) were purchased from Clonetics (catalog number cc-2702). The cells were rapidly thawed in a 37°C water bath and transferred to a 15 ml tube containing 10 ml of leukocyte growth media supplemented with DNase (prepared as described above). Cells were centrifuged at 200g for 10 minutes. The supernatant was removed and the cell pellet was resuspended in LGM-3 media supplemented with DNase. Cell density was determined using a hemocytometer. Cells were plated at a density of 1×10^6 cells/ml in a total volume of 30 ml in a T-75 flask (Corning). Half of the cells were stimulated with ionomycin and PMA at a final concentration of 1 µg/ml and 62 ng/ml, respectively. Cells were incubated at 37°C and at 5% CO₂ for 3 hours, then cells were scraped off the flask and collected into 50 ml tubes. Stimulated and resting cell populations were kept separate. Cells were centrifuged at 2000 rpm and the supernatant was removed. Cells were lysed in 6 ml of phenol/guanidine isothiocyanate solution (TRIZOL reagent, GibcoBRL), homogenized using a rotary homogenizer, and frozen at 80°. Total RNA and mRNA were isolated from these samples using the protocol described below.

45 ml of whole blood was drawn from a peripheral vein of four healthy human subjects into tubes containing anticoagulant. 50 µl RosetteSep (Stem Cell Technologies) cocktail per ml of blood was added, mixed well, and incubated for 20 minutes at room temperature. The mixture was diluted with an equal volume of PBS + 2% fetal bovine serum (FBS) and mixed by inversion. 30 ml of diluted mixture sample was layered on top of 15 ml DML medium (Stem Cell Technologies). The sample tube was centrifuged for 20 minutes at 1200xg at room temperature. The enriched T-lymphocyte cell layer at the plasma : medium interface was removed. Enriched cells were washed with PBS + 2% FBS and centrifuged at 1200 x g. The cell pellet was treated with 5 ml of erythrocyte lysis buffer (EL buffer, Qiagen) for 10 minutes on ice. The sample was centrifuged for 5 min at 1200g. Cells were plated at a density of 1×10^6 cells/ml in a total volume of 30 ml in a T-75 flask (Corning). Half of the cells were stimulated with ionomycin and PMA at a final concentration of 1 µg/ml and 62 ng/ml, respectively. Cells were incubated at 37°C and at 5% CO₂ for 3 hours, then cells were scraped off the flask and collected into 50 ml tubes. Stimulated and resting cell populations were kept separate. Cells were centrifuged at 2000 rpm

and the supernatant was removed. Cells were lysed in 6 ml of phenol/guanidine isothiocyanate solution (TRIZOL reagent, GibcoBRL), homogenized using a rotary homogenizer, and frozen at 80°. Total RNA and mRNA were isolated as described below.

Total RNA and mRNA were isolated using the following procedure: the homogenized samples were thawed and mixed by vortexing. Samples were lysed in a 1:0.2 mixture of Trizol and chloroform, respectively. For some samples, 6 ml of Trizol-chloroform was added. Variable amounts of Trizol-chloroform was added to other samples. Following lysis, samples were centrifuged at 3000 g for 15 min at 4°C. The aqueous layer was removed into a clean tube and 4 volumes of Buffer RLT (Qiagen) was added for every volume of aqueous layer. The samples were mixed thoroughly and total RNA was prepared from the sample by following the Qiagen Rneasy midi protocol for RNA cleanup (October 1999 protocol, Qiagen). For the final step, the RNA was eluted from the column twice with 250 µl RNase-free water. Total RNA was quantified using a spectrophotometer. Isolation of mRNA from total RNA sample was done using The Oligotex mRNA isolation protocol (Qiagen) was used to isolate mRNA from total RNA, according to the manufacturer's instructions (Qiagen, 7/99 version). mRNA was quantified by spectrophotometry.

Subtracted cDNA libraries were prepared using Clontech's PCR-Select cDNA Subtraction Kit (protocol number PT-1117-1) as described in the manufacturer's protocol. The protocol calls for two sources of RNA per library, designated "Driver" and "Tester." The following 6 libraries were made:

| <u>Library</u> | <u>Driver RNA</u> | <u>Tester RNA</u> |
|-----------------------|--------------------------|--------------------------|
| Buffy Coat Stimulated | Un-stimulated Buffy Coat | Stimulated Buffy Coat |
| Buffy Coat Resting | Stimulated Buffy Coat | Un-stimulated Buffy Coat |
| PBMC Stimulated | Un-stimulated PBMCs | Stimulated PBMCs |
| PBMC Resting | Stimulated PBMCs | Un-stimulated PBMCs |
| T-cell Stimulated | Un-stimulated T-cells | Stimulated T-cells |
| T-cell Resting | Stimulated T-cells | Un-stimulated T-cells |

The Clontech protocol results in the PCR amplification of cDNA products.

The PCR products of the subtraction protocol were ligated to the pGEM T-easy bacterial vector as described by the vector manufacturer (Promega 6/99 version). Ligated vector was transformed into competent bacteria using well-known techniques,

plated, and individual clones are picked, grown and stored as a glycerol stock at –80C. Plasmid DNA was isolated from these bacteria by standard techniques and used for sequence analysis of the insert. Unique cDNA sequences were searched in the Unigene database (build 133), and Unigene cluster numbers were identified that corresponded to the DNA sequence of the cDNA. Unigene cluster numbers were recorded in an Excel spreadsheet.

Example 2: Identification of nucleotide sequences for candidate library using data mining techniques

Existing and publicly available gene sequence databases were used to identify candidate nucleotide sequences for leukocyte expression profiling. Genes and nucleotide sequences with specific expression in leukocytes, for example, lineage specific markers, or known differential expression in resting or activated leukocytes were identified. Such nucleotide sequences are used in a leukocyte candidate nucleotide library, alone or in combination with nucleotide sequences isolated through cDNA library construction, as described above.

Leukocyte candidate nucleotide sequences were identified using three primary methods. First, the publically accessible publication database PubMed was searched to identify nucleotide sequences with known specific or differential expression in leukocytes. Nucleotide sequences were identified that have been demonstrated to have differential expression in peripheral blood leukocytes between subjects with and without particular disease(s) selected from Table 1. Additionally, genes and gene sequences that were known to be specific or selective for leukocytes or sub-populations of leukocytes were identified in this way.

Next, two publicly available databases of DNA sequences, Unigene (<http://www.ncbi.nlm.nih.gov/UniGene/>) and BodyMap (<http://bodymap.ims.u-tokyo.ac.jp/>), were searched for sequenced DNA clones that showed specificity to leukocyte lineages, or subsets of leukocytes, or resting or activated leukocytes.

The human Unigene database (build 133) was used to identify leukocyte candidate nucleotide sequences that were likely to be highly or exclusively expressed in leukocytes. We used the Library Differential Display utility of Unigene (<http://www.ncbi.nlm.nih.gov/UniGene/info/ddd.html>), which uses statistical methods (The Fisher Exact Test) to identify nucleotide sequences that have relative specificity

for a chosen library or group of libraries relative to each other. We compared the following human libraries from Unigene release 133:

546 NCI_CGAP_HSC1 (399)
 848 Human_mRNA_from_cd34+_stem_cells (122)
 105 CD34+DIRECTIONAL (150)
 3587 KRIBB_Human_CD4_intrathymic_T-cell_cDNA_library (134)
 3586 KRIBB_Human_DP_intrathymic_T-cell_cDNA_library (179)
 3585 KRIBB_Human_TN_intrathymic_T-cell_cDNA_library (127)
 3586 323 Activated_T-cells_I (740)
 376 Activated_T-cells_XX (1727)
 327 Monocytes,_stimulated_II (110)
 824 Proliferating_Erythroid_Cells_(LCB:ad_library) (665)
 825 429 Macrophage_II (105)
 387 Macrophage_I (137)
 669 NCI_CGAP_CLL1 (11626)
 129 Human_White_blood_cells (922)
 1400 NIH_MGC_2 (422)
 55 Human_promyelocyte (1220)
 1010 NCI_CGAP_CML1 (2541)
 2217 NCI_CGAP_Sub7 (218)
 1395 NCI_CGAP_Sub6 (2764)
 4874 NIH_MGC_48 (2524)

BodyMap, like Unigene, contains cell-specific libraries that contain potentially useful information about genes that may serve as lineage-specific or leukocyte specific markers (Okubo et al. 1992). We compared three leukocyte specific libraries, Granulocyte, CD4 T cell, and CD8 T cell, with the other libraries. Nucleotide sequences that were found in one or more of the leukocyte-specific libraries, but absent in the others, were identified. Clones that were found exclusively in one of the three leukocyte libraries were also included in a list of nucleotide sequences that could serve as lineage-specific markers.

Next, the sequence of the nucleotide sequences identified in PubMed or BodyMap were searched in Unigene (version 133), and a human Unigene cluster number was identified for each nucleotide sequence. The cluster number was

recorded in a Microsoft Excel™ spreadsheet, and a non-redundant list of these clones was made by sorting the clones by UniGene number, and removing all redundant clones using Microsoft Excel™ tools. The non-redundant list of UniGene cluster numbers was then compared to the UniGene cluster numbers of the cDNAs identified using differential cDNA hybridization, as described above in Example 1 (listed in Table 3 and the sequence listing). Only UniGene clusters that were not contained in the cDNA libraries were retained. Unigene clusters corresponding to 1911 candidate nucleotide sequences for leukocyte expression profiling were identified in this way and are listed in Table 3 and the sequence listing.

DNA clones corresponding to each UniGene cluster number are obtained in a variety of ways. First, a cDNA clone with identical sequence to part of, or all of the identified UniGene cluster is bought from a commercial vendor or obtained from the IMAGE consortium (<http://image.llnl.gov/>, the Integrated Molecular Analysis of Genomes and their Expression). Alternatively, PCR primers are designed to amplify and clone any portion of the nucleotide sequence from cDNA or genomic DNA using well-known techniques. Alternatively, the sequences of the identified UniGene clusters are used to design and synthesize oligonucleotide probes for use in microarray based expression profiling.

Example 3: DNA Sequencing and Processing of raw sequence data.

Clones of differentially expressed cDNAs (identified by subtractive hybridization, described above) were sequenced on an MJ Research BaseStation™ slab gel based fluorescent detection system, using BigDye™ (Applied Biosystems, Foster City, CA) terminator chemistry was used (Heiner et al., Genome Res 1998 May;8(5):557-61).

The fluorescent profiles were analyzed using the Phred sequence analysis program (Ewing et al, (1998), Genome Research 8: 175-185). Analysis of each clone results in a one pass nucleotide sequence and a quality file containing a number for each base pair with a score based on the probability that the determined base is correct. Each sequence files and its respective quality files were initially combined into single fasta format (Pearson, WR. Methods Mol Biol. 2000;132:185-219), multi-sequence file with the appropriate labels for each clone in the headers for subsequent automated analysis.

Initially, known sequences were analyzed by pair wise similarity searching using the blastn option of the blastall program obtained from the National Center for Biological Information, National Library of Medicine, National Institutes of Health (NCBI) to determine the quality score that produced accurate matching (Altschul SF, et al. J Mol Biol. 1990 Oct 5;215(3):403-10.). Empirically, it was determined that a raw score of 8 was the minimum that contained useful information. Using a sliding window average for 16 base pairs, an average score was determined. The sequence was removed (trimmed) when the average score fell below 8. Maximum reads were 950 nucleotides long.

Next, the sequences were compared by similarity matching against a database file containing the flanking vector sequences used to clone the cDNA, using the blastall program with the blastn option. All regions of vector similarity were removed, or “trimmed” from the sequences of the clones using scripts in the GAWK programming language, a variation of AWK (Aho AV et al, The Awk Programming Language (Addison-Wesley, Reading MA, 1988); Robbins, AD, “Effective AWK Programming” (Free Software Foundation, Boston MA, 1997). It was found that the first 45 base pairs of all the sequences were related to vector; these sequences were also trimmed and thus removed from consideration. The remaining sequences were then compared against the NCBI vector database (Kitts, P.A. et al. National Center for Biological Information, National Library of Medicine, National Institutes of Health, Manuscript in preparation (2001) using blastall with the blastn option. Any vector sequences that were found were removed from the sequences.

Messenger RNA contains repetitive elements that are found in genomic DNA. These repetitive elements lead to false positive results in similarity searches of query mRNA sequences versus known mRNA and EST databases. Additionally, regions of low information content (long runs of the same nucleotide, for example) also result in false positive results. These regions were masked using the program RepeatMasker2 found at <http://repeatmasker.genome.washington.edu> (Smit, AFA & Green, P “RepeatMasker” at <http://ftp.genome.washington.edu/RM/RepeatMasker.html>). The trimmed and masked files were then subjected to further sequence analysis.

Example 4: Further sequence analysis of novel nucleotide sequences identified by subtractive hybridization screening

cDNA sequences were further characterized using BLAST analysis. The BLASTN program was used to compare the sequence of the fragment to the UniGene, dbEST, and nr databases at NCBI (GenBank release 123.0; see Table 5). In the BLAST algorithm, the expect value for an alignment is used as the measure of its significance. First, the cDNA sequences were compared to sequences in Unigene (<http://www.ncbi.nlm.nih.gov/UniGene>). If no alignments were found with an expect value less than 10^{-25} , the sequence was compared to the sequences in the dbEST database using BLASTN. If no alignments were found with an expect value less than 10^{-25} , the sequence was compared to sequences in the nr database.

The BLAST analysis produced the following categories of results: a) a significant match to a known or predicted human gene, b) a significant match to a nonhuman DNA sequence, such as vector DNA or *E. coli* DNA, c) a significant match to an unidentified GenBank entry (a sequence not previously identified or predicted to be an expressed sequence or a gene), such as a cDNA clone, mRNA, or cosmid, or d) no significant alignments. If a match to a known or predicted human gene was found, analysis of the known or predicted protein product was performed as described below. If a match to an unidentified GenBank entry was found, or if no significant alignments were found, the sequence was searched against all known sequences in the human genome database (<http://www.ncbi.nlm.nih.gov/genome/seq/page.cgi?F=HsBlast.html&&ORG=Hs>, see Table 5).

If many unknown sequences were to be analyzed with BLASTN, the clustering algorithm CAP2 (Contig Assembly Program, version 2) was used to cluster them into longer, contiguous sequences before performing a BLAST search of the human genome. Sequences that can be grouped into contigs are likely to be cDNA from expressed genes rather than vector DNA, *E. coli* DNA or human chromosomal DNA from a noncoding region, any of which could have been incorporated into the library. Clustered sequences provide a longer query sequence for database comparisons with BLASTN, increasing the probability of finding a significant match to a known gene. When a significant alignment was found, further analysis of the putative gene was performed, as described below. Otherwise, the sequence of the

original cDNA fragment or the CAP2 contig is used to design a probe for expression analysis and further approaches are taken to identify the gene or predicted gene that corresponds to the cDNA sequence, including similarity searches of other databases, molecular cloning, and Rapid Amplification of cDNA Ends (RACE).

In some cases, the process of analyzing many unknown sequences with BLASTN was automated by using the BLAST network-client program `blastcl3`, which was downloaded from <ftp://ncbi.nlm.nih.gov/blast/network/netblast>.

When a cDNA sequence aligned to the sequence of one or more chromosomes, a large piece of the genomic region around the loci was used to predict the gene containing the cDNA. To do this, the contig corresponding to the mapped locus, as assembled by the RefSeq project at NCBI, was downloaded and cropped to include the region of alignment plus 100,000 bases preceding it and 100,000 bases following it on the chromosome. The result was a segment 200 kb in length, plus the length of the alignment. This segment, designated a putative gene, was analyzed using an exon prediction algorithm to determine whether the alignment area of the unknown sequence was contained within a region predicted to be transcribed (see Table 6).

This putative gene was characterized as follows: all of the exons comprising the putative gene and the introns between them were taken as a unit by noting the residue numbers on the 200kb+ segment that correspond to the first base of the first exon and the last base of the last exon, as given in the data returned by the exon prediction algorithm. The truncated sequence was compared to the UniGene, dbEST, and nr databases to search for alignments missed by searching with the initial fragment.

The predicted amino acid sequence of the gene was also analyzed. The peptide sequence of the gene predicted from the exons was used in conjunction with numerous software tools for protein analysis (see Table 7). These were used to classify or identify the peptide based on similarities to known proteins, as well as to predict physical, chemical, and biological properties of the peptides, including secondary and tertiary structure, flexibility, hydrophobicity, antigenicity (hydrophilicity), common domains and motifs, and localization within the cell or tissues. The peptide sequence was compared to protein databases, including SWISS-PROT, TrEMBL, GenPept, PDB, PIR, PROSITE, ProDom, PROSITE, Blocks,

PRINTS, and Pfam, using BLASTP and other algorithms to determine similarities to known proteins or protein subunits.

Example 5: Further sequence analysis of novel Clone 596H6

The sequence of clone 596H6 is provided below:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| ACTATATTTA | GGCACCCTG | CCATAAACTA | CCAAAAA | AATGTAATTC | 50 |
| CTAGAAGCTG | TGAAGAATAG | TAGTGTAGCT | AAGCACGGTG | TGTGGACAGT | 100 |
| GGGACATCTG | CCACCTGCAG | TAGGTCTCTG | CACTCCCAA | AGCAAATTAC | 150 |
| ATTGGCTTGA | ACTTCAGTAT | GCCCGGTTCC | ACCCTCCAGA | AACTTTTGTG | 200 |
| TTCTTTGTAT | AGAATTTAGG | AACTTCTGAG | GGCCACAAAT | ACACACATTA | 250 |
| AAAAAGGTAG | AATTTTGGAA | GATAAGATTC | TTCTAAAAA | GCTTCCCAAT | 300 |
| GCTTGAGTAG | AAAGTATCAG | TAGAGGTATC | AAGGGAGGAG | AGACTAGGTG | 350 |
| ACCACTAAAC | TCCTTCAGAC | TCTTAAAT | ACGATTCTTT | TCTCAAAGGG | 400 |
| GAAGAACGTC | AGTGCAGCGA | TCCCTTCACC | TTTAGCTAAA | GAATTGGACT | 450 |
| GTGCTGCTCA | AAATAAAGAT | CAGTTGGAGG | TANGATGTCC | AAGACTGAAG | 500 |
| GTAAAGGACT | AGTGCAAAC | GAAAGTGATG | GGGAAACAGA | CCTACGTATG | 550 |
| GAAGCCATGT | AGTGTTCTTC | ACAGGCTGCT | GTTGACTGAA | ATTCCTATCC | 600 |
| TCAAATTACT | CTAGACTGAA | GCTGCTTCCC | TTCAGTGAGC | AGCCTCTCCT | 650 |
| TCCAAGATTC | TGGAAAGCAC | ACCTGACTCC | AAACAAAGAC | TTAGAGCCCT | 700 |
| GTGTCAGTGC | TGCTGCTGCT | TTTACCAGAT | TCTCTAACCT | TCCGGGTAGA | 750 |

AGAG (SEQ ID NO: 8767)

This sequence was used as input for a series of BLASTN searches. First, it was used to search the UniGene database, build 132 (<http://www.ncbi.nlm.nih.gov/BLAST/>). No alignments were found with an expect value less than the threshold value of 10^{-25} . A BLASTN search of the database dbEST, release 041001, was then performed on the sequence and 21 alignments were found (<http://www.ncbi.nlm.nih.gov/BLAST/>). Ten of these had expect values less than 10^{-25} , but all were matches to unidentified cDNA clones. Next, the sequence was used to run a BLASTN search of the nr database, release 123.0. No significant alignment to any sequence in nr was found. Finally, a BLASTN search of the human genome was performed on the sequence (<http://www.ncbi.nlm.nih.gov/genome/seq/page.cgi?F=HsBlast.html&&ORG=Hs>).

A single alignment to the genome was found on contig NT_004698.3 (e=0.0). The region of alignment on the contig was from base 1,821,298 to base 1,822,054,

and this region was found to be mapped to chromosome 1, from base 105,552,694 to base 105,553,450. The sequence containing the aligned region, plus 100 kilobases on each side of the aligned region, was downloaded. Specifically, the sequence of chromosome 1 from base 105,452,694 to 105,653,450 was downloaded (http://www.ncbi.nlm.nih.gov/cgi-bin/Entrez/seq_reg.cgi?chr=1&from=105452694&to=105653450).

This 200,757 bp segment of the chromosome was used to predict exons and their peptide products as follows. The sequence was used as input for the Genscan algorithm (<http://genes.mit.edu/GENSCAN.html>), using the following Genscan settings:

Organism: vertebrate

Suboptimal exon cutoff: 1.00 (no suboptimal exons)

Print options: Predicted CDS and peptides

The region matching the sequence of clone 596H6 was known to span base numbers 100,001 to 100,757 of the input sequence. An exon was predicted by the algorithm, with a probability of 0.695, covering bases 100,601 to 101,094 (designated exon 4.14 of the fourth predicted gene). This exon was part of a predicted cistron that is 24,195 bp in length. The sequence corresponding to the cistron was noted and saved separately from the 200,757 bp segment. BLASTN searches of the Unigene, dbEST, and nr databases were performed on it.

At least 100 significant alignments to various regions of the sequence were found in the dbEST database, although most appeared to be redundant representations of a few exons. All matches were to unnamed cDNAs and mRNAs (unnamed cDNAs and mRNAs are cDNAs and mRNAs not previously identified, or shown to correspond to a known or predicted human gene) from various tissue types. Most aligned to a single region on the sequence and spanned 500 bp or less, but several consisted of five or six regions separated by gaps, suggesting the locations of exons in the gene. Several significant matches to entries in the UniGene database were found, as well, even after masking low-complexity regions and short repeats in the sequence. All matches were to unnamed cDNA clones.

At least 100 significant alignments were found in the nr database, as well. A similarity to hypothetical protein FLJ22457 (UniGene cluster Hs.238707) was found ($e=0.0$). The cDNA of this predicted protein has been isolated from B lymphocytes

(<http://www.ncbi.nlm.nih.gov/entrez/viewer.cgi?save=0&cmd=&cfm=on&f=1&view=gp&txt=0&val=13637988>).

Other significant alignments were to unnamed cDNAs and mRNAs.

Using Genscan, the following 730 residue peptide sequence was predicted from the putative gene:

| | | | | | |
|-------------|------------|------------|----------------|-------------|---|
| MDGLGRRLRA | SLRLKRGHGG | HWRLNEMPYM | KHEFDGGPPQ | DNSGEALKEP | 5 |
| ERAQEHSLPN | FAGGQHFFEY | LLVVSLLKKR | SEDDYEPIIT | YQFPKRENLL | 1 |
| RGQQEEEEERL | LKAIPFCFP | DGNEWASLTE | YPSLSCKTPG | LLAALVVEKA | 1 |
| QPRTCCHASA | PSAAPQARGP | DAPSPAAGQA | LPAGPGPRLP | KVYCIISCIG | 2 |
| CFGLFSKILD | EVEKRHQISM | AVIYPFMQGL | REAAFPAPGK | TVTLKSFIPD | 2 |
| SGTEFISLTR | PLDSHLEHVD | FSSLLHCLSF | EQILQIFASA | VLERKIIFLA | 3 |
| EGLREEEKDV | RDSTEVRGAG | ECHGFQRKGN | LGKQWGLCVE | DSVKMGDNQR | 3 |
| GTSCSTLSQC | IHAAAALLYP | FSWAHTYIPV | VPESLLATVC | CPTPFMVG VQ | 4 |
| MRFQQEVMSD | PMEEIQPAE | IKTVNPLGVY | EERGPEKASL | CLFQVLLVNL | 4 |
| CEGTFLMSVG | DEKDILPPKL | QDDILDSLQ | GINELKTAEQ | INEHVSGPFV | 5 |
| QFFVKIVGHY | ASYIKREANG | QGHFQERSFC | KALTSKTNRR | FVKKFVKTQL | 5 |
| FSLFIQAEK | SKNPPAEVTQ | VGNSSTCVVD | TWLEAAATAL | SHHYNIFNTE | 6 |
| HTLWSKGSAS | LHEVCGHVRT | RVKRKILFLY | VSLAFTMGKS | IFLVENKAMN | 6 |
| MTIKWTTSGR | PGHGDMFGVI | ESWGAAALLL | LTGRVRDTGK | SSSSTGHRAS | 7 |
| KSLVWSQVCF | PESWEERLLT | EGKQLQSRVI | SEQ ID NO:8768 | | |

Multiple analyses were performed using this prediction. First, a pairwise comparison of the sequence above and the sequence of FLJ22457, the hypothetical protein mentioned above, using BLASTP version 2.1.2

(<http://ncbi.nlm.nih.gov/BLAST/>), resulted in a match with an expect value of 0.0.

The peptide sequence predicted from clone 596H6 was longer and 19% of the region of alignment between the two resulted from gaps in hypothetical protein FLJ22457. The cause of the discrepancy might be alternative mRNA splicing, alternative post-translational processing, or differences in the peptide-predicting algorithms used to create the two sequences, but the homology between the two is significant.

BLASTP and TBLASTN were also used to search for sequence similarities in the SWISS-PROT, TrEMBL, GenBank Translated, and PDB databases. Matches to several proteins were found, among them a tumor cell suppression protein, HTS1. No

matches aligned to the full length of the peptide sequence, however, suggesting that similarity is limited to a few regions of the peptide.

TBLASTN produced matches to several proteins – both identified and theoretical – but again, no matches aligned to the full length of the peptide sequence. The best alignment was to the same hypothetical protein found in GenBank before (FLJ22457).

To discover similarities to protein families, comparisons of the domains (described above) were carried out using the Pfam and Blocks databases. A search of the Pfam database identified two regions of the peptide domains as belonging to the DENN protein family ($e=2.1 \times 10^{-33}$). The human DENN protein possesses an RGD cellular adhesion motif and a leucine-zipper-like motif associated with protein dimerization, and shows partial homology to the receptor binding domain of tumor necrosis factor alpha. DENN is virtually identical to MADD, a human MAP kinase-activating death domain protein that interacts with type I tumor necrosis factor receptor ([http://srs.ebi.ac.uk/srs6bin/cgi-bin/wgetz?-id+fS5n1GQsHf+-e+\[INTERPRO:'IPR001194'\]](http://srs.ebi.ac.uk/srs6bin/cgi-bin/wgetz?-id+fS5n1GQsHf+-e+[INTERPRO:'IPR001194'])). The search of the Blocks database also revealed similarities between regions of the peptide sequence and known protein groups, but none with a satisfactory degree of confidence. In the Blocks scoring system, scores over 1,100 are likely to be relevant. The highest score of any match to the predicted peptide was 1,058.

The Prosite, ProDom, PRINTS databases (all publicly available) were used to conduct further domain and motif analysis. The Prosite search generated many recognized protein domains. A BLASTP search was performed to identify areas of similarity between the protein query sequence and PRINTS, a protein database of protein fingerprints, groups of motifs that together form a characteristic signature of a protein family. In this case, no groups were found to align closely to any section of the submitted sequence. The same was true when the ProDom database was searched with BLASTP.

A prediction of protein structure was done by performing a BLAST search of the sequence against PDB, a database in which every member has tertiary structure information. No significant alignments were found by this method. Secondary and super-secondary structure was examined using the Garnier algorithm. Although it is only considered to be 60-65% accurate, the algorithm provided information on the locations and lengths of alpha-helices, beta-sheets, turns and coils.

The antigenicity of the predicted peptide was modeled by graphing hydrophilicity vs. amino acid number. This produced a visual representation of trends in hydrophilicity along the sequence. Many locations in the sequence showed antigenicity and five sites had antigenicity greater than 2. This information can be used in the design of affinity reagents to the protein.

Membrane-spanning regions were predicted by graphing hydrophobicity vs. amino acid number. Thirteen regions were found to be somewhat hydrophobic. The algorithm TMPred predicted a model with 6 strong transmembrane helices (http://www.ch.embnet.org/software/TMPRED_form.html).

NNPSL is a neural network algorithm developed by the Sanger Center. It uses amino acid composition and sequence to predict cellular location. For the peptide sequence submitted, its first choice was mitochondrial (51.1% expected accuracy). Its second choice was cytoplasmic (91.4% expected accuracy).

Example 6: Further sequence analysis of novel Clone 486E11

The sequence of clone 486E11 is provided below:

| | | | | | |
|------------|------------|------------|-----------------|------------|---|
| TAAAAGCAGG | CTGTGCACTA | GGGACCTAGT | GACCTTACTA | GAAAAAACTC | 5 |
| AAATTCTCTG | AGCCACAAGT | CCTCATGGGC | AAAATGTAGA | TACCACCACC | 1 |
| TAACCCTGCC | AATTCCTAT | CATTGTGACT | ATCAAATTAA | ACCACAGGCA | 1 |
| GGAAGTTGCC | TTGAAAACCT | TTTATAGTGT | ATATTACTGT | TCACATAGAT | 2 |
| NAGCAATTAA | CTTTACATAT | ACCCGTTTTT | AAAAGATCAG | TCCTGTGATT | 2 |
| AAAAGTCTGG | CTGCCCTAAT | TCACTTCGAT | TATACATTAG | GTAAAGCCA | 3 |
| TATAAAAGAG | GCACTACGTC | TTCGGAGAGA | TGAATGGATA | TTACAAGCAG | 3 |
| TAATGTTGGC | TTTGGAATAT | ACACATAATG | TCCACTTGAC | CTCATCTATT | 4 |
| TGACACAAAA | TGTAAACTAA | ATTATGAGCA | TCATTAGATA | CCTTGGCCTT | 4 |
| TTCAAATCAC | ACAGGGTCCT | AGATCTNNNN | NNNNNNNNNN | NNNNNNNNNN | 5 |
| NNNNNNNNNN | NNNNNNNNNN | NNNNNNNNNN | NNNNNNNNAC | TTGGGATTC | 5 |
| CTATATCTTT | GTCAGCTGTC | AACTTCAGTG | TTTTCAGGTT | AAATTCTATC | 6 |
| CATAGTCATC | CCAATATACC | TGCTTTAGAT | GATACAACCT | TCAAAAGATC | 6 |
| CGCTCTTCCT | CGTAAAAAGT | GGAG | SEQ ID NO: 8769 | | |

The BLASTN program was used to compare the sequence to the UniGene and dbEST databases. No significant alignments were found in either. It was then searched against the nr database and only alignments to unnamed genomic DNA clones were found.

CAP2 was used to cluster a group of unknowns, including clone 486E11. The sequence for 486E11 was found to overlap others. These formed a contig of 1,010 residues, which is shown below:

| | | | | | |
|------------|-----------------|------------|------------|-------------|-----|
| CGGACAGGTA | CCTAAAAGCA | GGCTGTGCAC | TAGGGACCTA | GTGACCTTAC | 50 |
| TAGAAAAAAC | TCAAATTCTC | TGAGCCACAA | GTCCTCATGG | GCAAAATGTA | 10 |
| GATACCACCA | CCTAACCCTG | CCAATTTCTT | ATCATTGTGA | CTATCAAATT | 15 |
| AAACCACAGG | CAGGAAGTTG | CCTTGAAAAC | TTTTTATAGT | GTATATTACT | 20 |
| GTTACATAG | ATNAGCAATT | AACTTTACAT | ATACCCGTTT | TTAAAAGATC | 25 |
| AGTCCTGTGA | TTAAAAGTCT | GGCTGCCCTA | ATTCACTTCG | ATTATACATT | 30 |
| AGGTAAAGC | CATATAAAAG | AGGCACTACG | TCTTCGGAGA | GATGAATGGA | 35 |
| TATTACAAGC | AGTAATTTTG | GCTTTGGAAT | ATACACATAA | TGTCCACTTG | 40 |
| ACCTCATCTA | TTTGACACAA | AATGTAAACT | AAATTATGAG | CATCATTAGA | 45 |
| TACCTTGGGC | CTTTTCAAAT | CACACAGGGT | CCTAGATCTG | NNNNNNNNNN | 50 |
| NNNNNNNNNN | NNNNNNNNNN | NNNNNNNNNN | NNNNNNNNNN | NNNNNNNNNN | 55 |
| NACTTTGGAT | TCTTATATCT | TTGTCAGCTG | TCAACTTCAG | TGTTTTTCAGG | 60 |
| NTAAATTCTA | TCCATAGTCA | TCCCAATATA | CCTGCTTTAG | ATGATACAAA | 65 |
| CTTCAAAAGA | TCCGGCTCTC | CCTCGTAAAA | CGTGGAGGAC | AGACATCAAG | 70 |
| GGGGTTTTCT | GAGTAAAGAA | AGGCAACCGC | TCGGCAAAAA | CTCACCCCTGG | 75 |
| CACAACAGGA | NCGAATATAT | ACAGACGCTG | ATTGAGCGTT | TTGCTCCATC | 80 |
| TTCACTTCTG | TTAAATGAAG | ACATTGATAT | CTAAAATGCT | ATGAGTCTAA | 85 |
| CTTTGTAAAA | TTAAAATAGA | TTTGTAGTTA | TTTTTCAAAA | TGAAATCGAA | 90 |
| AAGATACAAG | TTTTGAAGGC | AGTCTCTTTT | TCCACCCTGC | CCCTCTAGTG | 95 |
| TGTTTTACAC | ACTTCTCTGG | CCACTCCAAC | AGGGAAGCTG | GTCCAGGGCC | 100 |
| ATTATACAGG | SEQ ID NO: 8832 | | | | |

The sequence of the CAP2 contig was used in a BLAST search of the human genome. 934 out of 1,010 residues aligned to a region of chromosome 21. A gap of 61 residues divided the aligned region into two smaller fragments. The sequence of this region, plus 100 kilobases on each side of it, was downloaded and analyzed using the Genscan site at MIT (<http://genes.mit.edu/GENSCAN.html>), with the following settings:

Organism: vertebrate

Suboptimal exon cutoff: 1.00 (no suboptimal exons)

Print options: Predicted CDS and peptides

The fragment was found to fall within one of several predicted genes in the chromosome region. The bases corresponding to the predicted gene, including its predicted introns, were saved as a separate file and used to search GenBank again with BLASTN to find any ESTs or UniGene clusters identified by portions of the sequence not included in the original unknown fragment. The nr database contained no significant matches. At least 100 significant matches to various parts of the predicted gene were found in the dbEST database, but all of them were to unnamed cDNA clones. Comparison to UniGene produced fewer significant matches, but all matches were to unnamed cDNAs.

The peptide sequence predicted by Genscan was also saved. Multiple types of analyses were performed on it using the resources mentioned in Table 3. BLASTP and TBLASTN were used to search the TrEMBL protein database (<http://www.expasy.ch/sprot/>) and the GenBank nr database (<http://www.ncbi.nlm.nih.gov/BLAST/>), which includes data from the SwissProt, PIR, PRF, and PDB databases. No significant matches were found in any of these, so no gene identity or tertiary structure was discovered.

The peptide sequence was also searched for similarity to known domains and motifs using BLASTP with the Prosite, Blocks, Pfam, and ProDom databases. The searches produced no significant alignments to known domains. BLASTP comparison to the PRINTS database produced an alignment to the P450 protein family, but with a low probability of accuracy ($e=6.9$).

Two methods were used to predict secondary structure – the Garnier/Osguthorpe/Robson model and the Chou-Fasman model. The two methods differed somewhat in their results, but both produced representations of the peptide sequence with helical and sheet regions and locations of turns.

Antigenicity was plotted as a graph with amino acid number in the sequence on the x-axis and hydrophilicity on the y-axis. Several areas of antigenicity were observed, but only one with antigenicity greater than 2. Hydrophobicity was plotted in the same way. Only one region, from approximately residue 135 to residue 150, had notable hydrophobicity. TMpred, accessed through ExPASy, was used to predict transmembrane helices. No regions of the peptide sequence were predicted with reasonable confidence to be membrane-spanning helices.

NNPSL predicted that the putative protein would be found either in the nucleus (expected prediction accuracy = 51.1%) or secreted from the cell (expected prediction accuracy = 91.4%).

Example 7: Preparation of a leukocyte cDNA array comprising a candidate gene

library

Candidate genes and gene sequences for leukocyte expression profiling were identified through methods described elsewhere in this document. Candidate genes are used to obtain or design probes for peripheral leukocyte expression profiling in a variety of ways.

A cDNA microarray carrying 384 probes was constructed using sequences selected from the cDNA libraries described in example 1. cDNAs were selected from T-cell libraries, PBMC libraries and buffy coat libraries. A listing of the cDNA fragments used is given in Table 8.

96-Well PCR

Plasmids were isolated in 96-well format and PCR was performed in 96-well format. A master mix was made that contain the reaction buffer, dNTPs, forward and reverse primer and DNA polymerase was made. 99 ul of the master mix was aliquoted into 96-well plate. 1 ul of plasmid (1-2 ng/ul) of plasmid was added to the plate. The final reaction concentration was 10 mM Tris pH 8.3, 3.5 mM MgCl₂, 25 mM KCl, 0.4 mM dNTPs, 0.4 uM M13 forward primer, 0.4 M13 reverse primer, and 10 U of Taq Gold (Applied Biosystems). The PCR conditions were:

- Step 1 95C for 10 min
- Step 2 95C for 15 sec
- Step 3 56C for 30 sec
- Step 4 72C for 2 min 15 seconds
- Step 5 go to Step 2 39 times
- Step 6 72C for 10 minutes
- Step 7 4C for ever.

PCR Purification

PCR purification was done in a 96-well format. The ArrayIt (Telechem International, Inc.) PCR purification kit was used and the provided protocol was followed without modification. Before the sample was evaporated to dryness, the

concentration of PCR products was determined using a spectrophotometer. After evaporation, the samples were re-suspended in 1x Micro Spotting Solution (ArrayIt) so that the majority of the samples were between 0.2-1.0 ug/ul.

Array Fabrication

Spotted cDNA microarrays were then made from these PCR products by ArrayIt using their protocols (http://arrayit.com/Custom_Microarrays/Flex-Chips/flex-chips.html). Each fragment was spotted 3 times onto each array.

Candidate genes and gene sequences for leukocyte expression profiling were identified through methods described elsewhere in this document. Those candidate genes are used for peripheral leukocyte expression profiling. The candidate libraries can be used to obtain or design probes for expression profiling in a variety of ways.

Oligonucleotide probes are also prepared using the DNA sequence information for the candidate genes identified by differential hybridization screening (listed in Table 3 and the sequence listing) and/or the sequence information for the genes identified by database mining (listed in Table 2) is used to design complementary oligonucleotide probes. Oligo probes are designed on a contract basis by various companies (for example, Compugen, Mergen, Affymetrix, Telechem), or designed from the candidate sequences using a variety of parameters and algorithms as indicated at <http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi>. Briefly, the length of the oligonucleotide to be synthesized is determined, preferably greater than 18 nucleotides, generally 18-24 nucleotides, 24-70 nucleotides and, in some circumstances, more than 70 nucleotides. The sequence analysis algorithms and tools described above are applied to the sequences to mask repetitive elements, vector sequences and low complexity sequences. Oligonucleotides are selected that are specific to the candidate nucleotide sequence (based on a Blast n search of the oligonucleotide sequence in question against gene sequences databases, such as the Human Genome Sequence, UniGene, dbEST or the non-redundant database at NCBI), and have <50% G content and 25–70% G+C content. Desired oligonucleotides are synthesized using well-known methods and apparatus, or ordered from a company (for example Sigma). Oligonucleotides are spotted onto microarrays. Alternatively, oligonucleotides are synthesized directly on the array surface, using a variety of techniques (Hughes et al. 2001, Yershov et al. 1996, Lockhart et al 1996).

Example 8: Preparation of RNA from mononuclear cells for expression profiling

Blood was isolated from the subject for leukocyte expression profiling using the following methods:

Two tubes were drawn per patient. Blood was drawn from either a standard peripheral venous blood draw or directly from a large-bore intra-arterial or intravenous catheter inserted in the femoral artery, femoral vein, subclavian vein or internal jugular vein. Care was taken to avoid sample contamination with heparin from the intravascular catheters, as heparin can interfere with subsequent RNA reactions.

For each tube, 8 ml of whole blood was drawn into a tube (CPT, Becton-Dickinson order #362753) containing the anticoagulant Citrate, 25°C density gradient solution (e.g. Ficoll, Percoll) and a polyester gel barrier that upon centrifugation was permeable to RBCs and granulocytes but not to mononuclear cells. The tube was inverted several times to mix the blood with the anticoagulant. The tubes were centrifuged at 1750xg in a swing-out rotor at room temperature for 20 minutes. The tubes were removed from the centrifuge and inverted 5-10 times to mix the plasma with the mononuclear cells, while trapping the RBCs and the granulocytes beneath the gel barrier. The plasma/mononuclear cell mix was decanted into a 15ml tube and 5ml of phosphate-buffered saline (PBS) is added. The 15ml tubes were spun for 5 minutes at 1750xg to pellet the cells. The supernatant was discarded and 1.8 ml of RLT lysis buffer is added to the mononuclear cell pellet. The buffer and cells were pipetted up and down to ensure complete lysis of the pellet. The cell lysate was frozen and stored until it is convenient to proceed with isolation of total RNA.

Total RNA was purified from the lysed mononuclear cells using the Qiagen Rneasy Miniprep kit, as directed by the manufacturer (10/99 version) for total RNA isolation, including homogenization (Qias shredder columns) and on-column DNase treatment. The purified RNA was eluted in 50ul of water. The further use of RNA prepared by this method is described in Example 11, 24, and 23.

Some samples were prepared by a different protocol, as follows:

Two 8 ml blood samples were drawn from a peripheral vein into a tube (CPT, Becton-Dickinson order #362753) containing anticoagulant (Citrate), 25°C density gradient solution (Ficoll) and a polyester gel barrier that upon centrifugation is permeable to RBCs and granulocytes but not to mononuclear cells. The mononuclear cells and plasma remained above the barrier while the RBCs and granulocytes were

trapped below. The tube was inverted several times to mix the blood with the anticoagulant, and the tubes were subjected to centrifugation at 1750xg in a swing-out rotor at room temperature for 20 min. The tubes were removed from the centrifuge, and the clear plasma layer above the cloudy mononuclear cell layer was aspirated and discarded. The cloudy mononuclear cell layer was aspirated, with care taken to rinse all of the mononuclear cells from the surface of the gel barrier with PBS (phosphate buffered saline). Approximately 2 mls of mononuclear cell suspension was transferred to a 2ml microcentrifuge tube, and centrifuged for 3min. at 16,000 rpm in a microcentrifuge to pellet the cells. The supernatant was discarded and 1.8 ml of RLT lysis buffer (Qiagen) were added to the mononuclear cell pellet, which lysed the cells and inactivated Rnases. The cells and lysis buffer were pipetted up and down to ensure complete lysis of the pellet. Cell lysate was frozen and stored until it was convenient to proceed with isolation of total RNA.

RNA samples were isolated from 8 mL of whole blood. Yields ranged from 2 ug to 20ug total RNA for 8mL blood. A260/A280 spectrophotometric ratios were between 1.6 and 2.0, indicating purity of sample. 2ul of each sample were run on an agarose gel in the presence of ethidium bromide. No degradation of the RNA sample and no DNA contamination was visible.

Example 9: Preparation of Buffy Coat Control RNA for use in leukocyte expression profiling

Control RNA was prepared using total RNA from Buffy coats and/or total RNA from enriched mononuclear cells isolated from Buffy coats, both with and without stimulation with ionomycin and PMA. The following control RNAs were prepared:

Control 1: Buffy Coat Total RNA

Control 2: Mononuclear cell Total RNA

Control 3: Stimulated buffy coat Total RNA

Control 4: Stimulated mononuclear Total RNA

Control 5: 50% Buffy coat Total RNA / 50% Stimulated buffy coat Total RNA

Control 6: 50% Mononuclear cell Total RNA / 50% Stimulated Mononuclear Total RNA

Some samples were prepared using the following protocol: Buffy coats from 38 individuals were obtained from Stanford Blood Center. Each buffy coat is derived from ~350 mL whole blood from one individual. 10 ml buffy coat was removed from the bag, and placed into a 50 ml tube. 40 ml of Buffer EL (Qiagen) was added, the tube was mixed and placed on ice for 15 minutes, then cells were pelleted by centrifugation at 2000xg for 10 minutes at 4°C. The supernatant was decanted and the cell pellet was re-suspended in 10 ml of Qiagen Buffer EL. The tube was then centrifuged at 2000xg for 10 minutes at 4°C. The cell pellet was then re-suspended in 20 ml TRIZOL (GibcoBRL) per Buffy coat sample, the mixture was shredded using a rotary homogenizer, and the lysate was then frozen at -80°C prior to proceeding to RNA isolation.

Other control RNAs were prepared from enriched mononuclear cells prepared from Buffy coats. Buffy coats from Stanford Blood Center were obtained, as described above. 10 ml buffy coat was added to a 50 ml polypropylene tube, and 10 ml of phosphate buffer saline (PBS) was added to each tube. A polysucrose (5.7 g/dL) and sodium diatrizoate (9.0 g/dL) solution at a 1.077 +/-0.0001 g/ml density solution of equal volume to diluted sample was prepared (Histopaque 1077, Sigma cat. no 1077-1). This and all subsequent steps were performed at room temperature. 15 ml of diluted buffy coat/PBS was layered on top of 15 ml of the histopaque solution in a 50 ml tube. The tube was centrifuged at 400xg for 30 minutes at room temperature. After centrifugation, the upper layer of the solution to within 0.5 cm of the opaque interface containing the mononuclear cells was discarded. The opaque interface was transferred into a clean centrifuge tube. An equal volume of PBS was added to each tube and centrifuged at 350xg for 10 minutes at room temperature. The supernatant was discarded. 5 ml of Buffer EL (Qiagen) was used to resuspend the remaining cell pellet and the tube was centrifuged at 2000xg for 10 minutes at room temperature. The supernatant was discarded. The pellet was resuspended in 20 ml of TRIZOL (GibcoBRL) for each individual buffy coat that was processed. The sample was homogenized using a rotary homogenizer and frozen at -80C until RNA was isolated.

RNA was isolated from frozen lysed Buffy coat samples as follows: frozen samples were thawed, and 4 ml of chloroform was added to each buffy coat sample. The sample was mixed by vortexing and centrifuged at 2000xg for 5 minutes. The aqueous layer was moved to new tube and then repurified by using the RNeasy Maxi

RNA clean up kit, according to the manufacturer's instruction (Qiagen, PN 75162). The yield, purity and integrity were assessed by spectrophotometer and gel electrophoresis.

Some samples were prepared by a different protocol, as follows. The further use of RNA prepared using this protocol is described in Example 11.

50 whole blood samples were randomly selected from consented blood donors at the Stanford Medical School Blood Center. Each buffy coat sample was produced from ~350 mL of an individual's donated blood. The whole blood sample was centrifuged at $\sim 4,400 \times g$ for 8 minutes at room temperature, resulting in three distinct layers: a top layer of plasma, a second layer of buffy coat, and a third layer of red blood cells. 25 ml of the buffy coat fraction was obtained and diluted with an equal volume of PBS (phosphate buffered saline). 30 ml of diluted buffy coat was layered onto 15 ml of sodium diatrizoate solution adjusted to a density of 1.077 ± 0.001 g/ml (Histopaque 1077, Sigma) in a 50mL plastic tube. The tube was spun at 800 g for 10 minutes at room temperature. The plasma layer was removed to the 30 ml mark on the tube, and the mononuclear cell layer removed into a new tube and washed with an equal volume of PBS, and collected by centrifugation at 2000 g for 10 minutes at room temperature. The cell pellet was resuspended in 10 ml of Buffer EL (Qiagen) by vortexing and incubated on ice for 10 minutes to remove any remaining erythrocytes. The mononuclear cells were spun at 2000 g for 10 minutes at 4 degrees Celsius. The cell pellet was lysed in 25 ml of a phenol/guanidinium thiocyanate solution (TRIZOL Reagent, Invitrogen). The sample was homogenized using a PowerGene 5 rotary homogenizer (Fisher Scientific) and Omini disposable generator probes (Fisher Scientific). The Trizol lysate was frozen at -80 degrees C until the next step.

The samples were thawed out and incubated at room temperature for 5 minutes. 5 ml chloroform was added to each sample, mixed by vortexing, and incubated at room temperature for 3 minutes. The aqueous layers were transferred to new 50 ml tubes. The aqueous layer containing total RNA was further purified using the Qiagen RNeasy Maxi kit (PN 75162), per the manufacturer's protocol (October 1999). The columns were eluted twice with 1 ml Rnase-free water, with a minute incubation before each spin. Quantity and quality of RNA was assessed using standard methods. Generally, RNA was isolated from batches of 10 buffy coats at a

time, with an average yield per buffy coat of 870 µg, and an estimated total yield of 43.5 mg total RNA with a 260/280 ratio of 1.56 and a 28S/18S ratio of 1.78.

Quality of the RNA was tested using the Agilent 2100 Bioanalyzer using RNA 6000 microfluidics chips. Analysis of the electrophorograms from the Bioanalyzer for five different batches demonstrated the reproducibility in quality between the batches.

Total RNA from all five batches were combined and mixed in a 50 ml tube, then aliquoted as follows: 2 x 10 ml aliquots in 15 ml tubes, and the rest in 100 µl aliquots in 1.5 ml microcentrifuge tubes. The aliquots gave highly reproducible results with respect to RNA purity, size and integrity. The RNA was stored at -80°C.

Test hybridization of Reference RNA

The reference RNA (hereinafter, "R50") was hybridized to a spotted cDNA array (prepared as described in Example 10). There are a total of 1152 features on the array: 384 clones printed in triplicate. The R50 targets were fluorescently labeled with Cy-5 using methods described herein. In five array hybridizations, the reference RNA detected 94% of probes on the array with a Signal to Noise ratio of greater than three. 99% of probes on the array were detected with a signal to noise ratio of greater than one. Figure 8 shows one array hybridization. The probes are ordered from high to low in signal to noise ratio, and the log of median and the log of the background were plotted for each probe.

Example 10. RNA Labeling and hybridization to a leukocyte cDNA array of candidate nucleotide sequences.

Comparison of Guanidine-Silica to Acid-Phenol RNA Purification (GSvsAP)

These data are from a set of 12 hybridizations designed to identify differences between the signal strength from two different RNA purification methods. The two RNA methods used were guanidine-silica (GS, Qiagen) and acid-phenol (AP, Trizol, Gibco BRL). Ten tubes of blood were drawn from each of four people. Two were used for the AP prep, the other eight were used for the GS prep. The protocols for the leukocyte RNA preps using the AP and GS techniques were completed as described here:

Guanidine-silica (GS) method:

For each tube, 8ml blood was drawn into a tube containing the anticoagulant Citrate, 25°C density gradient solution and a polyester gel barrier that upon centrifugation is permeable to RBCs and granulocytes but not to mononuclear cells.

The mononuclear cells and plasma remained above the barrier while the RBCs and granulocytes were trapped below. CPT tubes from Becton-Dickinson (#362753) were used for this purpose. The tube was inverted several times to mix the blood with the anticoagulant. The tubes were immediately centrifuged @1750xg in a swinging bucket rotor at room temperature for 20 min. The tubes were removed from the centrifuge and inverted 5-10 times. This mixed the plasma with the mononuclear cells, while the RBCs and the granulocytes remained trapped beneath the gel barrier. The plasma/mononuclear cell mix was decanted into a 15ml tube and 5ml of phosphate-buffered saline (PBS) was added. The 15ml tubes are spun for 5 minutes at 1750xg to pellet the cells. The supernatant was discarded and 1.8 ml of RLT lysis buffer (guanidine isothiocyanate) was added to the mononuclear cell pellet. The buffer and cells were pipetted up and down to ensure complete lysis of the pellet. The cell lysate was then processed exactly as described in the Qiagen Rneasy Miniprep kit protocol (10/99 version) for total RNA isolation (including steps for homogenization (QiaShredder columns) and on-column DNase treatment. The purified RNA was eluted in 50ul of water.

Acid-phenol (AP) method:

For each tube, 8ml blood was drawn into a tube containing the anticoagulant Citrate, 25°C density gradient solution and a polyester gel barrier that upon centrifugation is permeable to RBCs and granulocytes but not to mononuclear cells. The mononuclear cells and plasma remained above the barrier while the RBCs and granulocytes were trapped below. CPT tubes from Becton-Dickinson (#362753) were used for this purpose. The tube was inverted several times to mix the blood with the anticoagulant. The tubes were immediately centrifuged @1750xg in a swinging bucket rotor at room temperature for 20 min. The tubes were removed from the centrifuge and inverted 5-10 times. This mixed the plasma with the mononuclear cells, while the RBCs and the granulocytes remained trapped beneath the gel barrier. The plasma/mononuclear cell mix was decanted into a 15ml tube and 5ml of phosphate-buffered saline (PBS) was added. The 15ml tubes are spun for 5 minutes @1750xg to pellet the cells. The supernatant was discarded and the cell pellet was lysed using 0.6 mL Phenol/guanidine isothiocyanate (e.g. Trizol reagent, GibcoBRL). Subsequent total RNA isolation proceeded using the manufacturers protocol.

RNA from each person was labeled with either Cy3 or Cy5, and then hybridized in pairs to the mini-array. For instance, the first array was hybridized with GS RNA from one person (Cy3) and GS RNA from a second person (Cy5).

Techniques for labeling and hybridization for all experiments discussed here were completed as detailed above in example 10. Arrays were prepared as described in example 7.

RNA isolated from subject samples, or control Buffy coat RNA, were labeled for hybridization to a cDNA array. Total RNA (up to 100 µg) was combined with 2 µl of 100 µM solution of an Oligo (dT)12-18 (GibcoBRL) and heated to 70°C for 10 minutes and place on ice. Reaction buffer was added to the tube, to a final concentration of 1xRT buffer (GibcoBRL), 10 mM DTT (GibcoBRL), 0.1 mM unlabeled dATP, dTTP, and dGTP, and 0.025 mM unlabeled dCTP, 200 pg of CAB (*A. thaliana* photosystem I chlorophyll a/b binding protein), 200 pg of RCA (*A. thaliana* RUBISCO activase), 0.25 mM of Cy-3 or Cy-5 dCTP, and 400 U Superscript II RT (GibcoBRL).

The volumes of each component of the labeling reaction were as follows: 20 µl of 5xRT buffer; 10 µl of 100 mM DTT; 1 µl of 10 mM dNTPs without dCTP; 0.5 µl of 5 mM CTP; 13 µl of H₂O; 0.02 µl of 10 ng/µl CAB and RCA; 1 µl of 40 Units/µl RNaseOUT Recombinant Ribonuclease Inhibitor (GibcoBRL); 2.5 µl of 1.0 mM Cy-3 or Cy-5 dCTP; and 2.0 µl of 200 Units/µl of Superscript II RT. The sample was vortexed and centrifuged. The sample was incubated at 4°C for 1 hour for first strand cDNA synthesis, then heated at 70°C for 10 minutes to quench enzymatic activity. 1 µl of 10 mg/ml of Rnase A was added to degrade the RNA strand, and the sample was incubated at 37°C for 30 minutes.

Next, the Cy-3 and Cy-5 cDNA samples were combined into one tube. Unincorporated nucleotides were removed using QIAquick RCR purification protocol (Qiagen), as directed by the manufacturer. The sample was evaporated to dryness and resuspended in 5 µl of water. The sample was mixed with hybridization buffer containing 5xSSC, 0.2% SDS, 2 mg/ml Cot-1 DNA (GibcoBRL), 1 mg/ml yeast tRNA (GibcoBRL), and 1.6 ng/µl poly dA40-60 (Pharmacia). This mixture was placed on the microarray surface and a glass cover slip was placed on the array (Corning). The microarray glass slide was placed into a hybridization chamber (ArrayIt). The chamber was then submerged in a water bath overnight at 62° C. The

microarray was removed from the cassette and the cover slip was removed by repeatedly submerging it to a wash buffer containing 1xSSC, and 0.1% SDS. The microarray slide was washed in 1xSSC/0.1% SDS for 5 minutes. The slide was then washed in 0.1%SSC/0.1% SDS for 5 minutes. The slide was finally washed in 0.1xSSC for 2 minutes. The slide was spun at 1000 rpm for 2 minutes to dry out the slide, then scanned on a microarray scanner (Axon Instruments, Union City, CA.).

Six hybridizations with 20 µg of RNA were performed for each type of RNA preparation (GS or AP). Since both the Cy3 and the Cy5 labeled RNA are from test preparations, there are six data points for each GS prepped, Cy3-labeled RNA and six for each GS-prepped, Cy5-labeled RNA. The mini array hybridizations were scanned on and Axon Instruments scanner using GenPix 3.0 software. The data presented were derived as follows. First, all features flagged as “not found” by the software were removed from the dataset for individual hybridizations. These features are usually due to high local background or other processing artifacts. Second, the median fluorescence intensity minus the background fluorescence intensity was used to calculate the mean background subtracted signal for each dye for each hybridization. In Figure 4, the mean of these means across all six hybridizations is graphed (n=6 for each column). The error bars are the SEM. This experiment shows that the average signal from AP prepared RNA is 47% of the average signal from GS prepared RNA for both Cy3 and Cy5.

Generation of expression data for leukocyte genes from peripheral leukocyte samples

Six hybridizations were performed with RNA purified from human blood leukocytes using the protocols given above. Four of the six were prepared using the GS method and 2 were prepared using the AP method. Each preparation of leukocyte RNA was labeled with Cy3 and 10 µg hybridized to the mini-array. A control RNA was batch labeled with Cy5 and 10 µg hybridized to each mini-array together with the Cy3-labeled experimental RNA.

The control RNA used for these experiments was Control 1: Buffy Coat RNA, as described above. The protocol for the preparation of that RNA is reproduced here:

Buffy Coat RNA Isolation:

Buffy coats were obtained from Stanford Blood Center (in total 38 individual buffy coats were used. Each buffy coat is derived from ~350 mL whole blood from

one individual. 10 ml buffy coat was taken and placed into a 50 ml tube and 40 ml of a hypochlorous acid (HOCl) solution (Buffer EL from Qiagen) was added. The tube was mixed and placed on ice for 15 minutes. The tube was then centrifuged at 2000xg for 10 minutes at 4°C. The supernatant was decanted and the cell pellet was re-suspended in 10 ml of hypochlorous acid solution (Qiagen Buffer EL). The tube was then centrifuged at 2000xg for 10 minutes at 4°C. The cell pellet was then re-suspended in 20 ml phenol/guanidine thiocyanate solution (TRIZOL from GibcoBRL) for each individual buffy coat that was processed. The mixture was then shredded using a rotary homogenizer. The lysate was then frozen at -80°C prior to proceeding to RNA isolation.

The arrays were then scanned and analyzed on an Axon Instruments scanner using GenePix 3.0 software. The data presented were derived as follows. First, all features flagged as “not found” by the software were removed from the dataset for individual hybridizations. Second, control features were used to normalize the data for labeling and hybridization variability within the experiment. The control features are cDNA for genes from the plant, *Arabidopsis thaliana*, that were included when spotting the mini-array. Equal amounts of RNA complementary to two of these cDNAs were added to each of the samples before they were labeled. A third was pre-labeled and equal amounts were added to each hybridization solution before hybridization. Using the signal from these genes, we derived a normalization constant (L_j) according to the following formula:

$$L_j = \frac{\frac{\sum_{i=1}^N BGSS_{j,i}}{N}}{\frac{\sum_{j=1}^K \frac{\sum_{i=1}^N BGSS_{j,i}}{N}}{K}}$$

where $BGSS_i$ is the signal for a specific feature as identified in the GenePix software as the median background subtracted signal for that feature, N is the number of *A. thaliana* control features, K is the number of hybridizations, and L is the normalization constant for each individual hybridization.

Using the formula above, the mean over all control features of a particular hybridization and dye (eg Cy3) was calculated. Then these control feature means for all Cy3 hybridizations were averaged. The control feature mean in one hybridization divided by the average of all hybridizations gives a normalization constant for that particular Cy3 hybridization.

The same normalization steps were performed for Cy3 and Cy5 values, both fluorescence and background. Once normalized, the background Cy3 fluorescence was subtracted from the Cy3 fluorescence for each feature. Values less than 100 were eliminated from further calculations since low values caused spurious results.

Figure 5 shows the average background subtracted signal for each of nine leukocyte-specific genes on the mini array. This average is for 3-6 of the above-described hybridizations for each gene. The error bars are the SEM. Figure 3: The ratio of Cy3 to Cy5 signal is shown for a number of genes. This ratio corrects for variability among hybridizations and allows comparison between experiments done at different times. The ratio is calculated as the Cy3 background subtracted signal divided by the Cy5 background subtracted signal. Each bar is the average for 3-6 hybridizations. The error bars are SEM.

Together, these results show that we can measure expression levels for genes that are expressed specifically in sub-populations of leukocytes. These expression measurements were made with only 10 µg of leukocyte total RNA that was labeled directly by reverse transcription. The signal strength can be increased by improved labeling techniques that amplify either the starting RNA or the signal fluorescence. In addition, scanning techniques with higher sensitivity can be used.

Genes in Figures 5 and 6:

| Gene Name/Description | GenBank Accession Number | Gene Name Abbreviation |
|---|-----------------------------|---------------------------|
| T cell-specific tyrosine kinase Mrna | L10717 | TKTCS |
| Interleukin 1 alpha (IL 1) mRNA, complete cds | NM_000575 | IL1A |
| T-cell surface antigen CD2 (T11) mRNA, complete cds | M14362 | CD2 |
| Interleukin-13 (IL-13) precursor gene, complete cds | U31120 | IL-13 |
| Thymocyte antigen CD1a mRNA, complete cds | M28825 | CD1a |

| | | |
|--|-----------|----------|
| CD6 mRNA for T cell glycoprotein CDS | NM_006725 | CD6 |
| MHC class II HLA-DQA1 mRNA, complete cds | U77589 | HLA-DQA1 |
| Granulocyte colony-stimulating factor | M28170 | CD19 |
| Homo sapiens CD69 antigen | NM_001781 | CD69 |

Example 11: Identification of diagnostic gene sets useful in diagnosis and treatment of Cardiac allograft rejection

An observational study was conducted in which a prospective cohort of cardiac transplant recipients were analyzed for associations between clinical events or rejection grades and expression of a leukocyte candidate nucleotide sequence library. Patients were identified at 4 cardiac transplantation centers while on the transplant waiting list or during their routing post-transplant care. All adult cardiac transplant recipients (new or re-transplants) who received an organ at the study center during the study period or within 3 months of the start of the study period were eligible. The first year after transplantation is the time when most acute rejection occurs and it is thus important to study patients during this period. Patients provided informed consent prior to study procedures.

Peripheral blood leukocyte samples were obtained from all patients at the following time points: prior to transplant surgery (when able), the same day as routinely scheduled screening biopsies, upon evaluation for suspected acute rejection (urgent biopsies), on hospitalization for an acute complication of transplantation or immunosuppression, and when Cytomegalovirus (CMV) infection was suspected or confirmed. Samples were obtained through a standard peripheral vein blood draw or through a catheter placed for patient care (for example, a central venous catheter placed for endocardial biopsy). When blood was drawn from an intravenous line, care was taken to avoid obtaining heparin with the sample as it can interfere with downstream reactions involving the RNA. Mononuclear cells were prepared from whole blood samples as described in Example 8. Samples were processed within 2 hours of the blood draw and DNA and serum were saved in addition to RNA. Samples were stored at -70°C or on dry ice and sent to the site of RNA preparation in a sealed container with ample dry ice. RNA was isolated from subject samples as

described in Example 8 and hybridized to a candidate library of differentially expressed leukocyte nucleotide sequences, as further described in Examples 20-22. Methods used for amplification, labeling, hybridization and scanning are described in example 23. Analysis of human transplant patient mononuclear cell RNA hybridized to a microarray is shown in Example 24.

From each patient, clinical information was obtained at the following time points: prior to transplant surgery (when available), the same day as routinely scheduled screening biopsies, upon evaluation for suspected acute rejection (e.g., urgent biopsies), on hospitalization for an acute complication of transplantation or immunosuppression, and when Cytomegalovirus (CMV) infection was suspected or confirmed. Data was collected directly from the patient, from the patient's medical record, from diagnostic test reports or from computerized hospital databases. It was important to collect all information pertaining to the study clinical correlates (diagnoses and patient events and states to which expression data is correlated) and confounding variables (diagnoses and patient events and states that may result in altered leukocyte gene expression. Examples of clinical data collected are: patient sex, date of birth, date of transplant, race, requirement for prospective cross match, occurrence of pre-transplant diagnoses and complications, indication for transplantation, severity and type of heart disease, history of left ventricular assist devices, all known medical diagnoses, blood type, HLA type, viral serologies (including CMV, Hepatitis B and C, HIV and others), serum chemistries, white and red blood cell counts and differentials, CMV infections (clinical manifestations and methods of diagnosis), occurrence of new cancer, hemodynamic parameters measured by catheterization of the right or left heart (measures of graft function), results of echocardiography, results of coronary angiograms, results of intravascular ultrasound studies (diagnosis of transplant vasculopathy), medications, changes in medications, treatments for rejection, and medication levels. Information was also collected regarding the organ donor, including demographics, blood type, HLA type, results of screening cultures, results of viral serologies, primary cause of brain death, the need for inotropic support, and the organ cold ischemia time.

Of great importance was the collection of the results of endocardial biopsy for each of the patients at each visit. Biopsy results were all interpreted and recorded using the international society for heart and lung transplantation (ISHLT) criteria, described below. Biopsy pathological grades were determined by experienced

pathologists at each center. It is desirable to have a single centralized pathologist determine the grades when an analysis is done using samples from multiple medical centers.

ISHLT Criteria

| Grade | Finding | Rejection Severity |
|--------------|--|-----------------------------|
| 0 | No lymphocytic infiltrates | None |
| 1A | Focal (perivascular or interstitial lymphocytic infiltrates without necrosis) | Borderline mild |
| 1B | Diffuse but sparse lymphocytic infiltrates without necrosis | Mild |
| 2 | One focus only with aggressive lymphocytic infiltrate and/or myocyte damage | Mild, focal moderate |
| 3A | Multifocal aggressive lymphocytic infiltrates and/or myocardial damage | Moderate |
| 3B | Diffuse inflammatory lymphocytic infiltrates with necrosis | Borderline Severe |
| 4 | Diffuse aggressive polymorphous lymphocytic infiltrates with edema hemorrhage and vasculitis, with necrosis | Severe |

Clinical data was entered and stored in a database. The database was queried to identify all patients and patient visits that meet desired criteria (for example, patients with > grade II biopsy results, no CMV infection and time since transplant < 12 weeks).

The collected clinical data (disease criteria) is used to define patient or sample groups for correlation of expression data. Patient groups are identified for comparison, for example, a patient group that possesses a useful or interesting clinical distinction, versus a patient group that does not possess the distinction. Examples of useful and interesting patient distinctions that can be made on the basis of collected clinical data are listed here (and further described in Table 2):

1. Rejection episode of at least moderate histologic grade, which results in treatment of the patient with additional corticosteroids, anti-T cell antibodies, or total lymphoid irradiation.

2. Rejection with histologic grade 2 or higher.
3. Rejection with histologic grade <2.
4. The absence of histologic rejection and normal or unchanged allograft function (based on hemodynamic measurements from catheterization or on echocardiographic data).
5. The presence of severe allograft dysfunction or worsening allograft dysfunction during the study period (based on hemodynamic measurements from catheterization or on echocardiographic data).
6. Documented CMV infection by culture, histology, or PCR, and at least one clinical sign or symptom of infection.
7. Specific graft biopsy rejection grades
8. Rejection of mild to moderate histologic severity prompting augmentation of the patient's chronic immunosuppressive regimen
9. Rejection of mild to moderate severity with allograft dysfunction prompting plasmaphoresis or a diagnosis of "humoral" rejection
10. Infections other than CMV, esp. Epstein Barr virus (EBV)
11. Lymphoproliferative disorder (also called, post-transplant lymphoma)
12. Transplant vasculopathy diagnosed by increased intimal thickness on intravascular ultrasound (IVUS), angiography, or acute myocardial infarction.
13. Graft Failure or Retransplantation
14. All cause mortality

Expression profiles of subject samples are examined to discover sets of nucleotide sequences with differential expression between patient groups, for example, by methods describes above and below.

Non-limiting examples of patient leukocyte samples to obtain for discovery of various diagnostic nucleotide sets are as follows:

- a. Leukocyte set to avoid biopsy or select for biopsy:

Samples : Grade 0 vs. Grades 1-4

- b. Leukocyte set to monitor therapeutic response:

Examine successful vs. unsuccessful drug treatment.

Samples:

Successful: Time 1: rejection, Time 2: drug therapy Time 3: no rejection

Unsuccessful: Time 1: rejection, Time 2: drug therapy; Time 3: rejection

- c. Leukocyte set to predict subsequent acute rejection.

Biopsy may show no rejection, but the patient may develop rejection shortly thereafter. Look at profiles of patients who subsequently do and do not develop rejection.

Samples:

Group 1 (Subsequent rejection): Time 1: Grade 0; Time 2: Grade>0

Group 2 (No subsequent rejection): Time 1: Grade 0, ; Time 2: Grade 0

Focal rejection may be missed by biopsy. When this occurs the patient may have a Grade 0, but actually has rejection. These patients may go on to have damage to the graft etc.

Samples:

Non-rejectors: no rejection over some period of time

Rejectors: an episode of rejection over same period

- d. Leukocyte set to diagnose subsequent or current graft failure:

Samples:

Echocardiographic or catheterization data to define worsening function over time and correlate to profiles.

- e. Leukocyte set to diagnose impending active CMV:

Samples:

Look at patients who are CMV IgG positive. Compare patients with subsequent (to a sample) clinical CMV infection verses no subsequent clinical CMV infection.

- f. Leukocyte set to diagnose current active CMV:

Samples:

Analyze patients who are CMV IgG positive. Compare patients with active current clinical CMV infection vs. no active current CMV infection.

Upon identification of a nucleotide sequence or set of nucleotide sequences that distinguish patient groups with a high degree of accuracy, that nucleotide sequence or set of nucleotide sequences is validated, and implemented as a diagnostic test. The use of the test depends on the patient groups that are used to discover the nucleotide set. For example, if a set of nucleotide sequences is discovered that have collective expression behavior that reliably distinguishes patients with no histological rejection or graft dysfunction from all others, a diagnostic is developed that is used to screen patients for the need for biopsy. Patients identified as having no rejection do not need biopsy, while others are subjected to a biopsy to further define the extent of disease. In another example, a diagnostic nucleotide set that determines continuing graft rejection associated with myocyte necrosis ($>$ grade I) is used to determine that a patient is not receiving adequate treatment under the current treatment regimen. After increased or altered immunosuppressive therapy, diagnostic profiling is conducted to

determine whether continuing graft rejection is progressing. In yet another example, a diagnostic nucleotide set(s) that determine a patient's rejection status and diagnose cytomegalovirus infection is used to balance immunosuppressive and anti-viral therapy.

Example 12: Identification of diagnostic nucleotide sets for kidney and liver allograft rejection

Diagnostic tests for rejection are identified using patient leukocyte expression profiles to identify a molecular signature correlated with rejection of a transplanted kidney or liver. Blood, or other leukocyte source, samples are obtained from patients undergoing kidney or liver biopsy following liver or kidney transplantation, respectively. Such results reveal the histological grade, i.e., the state and severity of allograft rejection. Expression profiles are obtained from the samples as described above, and the expression profile is correlated with biopsy results. In the case of kidney rejection, clinical data is collected corresponding to urine output, level of creatine clearance, and level of serum creatine (and other markers of renal function). Clinical data collected for monitoring liver transplant rejection includes, biochemical characterization of serum markers of liver damage and function such as SGOT, SGPT, Alkaline phosphatase, GGT, Bilirubin, Albumin and Prothrombin time.

Leukocyte nucleotide sequence expression profiles are collected and correlated with important clinical states and outcomes in renal or hepatic transplantation. Examples of useful clinical correlates are given here:

1. Rejection episode of at least moderate histologic grade, which results in treatment of the patient with additional corticosteroids, anti-T cell antibodies, or total lymphoid irradiation.
2. The absence of histologic rejection and normal or unchanged allograft function (based on tests of renal or liver function listed above).
3. The presence of severe allograft dysfunction or worsening allograft dysfunction during the study period (based on tests of renal and hepatic function listed above).
4. Documented CMV infection by culture, histology, or PCR, and at least one clinical sign or symptom of infection.
5. Specific graft biopsy rejection grades
6. Rejection of mild to moderate histologic severity prompting augmentation of the patient's chronic immunosuppressive regimen
7. Infections other than CMV, esp. Epstein Barr virus (EBV)
8. Lymphoproliferative disorder (also called, post-transplant lymphoma)
9. Graft Failure or Retransplantation
10. Need for hemodialysis or other renal replacement therapy for renal transplant patients.

11. Hepatic encephalopathy for liver transplant recipients.

12. All cause mortality

Subsets of the candidate library (or of a previously identified diagnostic nucleotide set), are identified, according to the above procedures, that have predictive and/or diagnostic value for kidney or liver allograft rejection.

Example 13: Identification of diagnostic nucleotide sequences sets for use in the diagnosis, prognosis, risk stratification, and treatment of Atherosclerosis, Stable Angina Pectoris, and acute coronary syndrome.

Prediction of complications of atherosclerosis: angina pectoris.

Over 50 million in the US have atherosclerotic coronary artery disease (CAD). Almost all adults have some atherosclerosis. The most important question is who will develop complications of atherosclerosis. Patients with angiographically-confirmed atherosclerosis are enrolled in a study, and followed over time. Leukocyte expression profiles are taken at the beginning of the study, and routinely thereafter. Some patients develop angina and others do not. Expression profiles are correlated with development of angina, and subsets of the candidate library (or a previously identified diagnostic nucleotide set) are identified, according to the above procedures, that have predictive and/or diagnostic value for angina pectoris.

Alternatively, patients are followed by serial angiography. Profiles are collected at the first angiography, and at a repeat angiography at some future time (for example, after 1 year). Expression profiles are correlated with progression of disease, measured, for example, by decrease in vessel lumen diameter. Subsets of the candidate library (or a previously identified diagnostic nucleotide set) are identified, according to the above procedures, that have predictive and/or diagnostic value for progression of atherosclerosis.

Prediction and/or diagnosis of acute coronary syndrome

The main cause of death due to coronary atherosclerosis is the occurrence of acute coronary syndromes: myocardial infarction and unstable angina. Patients with at a very high risk of acute coronary syndrome (e.g., patients with a history of acute coronary syndrome, patients with atherosclerosis, patients with multiple traditional risk factors, clotting disorders or lupus) are enrolled in a prospective study. Leukocyte expression profiles are taken at the beginning of the study period and patients are monitored for the occurrence of unstable angina and/or myocardial

infarction. Standard criteria for the occurrence of an event are used (serum enzyme elevation, EKG, nuclear imaging or other), and the occurrence of these events can be collected from the patient, the patient's physician, the medical record or medical database. Expression profiles (taken at the beginning of the study) are correlated with the occurrence of an acute event. Subsets of the candidate library (or a previously identified diagnostic nucleotide set) are identified, according to the above procedures, that have predictive value for occurrence of an acute event.

In addition, expression profiles (taken at the time that an acute event occurs) are correlated with the occurrence of an acute event. Subsets of the candidate library (or a previously identified diagnostic nucleotide set) are identified, according to the above procedures, that have diagnostic value for occurrence of an acute event.

Risk stratification: occurrence of coronary artery disease

The established and classic risks for the occurrence of coronary artery disease and complications of that disease are: cigarette smoking, diabetes, hypertension, hyperlipidemia and a family history of early atherosclerosis. Obesity, sedentary lifestyle, syndrome X, cocaine use, chronic hemodialysis and renal disease, radiation exposure, endothelial dysfunction, elevated plasma homocysteine, elevated plasma lipoprotein a, and elevated CRP. Infection with CMV and chlamydia infection are less well established, controversial or putative risk factors for the disease. These risk factors can be assessed or measured in a population.

Leukocyte expression profiles are measured in a population possessing risk factors for the occurrence of coronary artery disease. Expression profiles are correlated with the presence of one or more risk factors (that may correlate with future development of disease and complications). Subsets of the candidate library (or a previously identified diagnostic nucleotide set) are identified, according to the above procedures, that have predictive value for the development of coronary artery disease.

Additional examples of useful correlation groups in cardiology include:

1. Samples from patients with a high risk factor burden (e.g., smoking, diabetes, high cholesterol, hypertension, family history) versus samples from those same patients at different times with fewer risks, or versus samples from different patients with fewer or different risks.

2. Samples from patients during an episode of unstable angina or myocardial infarction versus paired samples from those same patients before the episode or after recovery, or from different patients without these diagnoses.

3. Samples from patients (with or without documented atherosclerosis) who subsequently develop clinical manifestations of atherosclerosis such as stable angina, unstable angina, myocardial infarction, or stroke, versus samples from patients (with or without atherosclerosis) who do not develop these manifestations over the same time period.

4. Samples from patients who subsequently respond to a given medication or treatment regimen versus samples from those same or different patients who subsequently do not respond to a given medication or treatment regimen.

Example 14: Identification of diagnostic nucleotide sets for use in diagnosing and treating Restenosis

Restenosis is the re-narrowing of a coronary artery after an angioplasty. Patients are identified who are about to, or have recently undergone angioplasty. Leukocyte expression profiles are measured before the angioplasty, and at 1 day and 1-2 weeks after angioplasty or stent placement. Patients have a follow-up angiogram at 3 months and/or are followed for the occurrence of clinical restenosis, e.g., chest pain due to re-narrowing of the artery, that is confirmed by angiography. Expression profiles are compared between patients with and without restenosis, and candidate nucleotide profiles are correlated with the occurrence of restenosis. Subsets of the candidate library (or a previously identified diagnostic nucleotide set) are identified, according to the above procedures, that have predictive value for the development of restenosis.

Example 15: Identification of diagnostic nucleotide sets for use in monitoring treatment and/or progression of Congestive Heart Failure

CHF affects greater than 5 million individuals in the US and the prevalence of this disorder is growing as the population ages. The disease is chronic and debilitating. Medical expenditures are huge due to the costs of drug treatments, echocardiograms and other tests, frequent hospitalization and cardiac transplantation. The primary causes of CHF are coronary artery disease, hypertension and idiopathic

cardiomyopathy. Congestive heart failure is the number one indication for heart transplantation.

There is ample recent evidence that congestive heart failure is associated with systemic inflammation. A leukocyte test with the ability to determine the rate of progression and the adequacy of therapy is of great interest. Patients with severe CHF are identified, e.g. in a CHF clinic, an inpatient service, or a CHF study or registry (such as the cardiac transplant waiting list/registry). Expression profiles are taken at the beginning of the study and patients are followed over time, for example, over the course of one year, with serial assessments performed at least every three months. Further profiles are taken at clinically relevant end-points, for example: hospitalization for CHF, death, pulmonary edema, worsening of Ejection Fraction or increased cardiac chamber dimensions determined by echocardiography or another imaging test, and/or exercise testing of hemodynamic measurements. Clinical data is collected from patients if available, including:

Serial C-Reactive Protein (CRP), other serum markers, echocardiography (e.g., ejection fraction or another echocardiographic measure of cardiac function), nuclear imaging, NYHA functional classes, hospitalizations for CHF, quality of life measures, renal function, transplant listing, pulmonary edema, left ventricular assist device use, medication use and changes.

Expression profiles correlating with progression of CHF are identified. Expression profiles predicting disease progression, monitoring disease progression and response to treatment, and predicting response to a particular treatment(s) or class of treatment(s) are identified. Subsets of the candidate library (or a previously identified diagnostic nucleotide set) are identified, according to the above procedures, that have predictive value for the progression of CHF. Such diagnostic nucleotide sets are also useful for monitoring response to treatment for CHF.

Example 16: Identification of diagnostic nucleotide sets for use in monitoring treatment and/or progression of Rheumatoid arthritis

Rheumatoid arthritis (hereinafter, "RA") is a chronic and debilitating inflammatory arthritis. The diagnosis of RA is made by clinical criteria and radiographs. A new class of medication, TNF blockers, are effective, but the drugs are expensive, have side effects and not all patients respond to treatment. In addition, relief of disease symptoms does not always correlate with inhibition of joint

destruction. For these reasons, an alternative mechanism for the titration of therapy is needed.

An observational study was conducted in which a cohort of patients meeting American College of Rheumatology (hereinafter "ARC") criteria for the diagnosis of RA was identified. Arnett et al. (1988) Arthritis Rheum 31:315-24. Patients gave informed consent and a peripheral blood mononuclear cell RNA sample was obtained by the methods as described herein. When available, RNA samples were also obtained from surgical specimens of bone or synovium from effected joints, and synovial fluid .

From each patient, the following clinical information was obtained if available:

Demographic information; information relating to the ACR criteria for RA; presence or absence of additional diagnoses of inflammatory and non-inflammatory conditions; data from laboratory test, including complete blood counts with differentials, CRP, ESR, ANA, Serum IL6, Soluble CD40 ligand, LDL, HDL, Anti-DNA antibodies, rheumatoid factor, C3, C4, serum creatinine and any medication levels; data from surgical procedures such as gross operative findings and pathological evaluation of resected tissues and biopsies; information on pharmacological therapy and treatment changes; clinical diagnoses of disease "flare"; hospitalizations; quantitative joint exams; results from health assessment questionnaires (HAQs); other clinical measures of patient symptoms and disability; physical examination results and radiographic data assessing joint involvement, synovial thickening, bone loss and erosion and joint space narrowing and deformity.

From these data, measures of improvement in RA are derived as exemplified by the ACR 20% and 50% response/improvement rates (Felson et al. 1996). Measures of disease activity over some period of time is derived from these data as are measures of disease progression. Serial radiography of effected joints is used for objective determination of progression (e.g., joint space narrowing, peri-articular osteoporosis, synovial thickening). Disease activity is determined from the clinical scores, medical history, physical exam, lab studies, surgical and pathological findings. The collected clinical data (disease criteria) is used to define patient or sample groups for correlation of expression data. Patient groups are identified for comparison, for example, a patient group that possesses a useful or interesting clinical distinction, verses a patient group that does not possess the distinction. Examples of useful and

interesting patient distinctions that can be made on the basis of collected clinical data are listed here:

1. Samples from patients during a clinically diagnosed RA flare versus samples from these same or different patients while they are asymptomatic.
2. Samples from patients who subsequently have high measures of disease activity versus samples from those same or different patients who have low subsequent disease activity.
3. Samples from patients who subsequently have high measures of disease progression versus samples from those same or different patients who have low subsequent disease progression.
4. Samples from patients who subsequently respond to a given medication or treatment regimen versus samples from those same or different patients who subsequently do not respond to a given medication or treatment regimen (for example, TNF pathway blocking medications).
5. Samples from patients with a diagnosis of osteoarthritis versus patients with rheumatoid arthritis.
6. Samples from patients with tissue biopsy results showing a high degree of inflammation versus samples from patients with lesser degrees of histological evidence of inflammation on biopsy.

Expression profiles correlating with progression of RA are identified. Subsets of the candidate library (or a previously identified diagnostic nucleotide set) are identified, according to the above procedures, that have predictive value for the progression of RA.

Diagnostic nucleotide set(s) are identified which predict respond to TNF blockade. Patients are profiled before and during treatment with these medications. Patients are followed for relief of symptoms, side effects and progression of joint destruction, e.g., as measured by hand radiographs. Expression profiles correlating with response to TNF blockade are identified. Subsets of the candidate library (or a previously identified diagnostic nucleotide set) are identified, according to the above procedures that have predictive value for response to TNF blockade.

Example 17: Identification of diagnostic nucleotide sets for diagnosis of Systemic Lupus Erythematosus

SLE is a chronic, systemic inflammatory disease characterized by dysregulation of the immune system. Clinical manifestations affect every organ system and include skin rash, renal dysfunction, CNS disorders, arthralgias and hematologic abnormalities. SLE clinical manifestations tend to both recur intermittently (or “flare”) and progress over time, leading to permanent end-organ damage.

An observational study was conducted in which a cohort of patients meeting American College of Rheumatology (hereinafter “ACR”) criteria for the diagnosis of SLE were identified. See Tan et al. (1982) Arthritis Rheum 25:1271-7. Patients gave informed consent and a peripheral blood mononuclear cell RNA sample was obtained by the methods as described herein.

From each patient, the following clinical information was obtained if available:

Demographic information, ACR criteria for SLE, additional diagnoses of inflammatory and non-inflammatory conditions, data from laboratory testing including complete blood counts with differentials, CRP, ESR, ANA, Serum IL6, Soluble CD40 ligand, LDL, HDL, Anti-DNA antibodies, rheumatoid factor, C3, C4, serum creatinine (and other measures of renal dysfunction) and any medication levels, data from surgical procedures such as gross operative findings and pathological evaluation of resected tissues and biopsies (e.g., renal, CNS), information on pharmacological therapy and treatment changes, clinical diagnoses of disease “flare”, hospitalizations, quantitative joint exams, results from health assessment questionnaires (HAQs), SLEDAIs (a clinical score for SLE activity that assess many clinical variables), other clinical measures of patient symptoms and disability, physical examination results and carotid ultrasonography.

The collected clinical data (disease criteria) is used to define patient or sample groups for correlation of expression data. Patient groups are identified for comparison, for example, a patient group that possesses a useful or interesting clinical distinction, verses a patient group that does not possess the distinction. Measures of disease activity in SLE are derived from the clinical data described above to divide patients (and patient samples) into groups with higher and lower disease activity over some period of time or at any one point in time. Such data are SLEDAI scores and

other clinical scores, levels of inflammatory markers or complement, number of hospitalizations, medication use and changes, biopsy results and data measuring progression of end-organ damage or end-organ damage, including progressive renal failure, carotid atherosclerosis, and CNS dysfunction. Further examples of useful and interesting patient distinctions that can be made on the basis of collected clinical data are listed here:

Samples from patients during a clinically diagnosed SLE flare versus samples from these same or different patients while they are asymptomatic or while they have a documented infection.

1. Samples from patients who subsequently have high measures of disease activity versus samples from those same or different patients who have low subsequent disease activity.

2. Samples from patients who subsequently have high measures of disease progression versus samples from those same or different patients who have low subsequent disease progression.

3. Samples from patients who subsequently respond to a given medication or treatment regimen versus samples from those same or different patients who subsequently do not respond to a given medication or treatment regimen.

4. Samples from patients with premature carotid atherosclerosis on ultrasonography versus patients with SLE without premature atherosclerosis.

Expression profiles correlating with progression of SLE are identified, including expression profiles corresponding to end-organ damage and progression of end-organ damage. Expression profiles are identified predicting disease progression or disease “flare”, response to treatment or likelihood of response to treatment, predict likelihood of “low” or “high” disease measures (optionally described using the SLEDAI score), and presence or likelihood of developing premature carotid atherosclerosis. Subsets of the candidate library (or a previously identified diagnostic nucleotide set) are identified, according to the above procedures, that have predictive value for the progression of SLE.

Example 18: Identification of a diagnostic nucleotide set for diagnosis of cytomegalovirus

Cytomegalovirus is a very important cause of disease in immunosuppressed patients, for example, transplant patients, cancer patients, and AIDS patients. The virus can cause inflammation and disease in almost any tissue (particularly the colon, lung, bone marrow and retina). It is increasingly important to identify patients with current or impending clinical CMV disease, particularly when immunosuppressive drugs are to be used in a patient, e.g. for preventing transplant rejection.

Leukocytes are profiled in patients with active CMV, impending CMV, or no CMV. Expression profiles correlating with diagnosis of active or impending CMV are identified. Subsets of the candidate library (or a previously identified diagnostic nucleotide set) are identified, according to the above procedures, that have predictive value for the diagnosis of active or impending CMV. Diagnostic nucleotide set(s) identified with predictive value for the diagnosis of active or impending CMV may be combined, or used in conjunction with, cardiac, liver and/or kidney allograft-related diagnostic gene set(s) (described in Examples 11 and 12).

In addition, or alternatively, CMV nucleotide sequences are obtained, and a diagnostic nucleotide set is designed using CMV nucleotide sequence. The entire sequence of the organism is known and all CMV nucleotide sequences can be isolated and added to the library using the sequence information and the approach described below. Known expressed genes are preferred. Alternatively, nucleotide sequences are selected to represent groups of CMV genes that are coordinately expressed (immediate early genes, early genes, and late genes) (Spector et al. 1990, Stamminger et al. 1990).

CMV nucleotide sequences were isolated as follows: Primers were designed to amplify known expressed CMV genes, based on the publically available sequence of CMV strain AD 169 (Genbank LOCUS: HEHCMVCG 229354 bp; DEFINITION Human cytomegalovirus strain AD169 complete genome; ACCESSION X17403; VERSION X17403.1 GI:59591). The following primer were used to PCR amplify nucleotide sequences from 175 ng of AD 169 viral genomic DNA (Advance Biotechnologies Incorporated) as a template:

| CMV GENE | PRIMER SEQUENCES | SEQ. ID. NO: |
|----------|-----------------------|--------------|
| UL21 5' | atgtggccgcttctgaaaaac | 8771 |

| | | |
|----------|----------------------------|------|
| UL21 3' | tcatggggtggggacgggg | 8772 |
| UL33 5' | gtacgcgctgctgggtcatg | 8773 |
| UL33 3' | tcataccccgctgaggttatg | 8774 |
| UL54 5' | cacggacgacgacgctgacg | 8775 |
| UL54 3' | gtacggcagaaaagccggctc | 8776 |
| UL55 5' | caccaaagacacgctgttacag | 8777 |
| UL55 3' | tcagacgttcttctctgctg | 8778 |
| UL75 5' | cagcggcgctcaacatttcac | 8779 |
| UL75 3' | tcagcatgtcttgagcatgcgg | 8780 |
| UL80 5' | ccctcccaactactactaccg | 8781 |
| UL80 3' | ttactcgagcttattgagcgag | 8782 |
| UL83 5' | cacgtcgggcgttatgacac | 8783 |
| UL83 3' | tcaacctcgggtgcttttggg | 8784 |
| UL97 5' | ctgtctgctcattctggcgg | 8785 |
| UL97 3' | ttactcgggaacagttggcg | 8786 |
| UL106 5' | atgatgaccgaccgcacgga | 8787 |
| UL106 3' | tcacggtggctcgatacactg | 8788 |
| UL107 5' | aagcttccttacagcataactgt | 8789 |
| UL107 3' | cctataacatgtatttgaaaaattg | 8790 |
| UL109 5' | atgatacacgactaccactgg | 8791 |
| UL109 3' | ttacgagcaagagttcatcacg | 8792 |
| UL112 5' | ctgcgtgtcctcgctgggt | 8793 |
| UL112 3' | tcacgagtcactcggaaagc | 8794 |
| UL113 5' | ctcgtcttctcggctccac | 8795 |
| UL113 3' | ttaatcgtcgaacacgccgcg | 8796 |
| UL122 5' | gatgcttgaacgaaggcgtc | 8797 |
| UL122 3' | ttactgagacttgttctcagg | 8798 |
| UL123 5' | gtagcctacacttggccacc | 8799 |
| UL123 3' | ttactggtcagccttgctcta | 8800 |
| IRL2 5' | acgtccctggtagacggg | 8801 |
| IRL2 3' | ttataagaaaagaagcacaagctc | 8802 |
| IRL3 5' | atgtattgtttcttttttacagaaag | 8803 |
| IRL3 3' | ttatattattatcaaacgaaaaacag | 8804 |
| IRL4 5' | cttctccttcttaatctcgg | 8805 |
| IRL4 3' | ctatacggagatcgcggtcc | 8806 |
| IRL5 5' | atgcatacatcacgcgtgcat | 8807 |
| IRL5 3' | ctaccatataaaaacgcagggg | 8808 |
| IRL7 5' | atgaaagcaagaggcagccg | 8809 |
| IRL7 3' | tcataaggtaacgatgctacttt | 8810 |
| IRL13 5' | atggactggcgatttacggtt | 8811 |
| IRL13 3' | ctacattgtgccatttctcagt | 8812 |
| US2 5' | atgaacaatctctggaaagcctg | 8813 |
| US2 3' | tcagcacacgaaaaaccgcac | 8814 |

| | | |
|---------|----------------------------|------|
| US3 5' | atgaagccggtgttggtgctc | 8815 |
| US3 3' | ttaaataaatcgagacgggcg | 8816 |
| US6 5' | atggatctcttgattcgtctcg | 8817 |
| US6 3' | tcaggagccacaacgtcgaatc | 8818 |
| US11 5' | cgcaaaacgctactggctcc | 8819 |
| US11 3' | tcaccactgggccgaaaacatc | 8820 |
| US18 5' | tacggctggccgcatcgt | 8821 |
| US18 3' | ttacaacaagctgaggagactc | 8822 |
| US27 5' | atgaccacctctacaaataatcaaac | 8823 |
| US27 3' | gtagaaacaagcgttgagtccc | 8824 |
| US28 5' | cgttgcggtgtctcagtcg | 8825 |
| US28 3' | tcatgctgtgtgtaccaggata | 8826 |

The PCR reaction conditions were 10 mM Tris pH 8.3, 3.5 mM MgCl₂, 25 mM KCl, 200 uM dNTP's, 0.2 uM primers, and 5 Units of Taq Gold. The cycle parameters were as follows:

1. 95°C for 30 sec
2. 95°C for 15 sec
3. 56°C for 30 sec
4. 72°C for 2 min
5. go to step 2, 29 times
6. 72°C for 2 min
7. 4°C forever

PCR products were gel purified, and DNA was extracted from the agarose using the QiaexII gel purification kit (Qiagen). PCR product was ligated into the T/A cloning vector p-GEM-T-Easy (Promega) using 3 ul of gel purified PCR product and following the Promega protocol. The products of the ligation reaction were transformed and plated as described in the p-GEM protocol. White colonies were picked and grow culture in LB-AMP medium. Plasmid was prepared from these cultures using Qiagen Miniprep kit (Qiagen). Restriction enzyme digested plasmid (Not I and EcoRI) was examined after agarose gel electrophoresis to assess insert size. When the insert was the predicted size, the plasmid was sequenced by well-known techniques to confirm the identity of the CMV gene. Using forward and reverse primers that are complimentary to sequences flanking the insert cloning site (M13F and M13R), the isolated CMV gene was amplified and purified as described above.

Amplified cDNAs were used to create a microarray as described above. In addition, 50mer oligonucleotides corresponding the CMV genes listed above were designed, synthesized and placed on a microarray using methods described elsewhere in the specification.

Alternatively, oligonucleotide sequences are designed and synthesized for oligonucleotide array expression analysis from CMV genes as described in examples 20-22.

Diagnostic nucleotide set(s) for expression of CMV genes is used in combination with diagnostic leukocyte nucleotide sets for diagnosis of other conditions, e.g. organ allograft rejection.

Example 19: Identification of diagnostic nucleotide sets for monitoring response to Statins

HMG-CoA reductase inhibitors, called "Statins," are very effective in preventing complications of coronary artery disease in either patients with coronary disease and high cholesterol (secondary prevention) or patients without known coronary disease and with high cholesterol (primary prevention). Examples of Statins are (generic names given) pravastatin, atorvastatin, and simvastatin. Monitoring response to Statin therapy is of interest. Patients are identified who are on or are about to start Statin therapy. Leukocytes are profiled in patients before and after initiation of therapy, or in patients already being treated with Statins. Data is collected corresponding to cholesterol level, markers of inflammation (e.g., C-Reactive Protein and the Erythrocyte Sedimentation Rate), measures of endothelial function (e.g., improved forearm resistance or coronary flow reserve) and clinical endpoints (new stable angina, unstable angina, myocardial infarction, ventricular arrhythmia, claudication). Patient groups can be defined based on their response to Statin therapy (cholesterol, clinical endpoints, endothelial function). Expression profiles correlating with response to Statin treatment are identified. Subsets of the candidate library (or a previously identified diagnostic nucleotide set) are identified, according to the above procedures, that have predictive value for the response to Statins. Members of candidate nucleotide sets with expression that is altered by Statins are disease target nucleotide sequences.

Example 20--Probe Selection for a 24,000 Feature Array

This Example describes the compilation of almost 8,000 unique genes and ESTs using sequences identified from the sources described below. The sequences of these genes and ESTs were used to design probes, as described in the following Example.

Tables 3A, 3B and 3C list the sequences identified in the subtracted leukocyte expression libraries. All sequences that were identified as corresponding to a known RNA transcript were represented at least once, and all unidentified sequences were represented twice – once by the sequence on file and again by the complementary sequence – to ensure that the sense (or coding) strand of the gene sequence was included.

Table 3A. Table 3A contained all those sequences in BioCardia's subtracted libraries that matched sequences in GenBank's nr, EST_Human, and UniGene databases with an acceptable level of confidence. All the entries in the table representing the sense strand of their genes were grouped together and all those representing the antisense strand were grouped. A third group contained those entries whose strand could not be determined. Two complementary probes were designed for each member of this third group.

Table 3B and 3C. Table 3B and 3C contained all those sequences in the leukocyte expression subtracted library that did not match sequences in GenBank's nr, EST_Human, and UniGene databases with an acceptable level of confidence, but which had a high probability of representing real mRNA sequences. Sequences in Table 3B did not match anything in the databases above but matched regions of the human genome draft and were spatially clustered along it, suggesting that they were exons, rather than genomic DNA included in the library by chance. Sequences in Table 3C also aligned well to regions of the human genome draft, but the aligned regions were interrupted by genomic DNA, meaning they were likely to be spliced transcripts of multiple exon genes.

Table 3B lists 510 clones and Table 3C lists 48 clones that originally had no similarity with any sequence in the public databases. Blastn searches conducted after the initial filing have identified sequences in the public database with high similarity (E values less than $1e-40$) to the sequences determined for these clones. Table 3B contained 272 clones and Table 3C contained 25 clones that were found to have high similarity to sequences in dbEST. The sequences of the similar dbEST clones were

used to design probes. Sequences from clones that contained no similar regions to any sequence in the database were used to design a pair of complementary probes.

Probes were designed from database sequences that had the highest similarity to each of the sequenced clones in Tables 3A, 3B, and 3C. Based on BLASTn searches the most similar database sequence was identified by locus number and the locus number was submitted to GenBank using batch Entrez (<http://www.ncbi.nlm.nih.gov/entrez/batchentrez.cgi?db=Nucleotide>) to obtain the sequence for that locus. The GenBank entry sequence was used because in most cases it was more complete or was derived from multi-pass sequencing and thus would likely have fewer errors than the single pass cDNA library sequences. When only UniGene cluster IDs were available for genes of interest, the respective sequences were extracted from the UniGene_unique database, build 137, downloaded from NCBI (<ftp://ncbi.nlm.nih.gov/repository/UniGene/>). This database contains one representative sequence for each cluster in UniGene.

Summary of BioCardia library clones used in probe design.

| Table | Sense Strand | Antisense Strand | Strand Undetermined |
|---------------|---------------------|-------------------------|----------------------------|
| Table 3A | 3621 | 763 | 124 |
| Table 3B | 142 | 130 | 238 |
| Table 3C | 19 | 6 | 23 |
| Totals | 3782 | 899 | 385 |

Literature Searches

Example 2 describes searches of literature databases. We also searched for research articles discussing genes expressed only in leukocytes or involved in inflammation and particular disease conditions, including genes that were specifically expressed or down-regulated in a disease state. Searches included, but were not limited to, the following terms and various combinations of these terms: inflammation, atherosclerosis, rheumatoid arthritis, osteoarthritis, lupus, SLE, allograft, transplant, rejection, leukocyte, monocyte, lymphocyte, mononuclear, macrophage, neutrophil, eosinophil, basophil, platelet, congestive heart failure, expression, profiling, microarray, inflammatory bowel disease, asthma, RNA expression, gene expression, granulocyte.

A UniGene cluster ID or GenBank accession number was found for each gene in the list. The strand of the corresponding sequence was determined, if possible, and the genes were divided into the three groups: sense (coding) strand, anti-sense strand, or strand unknown. The rest of the probe design process was carried out as described above for the sequences from the leukocyte subtracted expression library.

Database Mining

Database mining was performed as described in Example 2. In addition, the Library Browser at the NCBI UniGene web site (<http://www.ncbi.nlm.nih.gov/UniGene/lbrowse.cgi?ORG=Hs&DISPLAY=ALL>) was used to identify genes that are specifically expressed in leukocyte cell populations. All expression libraries available at the time were examined and those derived from leukocytes were viewed individually. Each library viewed through the Library Browser at the UniGene web site contains a section titled "Shown below are UniGene clusters of special interest only" that lists genes that are either highly represented or found only in that library. Only the genes in this section were downloaded from each library. Alternatively, every sequence in each library is downloaded and then redundancy between libraries is reduced by discarding all UniGene cluster IDs that are represented more than once.

A total of 439 libraries were downloaded, containing 35,819 genes, although many were found in more than one library. The most important libraries from the remaining set were separated and 3,914 genes remained. After eliminating all redundancy between these libraries and comparing the remaining genes to those listed in Tables 3A, 3B and 3C, the set was reduced to 2,573 genes in 35 libraries (listed below). From these, all genes in first 30 libraries were used to design probes. A random subset of genes was used from Library Lib.376, "Activated_T-cells_XX". From the last four libraries, a random subset of sequences listed as "ESTs, found only in this library" was used.

| Library ID | Library Name | Category | No. of sequences before reduction | No. of sequences used on array* |
|------------|---|--------------------|-----------------------------------|---------------------------------|
| | | | | |
| Lib.2228 | Human_leukocyte_MATCHMAKER_cDNA_Library | other/unclassified | 4 | 3 |

| | | | | |
|--------------|--|--------------------|--------------|------------|
| Lib.238 | RA-MO-III (activated monocytes from RA patient) | Blood | 2 | 1 |
| Lib.242 | Human_peripheral_blood_(Whole)_(Steve_Elledge) | Blood | 4 | 2 |
| Lib.2439 | Subtracted_cDNA_libraries_from_human_Jurkat_cells | other/unclassified | 4 | 1 |
| Lib.323 | Activated_T-cells_I | other/unclassified | 19 | 3 |
| Lib.327 | Monocytes,_stimulated_II | Blood | 92 | 35 |
| Lib.387 | Macrophage_I | other/unclassified | 84 | 24 |
| Lib.409 | Activated_T-cells_IV | other/unclassified | 37 | 10 |
| Lib.410 | Activated_T-cells_VIII | other/unclassified | 27 | 10 |
| Lib.411 | Activated_T-cells_V | other/unclassified | 41 | 9 |
| Lib.412 | Activated_T-cells_XII | other/unclassified | 29 | 12 |
| Lib.413 | Activated_T-cells_XI | other/unclassified | 13 | 6 |
| Lib.414 | Activated_T-cells_II | other/unclassified | 69 | 30 |
| Lib.429 | Macrophage_II | other/unclassified | 56 | 24 |
| Lib.4480 | Homo_sapiens_rheumatoid_arthritis_fibroblast-like_synovial | other/unclassified | 7 | 6 |
| Lib.476 | Macrophage,_subtracted_(total_cDNA) | other/unclassified | 11 | 1 |
| Lib.490 | Activated_T-cells_III | other/unclassified | 9 | 5 |
| Lib.491 | Activated_T-cells_VII | other/unclassified | 27 | 8 |
| Lib.492 | Activated_T-cells_IX | other/unclassified | 16 | 5 |
| Lib.493 | Activated_T-cells_VI | other/unclassified | 31 | 15 |
| Lib.494 | Activated_T-cells_X | other/unclassified | 18 | 5 |
| Lib.498 | RA-MO-I (activated peripheral blood monocytes from RA patient) | Blood | 2 | 1 |
| Lib.5009 | Homo_Sapiens_cDNA_Library_from_Peripheral_White_Blood_Cell | other/unclassified | 3 | 3 |
| Lib.6338 | human_activated_B_lymphocyte | Tonsils | 9 | 8 |
| Lib.6342 | Human_lymphocytes | other/unclassified | 2 | 2 |
| Lib.646 | Human_leukocyte_(M.L.Markelov) | other/unclassified | 1 | 1 |
| Lib.689 | Subtracted_cDNA_library_of_activated_B_lymphocyte | Tonsil | 1 | 1 |
| Lib.773 | PMA-induced_HL60_cell_subtraction_library (leukemia) | other/unclassified | 6 | 3 |
| Lib.1367 | cDNA_Library_from_rIL-2_activated_lymphocytes | other/unclassified | 3 | 2 |
| Lib.5018 | Homo_sapiens_CD4+_T-cell_clone_HA1.7 | other/unclassified | 6 | 3 |
| Lib.376 | Activated_T-cells_XX | other/unclassified | 999 | 119 |
| Lib.669 | NCI_CGAP_CLL1 (Lymphocyte) | Blood | 353 | 81† |
| Lib.1395 | NCI_CGAP_Sub6 (germinal center b-cells) | B cells germinal | 389 | 100† |
| Lib.2217 | NCI_CGAP_Sub7 (germinal center b-cells) | B cells germinal | 605 | 200† |
| Lib.289 | NCI_CGAP_GCB1 (germinal center b-cells) | Tonsil | 935 | 200† |
| Total | | | 3,914 | 939 |

* Redundancy of UniGene numbers between the libraries was eliminated.

† A subset of genes flagged as "Found only in this library" were taken.

Angiogenesis Markers

215 sequences derived from an angiogenic endothelial cell subtracted cDNA library obtained from Stanford University were used for probe design. Briefly, using well known subtractive hybridization procedures, (as described in, e.g., US Patent Numbers 5,958,738; 5,589,339; 5,827,658; 5,712,127; 5,643,761; 5,565,340) modified to normalize expression by suppressing over-representation of abundant RNA species while increasing representation of rare RNA species, a library was produced that is enriched for RNA species (messages) that are differentially expressed between test (stimulated) and control (resting) HUVEC populations. The subtraction/suppression protocol was performed as described by the kit manufacturer (Clontech, PCR-select cDNA Subtraction Kit).

Pooled primary HUVECs (Clonetics) were cultured in 15% FCS, M199 (GibcoBRL) with standard concentrations of Heparin, Penicillin, Streptomycin, Glutamine and Endothelial Cell Growth Supplement. The cells were cultured on 1% gelatin coated 10 cm dishes. Confluent HUVECs were photographed under phase contrast microscopy. The cells formed a monolayer of flat cells without gaps. Passage 2-5 cells were used for all experiments. Confluent HUVECs were treated with trypsin/EDTA and seeded onto collagen gels. Collagen gels were made according to the protocol of the Collagen manufacturer (Becton Dickinson Labware). Collagen gels were prepared with the following ingredients: Rat tail collagen type I (Collaborative Biomedical) 1.5 mg/mL, mouse laminin (Collaborative Biomedical) 0.5 mg/mL, 10% 10X media 199 (Gibco BRL). 1N NaOH, 10 X PBS and sterile water were added in amounts recommended in the protocol. Cell density was measured by microscopy. 1.2×10^6 cells were seeded onto gels in 6-well, 35 mm dishes, in 5% FCS M199 media. The cells were incubated for 2 hrs at 37 C with 5% CO₂. The media was then changed to the same media with the addition of VEGF (Sigma) at 30ng/mL media. Cells were cultured for 36 hrs. At 12, 24 and 36 hrs, the cells were observed with phase contrast microscopy. At 36 hours, the cells were observed elongating, adhering to each other and forming lumen structures. At 12 and 24 hrs media was aspirated and refreshed. At 36 hrs, the media was aspirated, the cells were rinsed with PBS and then treated with Collagenase (Sigma) 2.5mg/mL PBS for 5 min with active agitation until the collagen gels were liquefied. The cells were then centrifuged at 4C, 2000g for 10 min. The supernatant was removed and the cells

were lysed with 1 mL Trizol Reagent (Gibco) per 5×10^6 cells. Total RNA was prepared as specified in the Trizol instructions for use. mRNA was then isolated as described in the micro-fast track mRNA isolation protocol from Invitrogen. This RNA was used as the tester RNA for the subtraction procedure.

Ten plates of resting, confluent, p4 HUVECs, were cultured with 15 % FCS in the M199 media described above. The media was aspirated and the cells were lysed with 1 mL Trizol and total RNA was prepared according to the Trizol protocol. mRNA was then isolated according to the micro-fast track mRNA isolation protocol from Invitrogen. This RNA served as the control RNA for the subtraction procedure.

The entire subtraction cloning procedure was carried out as per the user manual for the Clontech PCR Select Subtraction Kit. The cDNAs prepared from the test population of HUVECs were divided into "tester" pools, while cDNAs prepared from the control population of HUVECs were designated the "driver" pool. cDNA was synthesized from the tester and control RNA samples described above. Resulting cDNAs were digested with the restriction enzyme RsaI. Unique double-stranded adapters were ligated to the tester cDNA. An initial hybridization was performed consisting of the tester pools of cDNA (with its corresponding adapter) and an excess of the driver cDNA. The initial hybridization results in a partial normalization of the cDNAs such that high and low abundance messages become more equally represented following hybridization due to a failure of driver/tester hybrids to amplify.

A second hybridization involved pooling unhybridized sequences from the first hybridization together with the addition of supplemental driver cDNA. In this step, the expressed sequences enriched in the two tester pools following the initial hybridization can hybridize. Hybrids resulting from the hybridization between members of each of the two tester pools are then recovered by amplification in a polymerase chain reaction (PCR) using primers specific for the unique adapters. Again, sequences originating in a tester pool that form hybrids with components of the driver pool are not amplified. Hybrids resulting between members of the same tester pool are eliminated by the formation of "panhandles" between their common 5' and 3' ends. This process is illustrated schematically in Figure 3. The subtraction was done in both directions, producing two libraries, one with clones that are upregulated in tube-formation and one with clones that are down-regulated in the process.

The resulting PCR products representing partial cDNAs of differentially expressed genes were then cloned (i.e., ligated) into an appropriate vector according to the manufacturer's protocol (pGEM-Teasy from Promega) and transformed into competent bacteria for selection and screening. Colonies (2180) were picked and cultured in LB broth with 50ug/mL ampicillin at 37C overnight. Stocks of saturated LB + 50 ug/mL ampicillin and 15% glycerol in 96-well plates were stored at -80C. Plasmid was prepared from 1.4mL saturated LB broth containing 50 ug/mL ampicillin. This was done in a 96 well format using commercially available kits according to the manufacturer's recommendations (Qiagen 96-turbo prep).

2 probes to represent 22 of these sequences required, therefore, a total of 237 probes were derived from this library.

Viral genes.

Several viruses may play a role in a host of disease including inflammatory disorders, atherosclerosis, and transplant rejection. The table below lists the viral genes represented by oligonucleotide probes on the microarray. Low-complexity regions in the sequences were masked using RepeatMasker before using them to design probes.

| Virus | Gene Name | Genome Location |
|---|---------------------------------|----------------------------|
| Adenovirus, type 2 Accession #J01917 | E1a | 1226..1542 |
| | E1b_1 | 3270...3503 |
| | E2a_2 | complement(24089..25885) |
| | E3-1 | 27609..29792 |
| | E4 (last exon at 3'-end) | complement(33193..32802) |
| | IX | 3576..4034 |
| | Iva2 | complement(4081..5417) |
| | DNA Polymerase | complement(5187..5418) |
| Cytomegalovirus (CMV) Accession #X17403 | HCMVTRL2 (IRL2) | 1893..2240 |
| | HCMVTRL7 (IRL7) | complement(6595..6843) |
| | HCMVUL21 | complement(26497..27024) |
| | HCMVUL27 | complement(32831..34657) |
| | HCMVUL33 | 43251..44423 |
| | HCMVUL54 | complement(76903..80631) |
| | HCMVUL75 | complement(107901..110132) |
| | HCMVUL83 | complement(119352..121037) |
| | HCMVUL106 | complement(154947..155324) |
| | HCMVUL109 | complement(157514..157810) |
| | HCMVUL113 | 161503..162800 |
| | HCMVUL122 | complement(169364..170599) |
| | HCMVUL123 (last exon at 3'-end) | complement(171006..172225) |
| | HCMVUS28 | 219200..220171 |
| Epstein-Barr virus (EBV) Accession # NC_001345 | Exon in EBNA-1 RNA | 67477..67649 |
| | Exon in EBNA-1 RNA | 98364..98730 |
| | BRLF1 | complement(103366..105183) |
| | BZLF1 (first of 3 exons) | complement(102655..103155) |
| | BMLF1 | complement(82743..84059) |
| | BALF2 | complement(161384..164770) |
| Human Herpesvirus 6 (HHV6) Accession #NC_001664 | U16/U17 | complement(26259..27349) |
| | U89 | complement(133091..135610) |
| | U90 | complement(135664..135948) |
| | U86 | complement(125989..128136) |
| | U83 | 123528..123821 |
| | U22 | complement(33739..34347) |
| | DR2 (DR2L) | 791..2653 |
| | DR7 (DR7L) | 5629..6720 |
| | U95 | 142941..146306 |
| | U94 | complement(141394..142866) |
| | U39 | complement(59588..62080) |
| | U42 | complement(69054..70598) |
| | U81 | complement(121810..122577) |

Strand Selection

It was necessary to design sense oligonucleotide probes because the labeling and hybridization protocol to be used with the microarray results in fluorescently-labeled antisense cRNA. All of the sequences we selected to design probes could be divided into three categories:

- (1) Sequences known to represent the sense strand
- (2) Sequences known to represent the antisense strand
- (3) Sequences whose strand could not be easily determined from their descriptions

It was not known whether the sequences from the leukocyte subtracted expression library were from the sense or antisense strand. GenBank sequences are reported with sequence given 5' to 3', and the majority of the sequences we used to design probes came from accession numbers with descriptions that made it clear whether they represented sense or antisense sequence. For example, all sequences containing "mRNA" in their descriptions were understood to be the sequences of the sense mRNA, unless otherwise noted in the description, and all IMAGE Consortium clones are directionally cloned and so the direction (or sense) of the reported sequence can be determined from the annotation in the GenBank record.

For accession numbers representing the sense strand, the sequence was downloaded and masked and a probe was designed directly from the sequence. These probes were selected as close to the 3' end as possible. For accession numbers representing the antisense strand, the sequence was downloaded and masked, and a probe was designed complementary to this sequence. These probes were designed as close to the 5' end as possible (i.e., complementary to the 3' end of the sense strand).

Minimizing Probe Redundancy.

Multiple copies of certain genes or segments of genes were included in the sequences from each category described above, either by accident or by design. Reducing redundancy within each of the gene sets was necessary to maximize the number of unique genes and ESTs that could be represented on the microarray.

Three methods were used to reduce redundancy of genes, depending on what information was available. First, in gene sets with multiple occurrences of one or more

UniGene numbers, only one occurrence of each UniGene number was kept. Next, each gene set was searched by GenBank accession numbers and only one occurrence of each accession number was conserved. Finally, the gene name, description, or gene symbol were searched for redundant genes with no UniGene number or different accession numbers. In reducing the redundancy of the gene sets, every effort was made to conserve the most information about each gene.

We note, however, that the UniGene system for clustering submissions to GenBank is frequently updated and UniGene cluster IDs can change. Two or more clusters may be combined under a new cluster ID or a cluster may be split into several new clusters and the original cluster ID retired. Since the lists of genes in each of the gene sets discussed were assembled at different times, the same sequence may appear in several different sets with a different UniGene ID in each.

Sequences from Table 3A were treated differently. In some cases, two or more of the leukocyte subtracted expression library sequences aligned to different regions of the same GenBank entry, indicating that these sequences were likely to be from different exons in the same gene transcript. In these cases, one representative library sequence corresponding to each presumptive exon was individually listed in Table 3A.

Compilation.

After redundancy within a gene set was sufficiently reduced, a table of approximately 8,000 unique genes and ESTs was compiled in the following manner. All of the entries in Table 3A were transferred to the new table. The list of genes produced by literature and database searches was added, eliminating any genes already contained in Table 3A. Next, each of the remaining sets of genes was compared to the table and any genes already contained in the table were deleted from the gene sets before appending them to the table.

| | <u>Probes</u> |
|---|---------------|
| BioCardia Subtracted Leukocyte Expression Library | |
| Table 3A | 4,872 |
| Table 3B | 796 |
| Table 3C | 85 |
| Literature Search Results | 494 |

| | |
|--|-------|
| Database Mining | 1,607 |
| Viral genes | |
| a. CMV | 14 |
| b. EBV | 6 |
| c. HHV 6 | 14 |
| d. Adenovirus | 8 |
| Angiogenesis markers: 215, 22 of which needed two probes | 237 |
| <i>Arabidopsis thaliana</i> genes | 10 |
| Total sequences used to design probes | 8,143 |

Example 21- Design of oligonucleotide probes

This section describes the design of four oligonucleotide probes using Array Designer Ver 1.1 (Premier Biosoft International, Palo Alto, CA).

Clone 40H12

Clone 40H12 was sequenced and compared to the nr, dbEST, and UniGene databases at NCBI using the BLAST search tool. The sequence matched accession number NM_002310, a 'curated RefSeq project' sequence, see Pruitt et al. (2000) Trends Genet. 16:44-47, encoding leukemia inhibitory factor receptor (LIFR) mRNA with a reported E value of zero. An E value of zero indicates there is, for all practical purposes, no chance that the similarity was random based on the length of the sequence and the composition and size of the database. This sequence, cataloged by accession number NM_002310, is much longer than the sequence of clone 40H12 and has a poly-A tail. This indicated that the sequence cataloged by accession number NM_002310 is the sense strand and a more complete representation of the mRNA than the sequence of clone 40H12, especially at the 3' end. Accession number "NM_002310" was included in a text file of accession numbers representing sense strand mRNAs, and sequences for the sense strand mRNAs were obtained by uploading a text file containing desired accession numbers as an Entrez search query using the Batch Entrez web interface and saving the results locally as a FASTA file. The following sequence was obtained, and the region of alignment of clone 40H12 is outlined:

CTCTCTCCCAGAACGTGTCTCTGCTGCAAGGCACCGGGCCCTTTCGCTCTGCAGAACTGC
ACTTGCAAGACCATTATCAACTCCTAATCCCAGCTCAGAAAGGGAGCCTCTGCGACTCAT
TCATCGCCCTCCAGGACTGACTGCATTGCACAGATGATGGATATTTACGTATGTTTGAAA
CGACCATCCTGGATGGTGGACAATAAAAGAATGAGGACTGCTTCAAATTTCCAGTGGCTG
TTATCAACATTTATTCTTCTATATCTAATGAATCAAGTAAATAGCCAGAAAAAGGGGGCT
CCTCATGATTTGAAGTGTGTAACATAAATTTGCAAGTGTGGAAGTGTCTTGGAAAGCA
CCCTCTGGAACAGGCCGTGGTACTGATTATGAAGTTTGCATTGAAAACAGGTCCCGTTCT
TGTTATCAGTTGGAGAAAACCAGTATTAATAATTCCAGCTCTTTCACATGGTGATTATGAA
ATAACAATAAATTCTCTACATGATTTTGGAAAGTCTACAAGTAAATTCACACTAAATGAA
CAAAACGTTTCCTTAATTCCAGATACTCCAGAGATCTTGAATTTGTCTGCTGATTTCTCA
ACCTCTACATTATACCTAAAGTGGAACGACAGGGGTTCAGTTTTTCCACACCGCTCAAAT
GTTATCTGGGAAATTAAAGTCTACGTAAAGAGAGTATGGAGCTCGTAAAATTAGTGACC
CACAACACAACCTCTGAATGGCAAAGATACACTTCATCACTGGAGTTGGGCCTCAGATATG
CCCTTGGAATGTGCCATTCATTTTGTGGAAATTAGATGCTACATTGACAATCTTCATTTT
TCTGGTCTCGAAGAGTGGAGTGAAGTGGAGCCCTGTGAAGAACATTTCTTGATACCTGAT
TCTCAGACTAAGGTTTTTCCTCAAGATAAAGTGATACTTGTAGGCTCAGACATAACATTT
TGTTGTGTGAGTCAAGAAAAAGTGTATCAGCACTGATTGGCCATACAACTGCCCTTG
ATCCATCTTGATGGGGAAAATGTTGCAATCAAGATTCGTAATATTTCTGTTTCTGCAAGT
AGTGGAACAAATGTAGTTTTTACAACCGAAGATAACATATTTGGAACCGTTATTTTTGCT
GGATATCCACCAGATACTCCTCAACAACCTGAATTGTGAGACACATGATTTAAAAGAAATT
ATATGTAGTTGGAATCCAGGAAGGGTGACAGCGTTGGTGGGCCCACGTGCTACAAGCTAC
ACTTTAGTTGAAAGTTTTTCAGGAAAATATGTTAGACTTAAAAGAGCTGAAGCACCTACA
AACGAAAGCTATCAATTATTATTTCAAATGCTTCCAAATCAAGAAATATATAATTTTACT
TTGAATGCTCACAATCCGCTGGGTGATCACAATCAACAATTTTAGTTAATATAACTGAA
AAAGTTTATCCCCATACTCCTACTTCATTCAAAGTGAAGGATATTAATTCAACAGCTGTT
AACTTTCTTGGCATTTACCAGGCAACTTTGCAAAGATTAATTTTTTATGTGAAATTGAA
ATTAAGAAATCTAATTCAGTACAAGAGCAGCGGAATGTCACAATCAAAGGAGTAGAAAAT
TCAAGTTATCTTGTGCTCTGGACAAGTTAAATCCATACACTCTATATACTTTTCGGATT
CGTTGTTCTACTGAAACTTTCTGGAAATGGAGCAAATGGAGCAATAAAAAACAACATTTA
ACAACAGAAGCCAGTCCTTCAAAGGGGCCTGATACTTGGAGAGAGTGGAGTTCTGATGGA
AAAAATTTAATAATCTATTGGAAGCCTTTACCCATTAATGAAGCTAATGGAAAAATACTT

TCCTACAATGTATCGTGTTTCATCAGATGAGGAAACACAGTCCCTTTCTGAAATCCCTGAT
CCTCAGCACAAAGCAGAGATACGACTTGATAAGAATGACTACATCATCAGCGTAGTGGCT
AAAAATTCTGTGGGCTCATCACCACCTTCCAAAATAGCGAGTATGGAAATTCCAAATGAT
GATCTCAAAATAGAACAAGTTGTTGGGATGGGAAAGGGGATTCTCCTCACCTGGCATTAC
GACCCCAACATGACTTGCGACTACGTCATTAAGTGGTGTAACCTCGTCTCGGTGCGAACCA
TGCCTTATGGACTGGAGAAAAGTTCCCTCAAACAGCACTGAACTGTAATAGAATCTGAT
GAGTTTCGACCAGGTATAAGATATAATTTTTTTCCTGTATGGATGCAGAAATCAAGGATAT
CAATTATTACGCTCCATGATTGGATATATAGAAGAATTGGCTCCCATTTGTTGCACCAAAT
TTTACTGTTGAGGATACTTCTGCAGATTTCGATATTAGTAAAATGGGAAGACATTCTGTG
GAAGAACTTAGAGGCTTTTTAAGAGGATATTTGTTTTACTTTGGAAAAGGAGAAAGAGAC
ACATCTAAGATGAGGGTTTTAGAATCAGGTCGTTCTGACATAAAAGTTAAGAATATTACT
GACATATCCCAGAAGACACTGAGAATTGCTGATCTTCAAGGTAAAACAAGTTACCACCTG
GTCTTGCGAGCCTATACAGATGGTGGAGTGGGCCCGGAGAAGAGTATGTATGTGGTGACA
AAGGAAAATTCTGTGGGATTAATTATTGCCATTCTCATCCCAGTGGCAGTGGCTGTCATT
GTTGGAGTGGTGACAAGTATCCTTTGCTATCGGAAACGAGAATGGATTAAAGAAACCTTC
TACCCTGATATTCCAAATCCAGAAAACCTGTAAAGCATTACAGTTTCAAAGAGTGTCTGT
GAGGGAAGCAGTGCTCTTAAACATTGGAAATGAATCCTTGTACCCCAAATAATGTTGAG
GTTCTGGAAACTCGATCAGCATTTCTTAAATAGAAGATACAGAAATAATTTCCCAGTA
GCTGAGCGTCCTGAAGATCGCTCTGATGCAGAGCCTGAAAACCATGTGGTTGTGTCCTAT
TGTCCACCCATCATTGAGGAAGAAATACCAAACCCAGCCGAGATGAAGCTGGAGGGACT
GCACAGGTTATTTACATTGATGTTTCAGTCGATGTATCAGCCTCAAGCAAAACCAGAAGAA
GAACAAGAAAATGACCCTGTAGGAGGGGCAGGCTATAAGCCACAGATGCACCTCCCCATT
AATTCTACTGTGGAAGATATAGCTGCAGAAGAGGACTTAGATAAAACTGCGGGTTACAGA
CCTCAGGCCAATGTAAATACATGGAATTTAGTGTCTCCAGACTCTCCTAGATCCATAGAC
AGCAACAGTGAGATTGTCTCATTTGGAAGTCCATGCTCCATTAATTTCCGACAATTTTTG
ATTCCTCCTAAAGATGAAGACTCTCCTAAATCTAATGGAGGAGGGTGGTCCTTTACAAAC
TTTTTTTCAGAACAAACCAAACGATTAACAGTGTACCGTGTCACTTCAGTCAGCCATCTC
AATAAGCTCTTACTGCTAGTGTGCTACATCAGCACTGGGCATTCTTGGAGGGATCCTGT
GAAGTATTGTTAGGAGGTGAACTTCACTACATGTTAAGTTACACTGAAAGTTCATGTGCT
TTTAATGTAGTCTAAAAGCCAAAGTATAGTGAATCCTCAATCCACAAAACCTCAA
GATTGGGAGCTCTTTGTGATCAAGCCAAAGAATTCTCATGTACTCTACCTTCAAGAAGCA
TTTCAAGGCTAATACCTACTTGTACGTACATGTAAACAAATCCCGCCGCAACTGTTTTTC

TGTTCCTGTTGTTTGTGGTTTTCTCATATGTATACTTGGTGGAATTGTAAGTGGATTTGCA
 GGCCAGGGAGAAAATGTCCAAGTAACAGGTGAAGTTTATTTGCCTGACGTTTACTCCTTT
 CTAGATGAAAACCAAGCACAGATTTTAAACTTCTAAGATTATTCTCCTCTATCCACAGC
 ATTCACAAAAATTAATATAATTTTTAATGTAGTGACAGCGATTTAGTGTTTTGTTTGATA
 AAGTATGCTTATTTCTGTGCCTACTGTATAATGGTTATCAAACAGTTGTCTCAGGGGTAC
 AAACTTTGAAAACAAGTGTGACACTGACCAGCCCAAATCATAATCATGTTTTCTTGCTGT
 GATAGGTTTTGCTTGCCTTTTCATTATTTTTTAGCTTTTATGCTTGCTTCCATTATTTCA
 GTTGTTGCCCTAATATTTAAATTTACACTTCTAAGACTAGAGACCCACATTTTTTAAA
 AATCATTTTATTTTGTGATACAGTGACAGCTTTATATGAGCAAATTCAATATTATTCATA
 AGCATGTAATTCCAGTGACTTACTATGTGAGATGACTACTAAGCAATATCTAGCAGCGTT
 AGTTCCATATAGTTCTGATTGGATTTCTGTTCTCCTGAGGAGACCATGCCGTTGAGCTTG
 GCTACCCAGGCAGTGGTGATCTTTGACACCTTCTGGTGGATGTTCTCCTCCACTCATGAGT
 CTTTTCATCATGCCACATTATCTGATCCAGTCCTCACATTTTTTAAATATAAACTAAAGA
 GAGAATGCTTCTTACAGGAACAGTTACCCAAGGGCTGTTTCTTAGTAAGTGTCAAACT
 GATCTGGATCCATGGGCATACCTGTGTTTCGAGGTGCAGCAATTGCTTGGTGAGCTGTGCA
 GAATTGATTGCCTTCAGCACAGCATCCTCTGCCACCCCTTGTTTCTCATAAGCGATGTCT
 GGAGTGATTGTGGTTCTTGGAAGAGCAGAAGGAAAACTAAAAAGTGTATCTTGTATTTT
 CCTGCCCCTCAGGTTGCCTATGTATTTTACCTTTTCATATTTAAGGCAAAAGTACTTGAA
 AATTTTAAGTGTCCGAATAAGATATGTCTTTTTTGTGTTTTTTTTTGGTTGGTTGTTTG
 TTTTTTATCATCTGAGATTCTGTAATGTATTTGCAAATAATGGATCAATTAATTTTTTTT
 GAAGCTCATATTGTATCTTTTTTAAAAACCATGTTGTGGAAAAAGCCAGAGTGACAAGTG
 ACAAATCTATTTAGGAACTCTGTGTATGAATCCTGATTTTAACTGCTAGGATTCAGCTA
 AATTTCTGAGCTTTATGATCTGTGGAATTTGGAATGAAATCGAATTCATTTTGTACATA
 CATAGTATATTAAACTATATAATAGTTCATAGAAATGTTTCAGTAATGAAAAATATATC
 CAATCAGAGCCATCCCGAAAAAATAAAAAA (SEQ ID No. : 8827)

The FASTA file, including the sequence of NM_002310, was masked using the RepeatMasker web interface (Smit, AFA & Green, P RepeatMasker at <http://ftp.genome.washington.edu/RM/RepeatMasker.html>, Smit and Green). Specifically, during masking, the following types of sequences were replaced with “N”s: SINE/MIR & LINE/L2, LINE/L1, LTR/MaLR, LTR/Retroviral, Alu, and other low

informational content sequences such as simple repeats. Below is the sequence following masking:

CTCTCTCCCAGAACGTGTCTCTGCTGCAAGGCACCGGGCCCTTTCGCTCTGCAGAACTG
CACTTGCAAGACCATTATCAACTCCTAATCCCAGCTCAGAAAGGGAGCCTCTGCGACTC
ATTCATCGCCCTCCAGGACTGACTGCATTGCACAGATGATGGATATTTACGTATGTTTG
AAACGACCATCCTGGATGGTGGACAATAAAAGAATGAGGACTGCTTCAAATTTCCAGTG
GCTGTTATCAACATTTATTCTTCTATATCTAATGAATCAAGTAAATAGCCAGAAAAAGG
GGGCTCCTCATGATTTGAAGTGTGTAACCTAACAATTTGCAAGTGTGGAAGTGTCTTGG
AAAGCACCCCTCTGGAACAGGCCGTGGTACTGATTATGAAGTTTGCATTGAAAACAGGTC
CCGTTCTTGTTATCAGTTGGAGAAAACCAGTATTAAATTCAGCTCTTTCACATGGTG
ATTATGAAATAACAATAAATTCTCTACATGATTTTGGGAAGTTCTACAAGTAAATTCACA
CTAAATGAACAAAACGTTTCCTTAATTCAGATACTCCAGAGATCTTGAATTTGTCTGC
TGATTTCTCAACCTCTACATTATACCTAAAGTGGAACGACAGGGGTTCAGTTTTTCCAC
ACCGCTCAAATGTTATCTGGGAAATTAAAGTTCTACGTAAAGAGAGTATGGAGCTCGTA
AAATTAGTGACCCACAACACAACCTCTGAATGGCAAAGATACACTTCATCACTGGAGTTG
GGCCTCAGATATGCCCTTGGAATGTGCCATTCATTTTGTGGAAATTAGATGCTACATTG
ACAATCTTCATTTTTCTGGTCTCGAAGAGTGAGTGACTGGAGCCCTGTGAAGAACATT
TCTTGGATACCTGATTCTCAGACTAAGGTTTTTCTCAAGATAAAGTGATACTTGTAGG
CTCAGACATAACATTTTGTGTGTGAGTCAAGAAAAAGTGTTATCAGCACTGATTGGCC
ATACAAACTGCCCTTGATCCATCTTGATGGGGAAAATGTTGCAATCAAGATTCGTAAT
ATTTCTGTTTCTGCAAGTAGTGGAACAAATGTAGTTTTTACAACCGAAGATAACATATT
TGGAACCGTTATTTTTGCTGGATATCCACCAGATACTCCTCAACAACCTGAATTGTGAGA
CACATGATTTAAAAGAAATTATATGTAGTTGGAATCCAGGAAGGGTGACAGCGTTGGTG
GGCCACGTGCTACAAGCTACACTTTAGTTGAAAGTTTTTTCAGGAAAATATGTTAGACT
TAAAAGAGCTGAAGCACCTACAAACGAAAGCTATCAATTATTATTTCAAATGCTTCCAA
ATCAAGAAATATATAATTTTACTTTGAATGCTCACAATCCGCTGGGTGATCACAATCA
ACAATTTTAGTTAATATAACTGAAAAAGTTTATCCCCATACTCCTACTTCATTCAAAGT
GAAGGATATTAATTCAACAGCTGTAAACTTTCTTGGCATTTACCAGGCAACTTTGCAA
AGATTAATTTTTTATGTGAAATTGAAATTAAGAAATCTAATTCAGTACAAGAGCAGCGG
AATGTCACAATCAAAGGAGTAGAAAATTCAGTTATCTTGTGCTCTGGACAAGTTAAA
TCCATACACTCTATATACTTTTCGGATTCTGTTGTTCTACTGAACTTTCTGGAAATGGA

GCAAATGGAGCAATAAAAAACAACATTTAACAACAGAAGCCAGTCCTTCAAAGGGGCCCT
GATACTTGGAGAGAGTGGAGTTCTGATGGAAAAATTTAATAATCTATTGGAAGCCTTT
ACCCATTAATGAAGCTAATGGAAAAATACTTTCTACAATGTATCGTGTTTCATCAGATG
AGGAAACACAGTCCCTTTCTGAAATCCCTGATCCTCAGCACAAAGCAGAGATACGACTT
GATAAGAATGACTACATCATCAGCGTAGTGGCTAAAAATTTCTGTGGGCTCATCACCACC
TTCCAAAATAGCGAGTATGGAAATTCCAAATGATGATCTCAAATAGAACAAGTTGTTG
GGATGGGAAAGGGGATTCTCCTCACCTGGCATTACGACCCCAACATGACTTGCGACTAC
GTCATTAAGTGGTGTAACCTCGTCTCGGTGGAACCATGCCTTATGGACTGGAGAAAAGT
TCCCTCAAACAGCACTGAACTGTAATAGAATCTGATGAGTTTCGACCAGGTATAAGAT
ATAATTTTTTCTGTATGGATGCAGAAATCAAGGATATCAATTATTACGCTCCATGATT
GGATATATAGAAGAATTGGCTCCCATTGTTGCACCAAATTTTACTGTTGAGGATACTTC
TGCAGATTCGATATTAGTAAAATGGGAAGACATTCTGTGGAAGAACTTAGAGGCTTTT
TAAGAGGATATTTGTTTTACTTTTGAAAAGGAGAAAGAGACACATCTAAGATGAGGGTT
TTAGAATCAGGTCGTTCTGACATAAAAGTTAAGAATATTACTGACATATCCCAGAAGAC
ACTGAGAATTGCTGATCTTCAAGGTAAAAAAGTTACCACCTGGTCTTGCGAGCCTATA
CAGATGGTGGAGTGGGCCCCGAGAAGAGTATGTATGTGGTGACAAAGGAAAATTCTGTG
GGATTAATTATTGCCATTCTCATCCCAGTGGCAGTGGCTGTCATTGTTGGAGTGGTGAC
AAGTATCCTTTGCTATCGGAAACGAGAATGGATTAAAGAAACCTTCTACCCTGATATTC
CAAATCCAGAAAACGTAAAGCATTACAGTTTCAAAGAGTGTCTGTGAGGGAAGCAGT
GCTCTTAAACATTGGAAATGAATCCTTGTACCCCAAATAATGTTGAGGTTCTGGAAAC
TCGATCAGCATTTCTTAAATAGAAGATACAGAAATAATTTCCCCAGTAGCTGAGCGTC
CTGAAGATCGCTCTGATGCAGAGCCTGAAAACCATGTGGTTGTGTCTTATTGTCCACCC
ATCATTGAGGAAGAAATACCAAACCCAGCCGCAGATGAAGCTGGAGGGACTGCACAGGT
TATTTACATTGATGTTTCAGTCGATGTATCAGCCTCAAGCAAACCCAGAAGAACAAG
AAAATGACCCTGTAGGAGGGGCAGGCTATAAGCCACAGATGCACCTCCCCATTAATTCT
ACTGTGGAAGATATAGCTGCAGAAGAGGACTTAGATAAACTGCGGGTTACAGACCTCA
GGCCAATGTAAATACATGGAATTTAGTGTCTCCAGACTCTCCTAGATCCATAGACAGCA
ACAGTGAGATTGTCTCATTTGGAAGTCCATGCTCCATTAATTTCCGACAATTTTTGATT
CCTCCTAAAGATGAAGACTCTCCTAAATCTAATGGAGGAGGGTGGTCCTTTACAAACTT
TTTTCAGAACAAACCAACGATTAACAGTGTACCGTGTCACTTCAGTCAGCCATCTCA
ATAAGCTCTTACTGCTAGTGTTGCTACATCAGCACTGGGCATTCTTGAGGGATCCTGT
GAAGTATTGTTAGGAGGTGAACTTCACTACATGTTAAGTTACACTGAAAGTTCATGTGC

TTTTAATGTAGTCTAAAAGCCAAAGTATAGTGACTCAGAATCCTCAATCCACAAAACCTC
AAGATTGGGAGCTCTTTGTGATCAAGCCAAAGAATTCTCATGTACTCTACCTTCAAGAA
GCATTTCAAGGCTAATACCTACTTGTACGTACATGTAAAACAAATCCCGCCGCAACTGT
TTTCTGTTCTGTTGTTTGTGGTTTTCTCATATGTATACTTGGTGGAATTGTAAGTGGA
TTGCAGGCCAGGGAGAAAATGTCCAAGTAACAGGTGAAGTTTATTTGCCTGACGTTTAC
TCCTTTCTAGATGAAAACCAAGCACAGATTTTAAAACCTTCTAAGATTATTCTCCTCTAT
CCACAGCATTACNNNNNNNNNNNNNNNNNNNNNGTAGTGACAGCGATTTAGTGTTTT
GTTTGATAAAGTATGCTTATTTCTGTGCCTACTGTATAATGGTTATCAAACAGTTGTCT
CAGGGGTACAACTTTGAAAACAAGTGTGACACTGACCAGCCCAAATCATAATCATGTT
TTCTTGCTGTGATAGGTTTTGCTTGCCTTTTCATTATTTTTTAGCTTTTATGCTTGCTT
CCATTATTTCAAGTTGGTTGCCCTAATATTTAAAATTTACACTTCTAAGACTAGAGACCC
ACATTTTTTAAAAATCATTTTATTTTGTGATACAGTGACAGCTTTATATGAGCAAATTC
AATATTATTCATAAGCATGTAATTCAGTGACTTACTATGTGAGATGACTACTAAGCAA
TATCTAGCAGCGTTAGTTCATATAGTTCTGATTGGATTTTCGTTCCCTCCTGAGGAGACC
ATGCCGTTGAGCTTGGCTACCCAGGCAGTGGTGATCTTTGACACCTTCTGGTGGAATGTT
CCTCCCACTCATGAGTCTTTTCATCATGCCACATTATCTGATCCAGTCCTCACATTTTT
AAATATAAACTAAAGAGAGAATGCTTCTTACAGGAACAGTTACCCAAGGGCTGTTTCT
TAGTAAGTGTACATAAACTGATCTGGATCCATGGGCATACCTGTGTTGAGGTGCAGCAA
TTGCTTGGTGAGCTGTGCAGAATTGATTGCCTTCAGCACAGCATCCTCTGCCCACCCTT
GTTTCTCATAAGCGATGTCTGGAGTGATTGTGGTTCTTGAAAAGCAGAAGGAAAAACT
AAAAAGTGTATCTTGTATTTTCCCTGCCCTCAGGTTGCCTATGTATTTTACCTTTTCAT
ATTTAAGGCAAAGTACTTGAAAATTTTAAGTGTC CGAATAAGATATGTCTTTTTTGT
TGTTTTTTTTTGGTTGGTTGTTTGTATCATCTGAGATTCTGTAATGTATTTGCAA
ATAATGGATCAATTAATTTTTTTGAAGCTCATATTGTATCTTTTTTAAAACCATGTTG
TGAAAAAAGCCAGAGTGACAAGTGACAAAATCTATTTAGGAACTCTGTGTATGAATCC
TGATTTTAACTGCTAGGATTCAGCTAAATTTCTGAGCTTTATGATCTGTGGAAATTTGG
AATGAAATCGAATTCATTTTGTACATACATAGTATATTAAACTATATAATAGTTCATA
GAAATGTTCAAGTAATGAAAAAATATATCCAATCAGAGCCATCCCGAAAAA

A SEQ ID No.: 8828

The length of this sequence was determined using batch, automated computational methods and the sequence, as sense strand, its length, and the desired location of the probe sequence near the 3' end of the mRNA was submitted to Array Designer Ver 1.1 (Premier Biosoft International, Palo Alto, CA). Search quality was set at 100%, number of best probes set at 1, length range set at 50 base pairs, Target T_m set at 75 C. degrees plus or minus 5 degrees, Hairpin max deltaG at 6.0 -kcal/mol., Self dimmer max deltaG at 6.0 -kcal/mol, Run/repeat (dinucleotide) max length set at 5, and Probe site minimum overlap set at 1. When none of the 49 possible probes met the criteria, the probe site would be moved 50 base pairs closer to the 5' end of the sequence and resubmitted to Array Designer for analysis. When no possible probes met the criteria, the variation on melting temperature was raised to plus and minus 8 degrees and the number of identical basepairs in a run increased to 6 so that a probe sequence was produced.

In the sequence above, using the criteria noted above, Array Designer Ver 1.1 designed a probe corresponding to oligonucleotide number 2280 in Table 8 and is indicated by underlining in the sequence above. It has a melting temperature of 68.4 degrees Celsius and a max run of 6 nucleotides and represents one of the cases where the criteria for probe design in Array Designer Ver 1.1 were relaxed in order to obtain an oligonucleotide near the 3' end of the mRNA (Low melting temperature was allowed).

Clone 463D12

Clone 463D12 was sequenced and compared to the nr, dbEST, and UniGene databases at NCBI using the BLAST search tool. The sequence matched accession number AI184553, an EST sequence with the definition line "qd60a05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733840 3' similar to gb:M29550 PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT 1 (HUMAN);, mRNA sequence." The E value of the alignment was 1.00×10^{-118} . The GenBank sequence begins with a poly-T region, suggesting that it is the antisense strand, read 5' to 3'. The beginning of this sequence is complementary to the 3' end of the mRNA sense strand. The accession number for this sequence was included in a text file of accession numbers representing antisense sequences. Sequences for antisense strand mRNAs were obtained by uploading a text file containing desired accession numbers as an Entrez

search query using the Batch Entrez web interface and saving the results locally as a FASTA file. The following sequence was obtained, and the region of alignment of clone 463D12 is outlined:

```

TTTTTTTTTTTTTTCTTAAATAGCATTATTTTCTCTCAAAAAGCCTATTATGTACTAA
CAAGTGTTCTCTAAATTAGAAAGGCATCACTACTAAAAATTTTATACATATTTTTTATA
TAAGAGAAGGAATATTGGGTACAACTCTGAATTTCTCTTTATGATTTCTCTTAAAGTAT
AGAACAGCTATTAAAATGACTAATATTGCTAAAAATGAAGGCTACTAAATTTCCCAAGA
ATTTTCGGTGGAATGCCCAAAAATGGTGTTAAGATATGCAGAAGGGCCCATTTCAAGCAA
AGCAATCTCTCCACCCCTTCATAAAAGATTTAAGCTAAAAAAAAAAAAAAAAAAGAAAGAAA
ATCCAACAGCTGAAGACATTGGGCTATTTATAAATCTTCTCCCAGTCCCCCAGACAGCC
TCACATGGGGGCTGTAAACAGCTAACTAAAATATCTTTGAGACTCTTATGTCCACACCC
ACTGACACAAGGAGAGCTGTAAACCACAGTGAAACTAGACTTTGCTTTCTTTAGCAAGT
ATGTGCCTATGATAGTAACTGGAGTAAATGTAACAAGTAATAAAACAAATTTTTTTTAA
AAATAAAAATTATACCTTTTTCTCCAACAAACGGTAAAGACCACGTGAAGACATCCATA
AAATTAGGCAACCAGTAAAGATGTGGAGAACCAGTAACTGTGCGAAATTCATCACATTA
TTTTCATACTTTAATACAGCAGCTTTAATTATTGGAGAACATCAAAGTAATTAGGTGCC
GAAAAACATTGTTATTAATGAAGGGAACCCCTGACGTTTGACCTTTTCTGTACCATCTA
TAGCCCTGGACTTGA (SEQ ID No.: 8829)

```

The FASTA file, including the sequence of AA184553, was then masked using the RepeatMasker web interface, as shown below. The region of alignment of clone 463D12 is outlined.

```

TTTTTTTTTTTTTTCTTAAATAGCATTATTTTCTCTCAAAAAGCCTATTATGTACTAA
CAAGTGTTCTCTAAATTAGAAAGGCATCACTACNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNGAGAAGGAATATTGGGTACAACTCTGAATTTCTCTTTATGATTTCTCTTAAAGTAT
AGAACAGCTATTAAAATGACTAATATTGCTAAAAATGAAGGCTACTAAATTTCCCAAGA
ATTTTCGGTGGAATGCCCAAAAATGGTGTTAAGATATGCAGAAGGGCCCATTTCAAGCAA
AGCAATCTCTCCACCCCTTCATAAAAGATTTAAGCTAAAAAAAAAAAAAAAAAAGAAAGAAA
ATCCAACAGCTGAAGACATTGGGCTATTTATAAATCTTCTCCCAGTCCCCCAGACAGCC
TCACATGGGGGCTGTAAACAGCTAACTAAAATATCTTTGAGACTCTTATGTCCACACCC

```

ACTGACACAAGGAGAGCTGTAACCACAGTGAACTAGACTTTGCTTTCCTTTAGCAAGT
ATGTGCCTATGATAGTAACTGGAGTAAATGTAAACAGNNNNNNNNNNNNNNNNNNNNNNNNNN
 NNNNNNNNNNNNNNNNCCTTTTCTCCAACAAACGGTAAAGACCACGTGAAGACATCCATA
 AAATTAGGCAACCAGTAAAGATGTGGAGAACCAGTAAACTGTCGAAATTCATCACATTA
 TTTTCATACTTTAATACAGCAGCTTTAATTATTGGAGAACATCAAAGTAATTAGGTGCC
 GAAAAACATTGTTATTAATGAAGGGAACCCCTGACGTTTGACCTTTTCTGTACCATCTA
 TAGCCCTGGACTTGA Masked version of 463D12 sequence. (SEQ ID
 NO:8830)

The sequence was submitted to Array Designer as described above, however, the desired location of the probe was indicated at base pair 50 and if no probe met the criteria, moved in the 3' direction. The complementary sequence from Array Designer was used, because the original sequence was antisense. The oligonucleotide designed by Array Designer corresponds to oligonucleotide number 4342 in Table 8 and is complementary to the underlined sequence above. The probe has a melting temperature of 72.7 degrees centigrade and a max run of 4 nucleotides.

Clone 72D4

Clone 72D4 was sequenced and compared to the nr, dbEST, and UniGene databases at NCBI using the BLAST search tool. No significant matches were found in any of these databases. When compared to the human genome draft, significant alignments were found to three consecutive regions of the reference sequence NT_008060, as depicted below, suggesting that the insert contains three spliced exons of an unidentified gene.

| Residue numbers on clone 72D4 sequence | Matching residue numbers on NT_008060 |
|---|--|
| 1 – 198 | 478646 – 478843 |
| 197 – 489 | 479876 – 480168 |
| 491 – 585 | 489271 – 489365 |

Because the reference sequence contains introns and may represent either the coding or noncoding strand for this gene, BioCardia's own sequence file was used to design the oligonucleotide. Two complementary probes were designed to ensure that the

sense strand was represented. The sequence of the insert in clone 72D4 is shown below, with the three putative exons outlined.

```

CAGGTCACACAGCACATCAGTGGCTACATGTGAGCTCAGACCTGGGTCTGCT
GCTGTCTGTCTTCCCAATATCCATGACCTTGACGATGATGCAGGTGTCTAGGGAT
ACGTCCATCCCCGTCCTGCTGGAGCCCAGAGCACGGAAGCCTGGCCCTCCGA
GGAGACAGAAGGGAGTGTCTGGACACCATGACGAGAGCTTGGCAGAATAAAT
AACTTCTTTAAACAATTTTACGGCATGAAGAAATCTGGACCAGTTTATTAAAT
GGGATTTCTGCCACAAACCTTGGAAGAATCACATCATCTTANNCCCAAGTGA
AAACTGTGTTGCGTAACAAAGAACATGACTGCGCTCCACACATACATCATTG
CCCGGCGAGGCGGGACACAAGTCAACGACGGAACACTTGAGACAGGCCTAC
AACTGTGCACGGGTCAGAAGCAAGTTTAAGCCATACTTGCTGCAGTGAGACT
ACATTTCTGTCTATAGAAGATACTGACTTGATCTGTTTTTCAGCTCCAGTTC
CCAGATGTGCGTGTTGTGGTCCCAAGTATCACCTTCCAATTTCTGGGAGCA
GTGCTCTGGCCGATCCTTGCCGCGCGGATAAAAAC (SEQ ID NO.: 8445)

```

The sequence was submitted to RepeatMasker, but no repetitive sequences were found. The sequence shown above was used to design the two 50-mer probes using Array Designer as described above. The probes are shown in bold typeface in the sequence depicted below. The probe in the sequence is oligonucleotide number 6415 (SEQ ID NO.: 6415) in Table 8 and the complementary probe is oligonucleotide number 6805 (SEQ ID NO.:6805).

```

CAGGTCACACAGCACATCAGTGGCTACATGTGAGCTCAGACCTGGGTCTGCTGTCT
GTCTTCCCAATATCCATGACCTTGACTGATGCAGGTGTCTAGGGATACGTCCATCCCCG
TCCTGCTGGAGCCCAGAGCACGGAAGCCTGGCCCTCCGAGGAGACAGAAGGGAGTGTCTG
GACACCATGACGAGAGCTTGGCAGAATAAATAACTTCTTTAAACAATTTTACGGCATGA
AGAAATCTGGACCAGTTTATTAAATGGGATTTCTGCCACAAACCTTGGAAGAATCACAT
CATCTTANNCCCAAGTGAAACTGTGTTGCGTAACAAAGAACATGACTGCGCTCCACAC
ATACATCATTGCCCGGCGAGGCGGGACACAAGTCAACGACGGAACACTTGAGACAGGCC

```

TACAACTGTGCACGGGTCAGAAGCAAGTTTAAGCCATACTTGCTGCAGTGAGACTACAT
 TTCTGTCTATAGAAGATACCTGACTTGATCTGTTTTTCAGCTCCAGTTCCCAGATGTGC
 ← ---GTCAAGGGTCTACACG
 GTGTTGTGGTCCCCAAGTATCACCTTCCAATTTCTGGGAG--→
CACAACACCAGGGGTTCATAGTGGAAGGTTAAAG-5'

CAGTGCTCTGGCCGGATCCTTGCCGCGCGGATAAAAACT---→

Confirmation of probe sequence

Following probe design, each probe sequence was confirmed by comparing the sequence against dbEST, the UniGene cluster set, and the assembled human genome using BLASTn at NCBI. Alignments, accession numbers, gi numbers, UniGene cluster numbers and names were examined and the most common sequence used for the probe. The final probe set was compiled into Table 8.

Example 22 - Production of an array of 8000 spotted 50mer oligonucleotides

We produced an array of 8000 spotted 50mer oligonucleotides. Examples 20 and 21 exemplify the design and selection of probes for this array.

Sigma-Genosys (The Woodlands, TX) synthesized un-modified 50-mer oligonucleotides using standard phosphoramidite chemistry, with a starting scale of synthesis of 0.05 μ mole (see, e.g., R. Meyers, ed. (1995) Molecular Biology and Biotechnology: A Comprehensive Desk Reference). Briefly, to begin synthesis, a 3' hydroxyl nucleoside with a dimethoxytrityl (DMT) group at the 5' end was attached to a solid support. The DMT group was removed with trichloroacetic acid (TCA) in order to free the 5'-hydroxyl for the coupling reaction. Next, tetrazole and a phosphoramidite derivative of the next nucleotide were added. The tetrazole protonates the nitrogen of the phosphoramidite, making it susceptible to nucleophilic attack. The DMT group at the 5'-end of the hydroxyl group blocks further addition of nucleotides in excess. Next, the inter-nucleotide linkage was converted to a phosphotriester bond in an oxidation step using an oxidizing agent and water as the oxygen donor. Excess nucleotides were filtered

out and the cycle for the next nucleotide was started by the removal of the DMT protecting group. Following the synthesis, the oligo was cleaved from the solid support. The oligonucleotides were desalted, resuspended in water at a concentration of 100 or 200 μM , and placed in 96-deep well format. The oligonucleotides were re-arrayed into Whatman Uniplate 384-well polypropylene V bottom plates. The oligonucleotides were diluted to a final concentration 30 μM in 1X Micro Spotting Solution Plus (Telechem/arrayit.com, Sunnyvale, CA) in a total volume of 15 μl . In total, 8,031 oligonucleotides were arrayed into twenty-one 384-well plates.

Arrays were produced on Telechem/arrayit.com Super amine glass substrates (Telechem/arrayit.com), which were manufactured in 0.1 mm filtered clean room with exact dimensions of 25x76x0.96 mm. The arrays were printed using the Virtek Chipwriter with a Telechem 48 pin Micro Spotting Printhead. The Printhead was loaded with 48 Stealth SMP3B TeleChem Micro Spotting Pins, which were used to print oligonucleotides onto the slide with the spot size being 110-115 microns in diameter.

Example 23- Amplification, labeling, and hybridization of total RNA to an oligonucleotide microarray

Amplification, labeling, hybridization and scanning

Samples consisting of at least 2 μg of intact total RNA were further processed for array hybridization. Amplification and labeling of total RNA samples was performed in three successive enzymatic reactions. First, a single-stranded DNA copy of the RNA was made (hereinafter, "ss-cDNA"). Second, the ss-cDNA was used as a template for the complementary DNA strand, producing double-stranded cDNA (hereinafter, "ds-cDNA, or cDNA"). Third, linear amplification was performed by in vitro transcription from a bacterial T₇ promoter. During this step, fluorescent-conjugated nucleotides were incorporated into the amplified RNA (hereinafter, "aRNA").

The first strand cDNA was produced using the Invitrogen kit (Superscript II). The first strand cDNA was produced in a reaction composed of 50 mM Tris-HCl (pH 8.3), 75 mM KCl, and 3 mM MgCl₂ (1x First Strand Buffer, Invitrogen), 0.5 mM dGTP, 0.5 mM dATP, 0.5 mM dTTP, 0.5 mM dCTP, 10 mM DTT, 10 U reverse transcriptase (Superscript II, Invitrogen, #18064014), 15 U RNase inhibitor (RNAGuard, Amersham

Pharmacia, #27-0815-01), 5 μ M T7T24 primer

(5'-GGCCAGTGAATTGTAATACGACTCACTATAGGGAGGCGGTTTTTTTTTTTTTTT
TTTTTTTTTTTTTT-3'), (SEQ ID NO.:8831) and 2 μ g of selected sample total RNA.

Several purified, recombinant control mRNAs from the plant *Arabidopsis thaliana* were added to the reaction mixture: 20 pg of CAB and RCA, 14 pg of LTP4 and NAC1, and 2 pg of RCP1 and XCP2 (Stratagene, #252201, #252202, #252204, #252208, #252207, #252206 respectively). The control RNAs allow the estimate of copy numbers for individual mRNAs in the clinical sample because corresponding sense oligonucleotide probes for each of these plant genes are present on the microarray. The final reaction volume of 40 μ l was incubated at 42°C for 60 min.

For synthesis of the second cDNA strand, DNA polymerase and RNase were added to the previous reaction, bringing the final volume to 150 μ l. The previous contents were diluted and new substrates were added to a final concentration of 20 mM Tris-HCl (pH 7.0) (Fisher Scientific, Pittsburgh, PA #BP1756-100), 90 mM KCl (Teknova, Half Moon Bay, CA, #0313-500), 4.6 mM MgCl₂ (Teknova, Half Moon Bay, CA, #0304-500), 10 mM (NH₄)₂SO₄ (Fisher Scientific #A702-500) (1x Second Strand buffer, Invitrogen), 0.266 mM dGTP, 0.266 mM dATP, 0.266 mM dTTP, 0.266 mM dCTP, 40 U *E. coli* DNA polymerase (Invitrogen, #18010-025), and 2 U RNaseH (Invitrogen, #18021-014). The second strand synthesis took place at 16°C for 120 minutes.

Following second-strand synthesis, the ds-cDNA was purified from the enzymes, dNTPs, and buffers before proceeding to amplification, using phenol-chloroform extraction followed by ethanol precipitation of the cDNA in the presence of glycogen. Alternatively, a silica-gel column is used to purify the cDNA (e.g. Qiaquick PCR cleanup from Qiagen, #28104). The cDNA was collected by centrifugation at >10,000 \times g for 30 minutes, the supernatant is aspirated, and 150 μ l of 70% ethanol, 30% water was added to wash the DNA pellet. Following centrifugation, the supernatant was removed, and residual ethanol was evaporated at room temperature.

Linear amplification of the cDNA was performed by in vitro transcription of the cDNA. The cDNA pellet from the step described above was resuspended in 7.4 μ l of water, and in vitro transcription reaction buffer was added to a final volume of 20 μ l

containing 7.5 mM GTP, 7.5 mM ATP, 7.5 mM TTP, 2.25 mM CTP, 1.025 mM Cy3-conjugated CTP (Perkin Elmer; Boston, MA, #NEL-580), 1x reaction buffer (Ambion, Megascript Kit, Austin, TX and #1334) and 1 % T₇ polymerase enzyme mix (Ambion, Megascript Kit, Austin, TX and #1334). This reaction was incubated at 37°C overnight. Following in vitro transcription, the RNA was purified from the enzyme, buffers, and excess NTPs using the RNeasy kit from Qiagen (Valencia, CA; # 74106) as described in the vendor's protocol. A second elution step was performed and the two eluates were combined for a final volume of 60 µl. RNA is quantified using an Agilent 2100 bioanalyzer with the RNA 6000 nano LabChip.

Reference RNA was prepared as described above, except that 10 µg of total RNA was the starting material for amplification, and Cy5-CTP was incorporated instead of Cy3CTP. Reference RNA from five reactions was pooled together and quantitated as described above.

Hybridization to an array

RNA was prepared for hybridization as follows: for an 18mm×55mm array, 20 µg of amplified RNA (aRNA) was combined with 20 µg of reference aRNA. The combined sample and reference aRNA was concentrated by evaporating the water to 5 µl in a vacuum evaporator. Five µl of 20 mM zinc acetate was added to the aRNA and the mix incubated at 60°C for 10 minutes to fragment the RNA into 50-200 bp pieces. Following the incubation, 40 µl of hybridization buffer was added to achieve final concentrations of 5×SSC and 0.20 %SDS with 0.1 µg/ul of Cot-1 DNA (Invitrogen) as a competitor DNA. The final hybridization mix was heated to 98°C, and then reduced to 50°C at 0.1°C per second.

Alternatively, formamide is included in the hybridization mixture to lower the hybridization temperature.

The hybridization mixture was applied to the microarray surface, covered with a glass coverslip (Corning, #2935-246), and incubated in a humidified chamber (Telechem, AHC-10) at 62°C overnight. Following incubation, the slides were washed in 2×SSC, 0.1% SDS for two minutes, then in 2×SSC for two minutes, then in 0.2×SSC for two

minutes. The arrays were spun at 1000×g for 2 minutes to dry them. The dry microarrays are then scanned by methods described above.

Example 24: Analysis of Human Transplant Patient Mononuclear cell RNA Hybridized to a 24,000 Feature Microarray.

Patients who had recently undergone cardiac transplant and were being monitored for rejection by biopsy were selected and enrolled in a clinical study, as described in Example 11. Blood was drawn from several patients and mononuclear cells isolated as described in Example 8. The rejection grade determined from the biopsy is presented in Table 9 for some of the patient samples. Four samples (14-0001-2, 14-0001-3, 14-0005-1 and 14-0005-2) from one center were selected for further examination. Two sets of paired samples were available that allowed comparison of severe rejection (rejection grade 3A) to minimal or no rejection (rejection grade 1 or 0). These two groups are designated “high rejection grade” and “low rejection grade”, respectively.

Additional RNA was isolated from the mononuclear cells of enrolled cardiac allograft recipients as described in Example 8. The yield of RNA from 8 ml of blood is shown in Table 9, below.

1 or 2 µg of total RNA was amplified by making cDNA copies using a T7T24 primer and subsequent in vitro transcription, as described in Example 23. This “target” amplified RNA was labeled by incorporation of Cy3-conjugated nucleotides, as described in Example 23. The amplified RNA was quantified by analysis at A260 on a spectrophotometer.

Hybridization to the 8,000 probe (24,000-feature) microarray (described in Examples 20-22) was performed essentially as described in Example 23. 20 µg of amplified and labeled RNA was combined with 20 µg of R50 reference RNA that was labeled and prepared as described in Example 9.

The sample and reference amplified and labeled RNAs were combined and fragmented at 95°C for 30 min, as described in Example 23. The fragmented RNA was mixed with 40 µl of hybridization solution (to bring the total to 50 µl) and applied to the 8,000-probe, 24,000-feature microarray and covered with a 21mm×60mm coverslip. The arrays were hybridized overnight and washed as described in Example 23.

Once hybridized and washed, the arrays were scanned as described in Example 23. The full image produced by the Agilent scanner G2565AA was flipped, rotated, and split into two images (one for each signal channel) using TIFFSplitter (Agilent, Palo Alto, CA). The two channels are the output at 532 nm (Cy3-labeled sample) and 633 nm (Cy5-labeled R50). The individual images were loaded into GenePix 3.0 (Axon Instruments, Union City, CA) and the software was used to determine the median pixel intensity for each feature (F_i) and the median pixel intensity of the local background for each feature (B_i) in both channels. The standard deviation (SDF_i and SDB_i) for each is also determined. Features for which GenePix could not discriminate the feature from the background were “flagged”, and the data were deleted from further consideration.

From the remaining data, the following calculations were performed.

The first calculation performed was the signal to noise ratio:

$$S/N = \frac{F_i - B_i}{SDB_i}$$

All features with a S/N less than 3 in either channel were removed from further consideration. All features that did not have GenePix flags and passed the S/N test were considered usable features. The background-subtracted signal (hereinafter, “BGSS”) was calculated for each usable feature in each channel ($BGSS_i = F_i - B_i$).

The BGSS was used for the scaling step within each channel. The median BGSS for all usable features was calculated. The $BGSS_i$ for each feature was divided by the median BGSS. The median BGSS for the scaled data then became 1 for each channel on each array. This operation did not change the distribution of the data, but did allow each to be directly compared

The scaled $BGSS_i$ (S_i) for each feature was used to calculate the ratio of the Cy3 to the Cy5 signal:

$$R_n = \frac{Cy3S_i}{Cy5S_i}$$

The ratio data from the triplicate features were combined for each probe on the array. If all three features were still usable, their average was taken (R_p) and the coefficient of variation (hereinafter “CV”) was determined. If the CV was less than 15%, the average was carried forward for that probe. If the CV was greater than 15% for the triplicate features, then the average of the two features with the closest R_n values were used. If there were only two usable features for a given probe, the average of the two features was used. If there was only one usable feature for a given probe, the value of that feature was used.

The logarithm of the average ratio was taken for each probe ($\log R_p$). This value was used for comparison among arrays. For comparison of gene expression in high rejection grade patients to gene expression from low rejection grade patients, the average was taken for each probe for hybridizations 107739 and 107741 (high rejection grades) and 107740 and 107742 (low rejection grades). Since there were only two patients, each with a change from high to low rejection grade, there should be less variability in the data than if all four samples were from different patients. The results of this comparison were plotted in Figure 9. The X-axis is the high rejection grade average (the average of each probe for hybridizations of samples from high rejection grade patients) and the Y-axis is the low rejection grade average. There was complete data for 5562 probes, all plotted in Figure 9. Each “point” in the graph corresponded to a probe on the microarray.

A “cluster” of points were shaded in white. Points within the cluster represented genes with expression that is not significantly changed from one sample group to the other. The far ends of the cluster corresponded to genes that are expressed at either low or high levels in each group.

Outlier points, corresponding to genes with differential expression between high and low rejection grade patients, were shaded black and are further described in Table 10. There was one point above the cluster (indicating that expression was relatively higher in the low rejection grade than in the low rejection grade), and 7 points below the cluster (indicating that expression was relatively higher in the high rejection grade than in the low rejection grade).

Many of the differentially expressed genes had unknown or poorly described functions. One, corresponding to probe number 8091, was known in the public databases only as a predicted mRNA and protein.

Using the data from samples 107739 (Grade 3A rejection) and 107742 (Grade 0), a scaled ratio of sample (Cy3) to reference (Cy5) expression was determined using the same techniques. The ratio of was taken of these scaled ratios, denoted “the ratio of scaled ratios (hereinafter, “SR”). Replicate features were not combined and all probes with $S/N < 3$ in either channel were filtered out. Some probes with differential expression between these two samples are shown in Figure 10. In this Figure, the probes are sorted from the top to the bottom by relative expression in the first grade 0 sample vs grade 3A (ratio of SRs, grade 0/3A).

Diagnostic accuracy for sample classification is determined using additional samples and suitable methods for correlation analysis.

Comparing Figure 10 and Table 10, genes of particular interest include those corresponding to SEQ ID NO:2476, SEQ ID NO: 2407, SEQ ID NO:2192, SEQ ID NO: 2283, SEQ ID NO:6025, SEQ ID NO: 4481, SEQ ID NO:3761, SEQ ID NO: 3791, SEQ ID NO:4476, SEQ ID NO: 4398, SEQ ID NO:7401, SEQ ID NO: 1796, SEQ ID NO:4423, SEQ ID NO: 4429, SEQ ID NO:4430, SEQ ID NO: 4767, SEQ ID NO:4829 and SEQ ID NO: 8091.

Table 1

| Disease Classification | Disease/Patient Group |
|-------------------------------|---|
| Cardiovascular Disease | Atherosclerosis Unstable angina Myocardial Infarction Restenosis after angioplasty Congestive Heart Failure Myocarditis Endocarditis Endothelial Dysfunction Cardiomyopathy Cardiovascular drug use |
| Endocrine Disease | Diabetes Mellitus I and II Thyroiditis Addison's Disease |
| Infectious Disease | Hepatitis A, B, C, D, E, G Malaria Tuberculosis HIV Pneumocystis Carinii Giardia Toxoplasmosis Lyme Disease Rocky Mountain Spotted Fever Cytomegalovirus Epstein Barr Virus Herpes Simplex Virus Clostridium Difficile Colitis Meningitis (all organisms) Pneumonia (all organisms) Urinary Tract Infection (all organisms) Infectious Diarrhea (all organisms) Anti-infectious drug use |
| Angiogenesis | Pathologic angiogenesis Physiologic angiogenesis Treatment induced angiogenesis Pro or anti-angiogenic drug use |
| Inflammatory/Rheumatic | Rheumatoid Arthritis Systemic Lupus Erythematosus Sjogrens Disease CREST syndrome Scleroderma Ankylosing Spondylitis Crohn's Ulcerative Colitis Primary Sclerosing Cholangitis |

Table 1 (continued)

| Disease Classification | Disease/Patient Group |
|-------------------------------|--|
| Inflammatory/Rheumatic | Appendicitis Diverticulitis Primary Biliary Sclerosis Wegener's Granulomatosis Polyarteritis nodosa Whipple's Disease Psoriasis Microscopic Polyangiitis Takayasu's Disease Kawasaki's Disease Autoimmune hepatitis Asthma Churg-Strauss Disease Beurger's Disease Raynaud's Disease Cholecystitis Sarcoidosis Asbestosis Pneumoconioses Antinflammatory drug use |
| Transplant Rejection | Heart Lung Liver Pancreas Bowel Bone Marrow Stem Cell Graft versus host disease Transplant vasculopathy Skin Cornea Immunosuppressive drug use |
| Malignant Disorders | Leukemia Lymphoma Carcinoma Sarcoma |
| Neurological Disease | Alzheimer's Dementia Pick's Disease Multiple Sclerosis Guillain Barre Syndrome Peripheral Neuropathy |

Table 2: Candidate genes, Database mining

Unigene clusters are listed.

Cluster numbers are defined as in Unigene build #133 uploaded on: Fri Apr 20 2001

| | | | |
|--|--------------------------|--|--------------------------|
| CD50 | Hs.99995 | Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA. | Hs.79194 |
| CD70 = CD27L | Hs.99899 | Nucleolin (NCL) | Hs.79110 |
| MDC | Hs.97203 | MAPK14 | Hs.79107 |
| CD3z | Hs.97087 | CD100 | Hs.79089 |
| CD19 | Hs.96023 | OX-2 | Hs.79015 |
| | Hs.95388 | PCNA | Hs.78996 |
| CD3d | Hs.95327 | | Hs.78909 |
| | Hs.9456 | GRO-a | Hs.789 |
| interleukin 6 | Hs.93913 | CDw32A | Hs.78864 |
| phospholipaseA2 | Hs.93304 | H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP). | Hs.78683 |
| Human mRNA for KIAA0128 gene, partial cds. | Hs.90998 | CD41b = LIBS1 | Hs.785 |
| CD48 | Hs.901 | ANXA1 (LPC1) | Hs.78225 |
| heat shock 70kD protein 1A | Hs.8997 | CD31 | Hs.78146 |
| TxA2 receptor | Hs.89887 | Homo sapiens TERF1 (TRF1)-interacting nuclear factor 2 (TINF2), mRNA. | Hs.7797 |
| fragile X mental retardation protein (FMR-1) | Hs.89764 | major histocompatibility complex, class I, B | Hs.77961 |
| CD20 | Hs.89751 | LOX1 | Hs.77729 |
| ENA-78 | Hs.89714 | major histocompatibility complex, class II, DM alpha | Hs.77522 |
| IL-2 | Hs.89679 | CD64 | Hs.77424 |
| CD79b | Hs.89575 | CD71 | Hs.77356 |
| CD2 | Hs.89476 | | Hs.77054 |
| SDF-1=CXCR4 | Hs.89414 | HLA-DRA | Hs.76807 |
| CD61 | Hs.87149 | CD105 | Hs.76753 |
| IFN-g | Hs.856 | | Hs.76691 |
| CD34 | Hs.85289 | TNF-alpha | Hs.76507 |
| CD104 | Hs.85266 | LCP1 | Hs.76506 |
| CD8 | Hs.85258 | TMSB4X | Hs.75968 |
| IGF-1 | Hs.85112 | PAI2 | Hs.75716 |
| CD103 | Hs.851 | MIP-1b | Hs.75703 |
| IL-13 | Hs.845 | CD58 | Hs.75626 |
| RPA1 | Hs.84318 | CD36 | Hs.75613 |
| CD74 | Hs.84298 | hnRNP A2 / hnRNP B1 | Hs.75598 |
| CD132 | Hs.84 | CD124 | Hs.75545 |
| CD18 | Hs.83968 | MIP-3a | Hs.75498 |
| Cathepsin K | Hs.83942 | beta-2-microglobulin | Hs.75415 |
| CD80 | Hs.838 | FPR1 | Hs.753 |
| CD46 | Hs.83532 | Topo2B | Hs.75248 |
| NFKB1 | Hs.83428 | interleukin enhancer binding factor 2, 45kD | Hs.75117 |
| IL-18 | Hs.83077 | chloride intracellular channel 1 | Hs.74276 |
| interleukin 14 | Hs.83004 | EGR3 | Hs.74088 |
| L-selectin = CD62L | Hs.82848 | MIP-1a | Hs.73817 |
| CD107b | Hs.8262 | CD62P = p-selectin | Hs.73800 |
| CD69 | Hs.82401 | CD21 | Hs.73792 |
| CD95 | Hs.82359 | APE | Hs.73722 |
| CD53 | Hs.82212 | IL12Rb2 | Hs.73165 |

Table 2: Candidate genes, Database mining

| | | | |
|--|---------------------------|--|---------------------------|
| Human lymphocyte specific interferon regulatory factor/interferon regulatory factor 4 (LSIRF/IRF4) mRNA, complete cds. | Hs.82132 | NFKB2 | Hs.73090 |
| IL-16 | Hs.82127 | I-309 | Hs.72918 |
| DUT | Hs.82113 | immunoglobulin superfamily, member 4 | Hs.70337 |
| CDw121a | Hs.82112 | IL-3 | Hs.694 |
| PAI-1 | Hs.82085 | | Hs.6895 |
| TGF- β R2 | Hs.82028 | NTH1 | Hs.66196 |
| CD117 | Hs.81665 | CD40L | Hs.652 |
| HLA-DPB1 | Hs.814 | IL-11R | Hs.64310 |
| NFKBIA | Hs.81328 | Homo sapiens toll-like receptor 2 (TLR2) mRNA. | Hs.63668 |
| CD6 | Hs.81226 | ferritin H chain | Hs.62954 |
| IL-1 RA | Hs.81134 | IL8 | Hs.624 |
| UBE2B (RAD6B) | Hs.811 | Tissue Factor | Hs.62192 |
| Lyn | Hs.80887 | F-box only protein 7 | Hs.5912 |
| STAT4 | Hs.80642 | CD5 | Hs.58685 |
| UBE2A (RAD6A) | Hs.80612 | guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 | Hs.5662 |
| Fractalkine | Hs.80420 | SCYA11 | Hs.54460 |
| IK cytokine, down-regulator of HLA II | Hs.8024 | IK1 | Hs.54452 |
| | Hs.79933 | CCR1 | Hs.516 |
| CD79a | Hs.79630 | Homo sapiens TRAIL receptor 2 mRNA, complete cds. | Hs.51233 |
| | Hs.7942 | CD11c | Hs.51077 |
| nuclear factor, interleukin 3 regulated | Hs.79334 | CD66a | Hs.50964 |
| CD83 | Hs.79197 | JAK1 | Hs.50651 |
| DC-CK1 | Hs.16530 | Homo sapiens programmed cell death 4 (PDCD4), mRNA. | Hs.100407 |
| CCR7 | Hs.1652 | SCYB13 (CXCL13) | Hs.100431 |
| TLR4 | Hs.159239 | SMAD7 | Hs.100602 |
| EST | Hs.158975 | RAD51L1 (RAD51B) | Hs.100669 |
| EST | Hs.158966 | PPARG | Hs.100724 |
| EST | Hs.158965 | transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) | Hs.101047 |
| EST | Hs.158943 | major histocompatibility complex, class I-like sequence | Hs.101840 |
| EST | Hs.158894 | immunoglobulin superfamily containing leucine-rich repeat | Hs.102171 |
| EST | Hs.158877 | CD166 | Hs.10247 |
| EST | Hs.157815 | fibroblast tropomyosin TM30 (pl) | Hs.102824 |
| EST | Hs.157813 | interleukin 1 receptor-like 2 | Hs.102865 |
| ESTs | Hs.157569 | GTF2H4 | Hs.102910 |
| immunoglobulin kappa constant | Hs.156110 | | Hs.10326 |
| INPP5D | Hs.155939 | Human ITAC (IBICK) | Hs.103982 |
| C3AR1 | Hs.155935 | novel protein with MAM domain | Hs.104311 |
| PRKDC | Hs.155637 | ESTs, Weakly similar to interleukin enhancer binding factor 2 [H.sapiens] | Hs.105125 |

Table 2: Candidate genes, Database mining

| | | | |
|--|------------------|--|------------------|
| MHC class II HLA-DRw53-associated glycoprotein | <u>Hs.155122</u> | Homo sapiens clone 24686 mRNA sequence. | Hs.105509 |
| CD73 | <u>Hs.153952</u> | | Hs.105532 |
| CD37 | <u>Hs.153053</u> | Homo sapiens granulysin (GNLY), transcript variant 519, mRNA. | Hs.105806 |
| IFNAR1 | <u>Hs.1513</u> | CD77 | Hs.105956 |
| Homo sapiens solute carrier family 21 (organic anion transporter), member 11 (SLC21A11), mRNA. | Hs.14805 | RD RNA-binding protein | <u>Hs.106061</u> |
| EST | <u>Hs.146627</u> | | Hs.106673 |
| SET translocation (myeloid leukemia-associated) | <u>Hs.145279</u> | | Hs.10669 |
| EST | Hs.144119 | Homo sapiens clone 24818 mRNA sequence. | Hs.106823 |
| ESTs | <u>Hs.143534</u> | | Hs.106826 |
| STAT3 | <u>Hs.142258</u> | | Hs.10712 |
| CD96 | <u>Hs.142023</u> | | Hs.107149 |
| CD23 | <u>Hs.1416</u> | hypothetical protein | <u>Hs.10729</u> |
| EGR2 | <u>Hs.1395</u> | Tachykinin Receptor 1 | Hs.1080 |
| CDw84 | <u>Hs.137548</u> | glycophorin A | Hs.108694 |
| <u>CD55</u> | <u>Hs.1369</u> | Histone H1x | Hs.109804 |
| EST | <u>Hs.135339</u> | CD66d | Hs.11 |
| GM-CSF | <u>Hs.1349</u> | interleukin 17 | Hs.110040 |
| EST | <u>Hs.133175</u> | | Hs.110131 |
| CD1a | <u>Hs.1309</u> | major histocompatibility complex, class I, F | <u>Hs.110309</u> |
| CD10 | <u>Hs.1298</u> | REV1 | Hs.110347 |
| HVEM | <u>Hs.129708</u> | HCR | Hs.110746 |
| C9 | <u>Hs.1290</u> | VWF | Hs.110802 |
| C6 | <u>Hs.1282</u> | high affinity immunoglobulin epsilon receptor beta subunit | <u>Hs.11090</u> |
| C1R | <u>Hs.1279</u> | interleukin 22 receptor | Hs.110915 |
| IL-1b | <u>Hs.126256</u> | | Hs.110978 |
| CD9 | <u>Hs.1244</u> | Homo sapiens ubiquitin specific protease 6 (Tre-2 oncogene) (USP6), mRNA. | Hs.111065 |
| | <u>Hs.12305</u> | | Hs.111128 |
| Homo sapiens Vanin 2 (VNN2) mRNA. | Hs.121102 | MMP2 | Hs.111301 |
| Hsp10 | Hs.1197 | major histocompatibility complex, class II, DN alpha | <u>Hs.11135</u> |
| CD59 | <u>Hs.119663</u> | LTBR | <u>Hs.1116</u> |
| CD51 | <u>Hs.118512</u> | ESTs, Weakly similar to A41285 interleukin enhancer-binding factor ILF-1 [H.sapiens] | <u>Hs.111941</u> |
| CD49a | <u>Hs.116774</u> | Homo sapiens STRIN protein (STRIN), mRNA. | Hs.112144 |
| CD72 | <u>Hs.116481</u> | MSH5 | Hs.112193 |
| HLA-DMB | <u>Hs.1162</u> | TCRg | Hs.112259 |
| MCP-4 | <u>Hs.11383</u> | | Hs.11307 |
| | <u>Hs.111554</u> | CMKRL2 | Hs.113207 |

Table 2: Candidate genes, Database mining

| | | | |
|---|-----------|--|-----------|
| ferritin L chain | Hs.111334 | CCR8 | Hs.113222 |
| TGF-b | Hs.1103 | LILRA3 | Hs.113277 |
| Homo sapiens ras homolog gene family, member H (ARHH), mRNA. | Hs.109918 | Human CXCR-5 (BLR-1) | Hs.113916 |
| lysosomal alpha-mannosidase (MANB) | Hs.108969 | RAD51C | Hs.11393 |
| | Hs.108327 | myosin, heavy polypeptide 8, skeletal muscle, perinatal | Hs.113973 |
| granzyme B | Hs.1051 | CD42a | Hs.1144 |
| HCC-4 | Hs.10458 | TNFRSF11A | Hs.114676 |
| | Hs.10362 | | Hs.114931 |
| | Hs.102630 | MSH4 | Hs.115246 |
| | Hs.101382 | Homo sapiens dendritic cell immunoreceptor (DCIR), mRNA. | Hs.115515 |
| C4BPA | Hs.1012 | REV3L (POLZ) | Hs.115521 |
| CD125 | Hs.100001 | JAK2 | Hs.115541 |
| TERF2 | Hs.100030 | OPG ligand | Hs.115770 |
| LIG3 | Hs.100299 | PCDH12 | Hs.115897 |
| | Hs.157489 | | Hs.166235 |
| EST | Hs.157560 | POLE1 | Hs.166846 |
| EST | Hs.157808 | regulatory factor X, 5 (influences HLA class II expression) | Hs.166891 |
| EST | Hs.157811 | PIG-F (phosphatidyl-inositol-glycan class F) | Hs.166982 |
| | Hs.158127 | ESTs, Moderately similar to ILF1_HUMAN INTERLEUKIN ENHANCER-BINDING FACTOR 1 [H.sapiens] | Hs.167154 |
| interleukin 18 receptor accessory protein | Hs.158315 | HLA-DRB6 | Hs.167385 |
| CCR3 | Hs.158324 | ret finger protein-like 3 | Hs.167751 |
| Human DNA sequence from clone CTA-390C10 on chromosome 22q11.21-12.1 Contains an Immunoglobulin-like gene and a pseudogene similar to Beta Crystallin, ESTs, STSs, GSSs and taga and tat repeat polymorphisms | Hs.158352 | CD56 | Hs.167988 |
| ESTs | Hs.158576 | RBT1 | Hs.169138 |
| | Hs.158874 | APOE | Hs.169401 |
| EST | Hs.158875 | | Hs.16944 |
| EST | Hs.158876 | | Hs.169470 |
| EST | Hs.158878 | MMP12 | Hs.1695 |
| EST | Hs.158956 | CD161 | Hs.169824 |
| EST | Hs.158967 | tenascin XB | Hs.169886 |
| EST | Hs.158969 | | Hs.170027 |
| EST | Hs.158971 | | Hs.170150 |
| EST | Hs.158988 | C4A | Hs.170250 |

Table 2: Candidate genes, Database mining

| | | | |
|---|------------------|--|------------------|
| CD120a=TNFR-1 | <u>Hs.159</u> | TP53BP1 | Hs.170263 |
| EST | Hs.159000 | ESTs | Hs.170274 |
| | Hs.159013 | ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens] | Hs.170338 |
| EST | Hs.159025 | ESTs | Hs.170578 |
| EST | Hs.159059 | EST | Hs.170579 |
| IL18R1 | <u>Hs.159301</u> | ESTs | Hs.170580 |
| ftp-3 | Hs.159494 | EST | Hs.170581 |
| CASP8 | Hs.159651 | ESTs | Hs.170583 |
| EST | Hs.159655 | EST | Hs.170586 |
| EST | Hs.159660 | EST | Hs.170588 |
| EST | Hs.159678 | EST | Hs.170589 |
| kallikrein 12 (KLK12) | Hs.159679 | | Hs.170772 |
| EST | Hs.159682 | ESTs | Hs.170786 |
| EST | Hs.159683 | EST | Hs.170909 |
| EST | Hs.159693 | EST | Hs.170912 |
| EST | Hs.159706 | EST | Hs.170933 |
| EST | Hs.159718 | ESTs | Hs.171004 |
| SPO11 | Hs.159737 | EST | Hs.171095 |
| EST | Hs.159754 | EST | Hs.171098 |
| EST | Hs.160401 | ESTs | Hs.171101 |
| EST | Hs.160405 | EST | Hs.171108 |
| EST | Hs.160408 | ESTs | Hs.171110 |
| EST | Hs.160410 | ESTs | Hs.171113 |
| EST | Hs.160423 | ESTs | Hs.171117 |
| RPA3 | Hs.1608 | EST | Hs.171119 |
| ESTs | Hs.160946 | ESTs | Hs.171120 |
| EST | Hs.160956 | EST | Hs.171122 |
| ESTs | Hs.160978 | EST | Hs.171123 |
| EST | Hs.160980 | EST | Hs.171124 |
| EST | Hs.160981 | EST | Hs.171140 |
| EST | Hs.160982 | EST | Hs.171216 |
| EST | Hs.160983 | EST | Hs.171260 |
| Tachykinin Receptor 2 | Hs.161305 | ESTs | Hs.171264 |
| RAD17 (RAD24) | Hs.16184 | RIP | Hs.171545 |
| Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds. | Hs.162808 | ESTs, Weakly similar to immunoglobulin superfamily member [D.melanogaster] | <u>Hs.171697</u> |
| Human alpha-1 Ig germline C-region membrane-coding region, 3' end | <u>Hs.163271</u> | CD22 | <u>Hs.171763</u> |
| GCP-2 | <u>Hs.164021</u> | | Hs.171776 |
| | Hs.164284 | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C | <u>Hs.171921</u> |
| EST | Hs.164331 | interleukin 11 | <u>Hs.1721</u> |
| | Hs.164427 | <u>CD11b</u> | <u>Hs.172631</u> |
| | Hs.165568 | EST, Highly similar to APS [H.sapiens] | Hs.172656 |
| ER | Hs.1657 | ALK1 | Hs.172670 |

Table 2: Candidate genes, Database mining

| | | | |
|---|-----------|---|-----------|
| EST, Highly similar to JM26 [H.sapiens] | Hs.165701 | | Hs.172674 |
| EST | Hs.165702 | CD123 | Hs.172689 |
| EST | Hs.165704 | ESTs | Hs.172822 |
| EST | Hs.165732 | Colla1 | Hs.172928 |
| regulatory factor X, 3 (influences HLA class II expression) | Hs.166019 | | Hs.172998 |
| LIG4 | Hs.166091 | | Hs.173081 |
| TNFSF18 | Hs.248197 | myosin, heavy polypeptide 3, skeletal muscle, embryonic | Hs.173084 |
| EST | Hs.248228 | | Hs.173201 |
| H.sapiens rearranged gene for kappa immunoglobulin subgroup V kappa IV | Hs.248756 | Mediterranean fever (MEFV) | Hs.173730 |
| caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase) | Hs.2490 | | Hs.173749 |
| EST | Hs.249031 | interleukin 1 receptor accessory protein | Hs.173880 |
| TNFRSF10A | Hs.249190 | EST, Weakly similar to RL13_HUMAN 60S RIBOSOMAL PROTEIN L13 [H.sapiens] | Hs.174231 |
| immunoglobulin lambda variable 3-10 | Hs.249208 | EST | Hs.174242 |
| Homo sapiens mRNA for single-chain antibody, complete cds | Hs.249245 | EST | Hs.174300 |
| EST | Hs.250473 | EST | Hs.174634 |
| ESTs | Hs.250591 | EST | Hs.174635 |
| ESTs | Hs.250605 | EST | Hs.174650 |
| | Hs.25063 | EST | Hs.174673 |
| Human DNA sequence from clone RP1-149A16 on chromosome 22 Contains an IGLC (Immunoglobulin Lambda Chain C) pseudogene, the RFPL3 gene for Ret finger protein-like 3, the RFPL3S gene for Ret finger protein-like 3 antisense, the gene for a novel Immunoglobulin Lambda Chain V family protein, the gene for a novel protein similar to mouse RGDS (RALGDS, RALGEF, Guanine Nucleotide Dissociation Stimulator A) and rabbit oncogene RSC, the gene for a novel protein (ortholog of worm F16A11.2 and bacterial and archaea-bacterial predicted proteins), the gene for a novel protein similar to BPI (Bacterial Permeability-Increasing Protein) and rabbit LBP (Liposaccharide-Binding Protein) and the 5' part of a novel gene. Contains ESTs, STSSs, GSSs and three putative CpG islands | Hs.250675 | EST | Hs.174716 |
| ACE | Hs.250711 | EST | Hs.174740 |
| TREX2 | Hs.251398 | EST | Hs.174778 |

Table 2: Candidate genes, Database mining

| | | | |
|--|------------------|--|------------------|
| Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs | <u>Hs.251417</u> | EST | Hs.174779 |
| EST | Hs.251539 | EST, Weakly similar to RL13_HUMAN 60S RIBOSOMAL PROTEIN L13 [H.sapiens] | Hs.174780 |
| EST | Hs.251540 | (KIAA0033) for ORF, partial cds. | Hs.174905 |
| C3 | <u>Hs.251972</u> | | Hs.175270 |
| EST | Hs.252273 | EST | Hs.175281 |
| EST | Hs.252359 | EST | Hs.175300 |
| ESTs, Moderately similar to T2DT_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 105 KDA SUBUNIT [H.sapiens] | Hs.252867 | EST | Hs.175336 |
| EST, Moderately similar to RS2_HUMAN 40S RIBOSOMAL PROTEIN S2 [H.sapiens] | Hs.253150 | EST | Hs.175388 |
| EST | Hs.253151 | | Hs.175437 |
| EST | Hs.253154 | EST, Weakly similar to salivary proline-rich protein precursor [H.sapiens] | Hs.175777 |
| EST | Hs.253165 | EST | Hs.175803 |
| EST | Hs.253166 | ESTs | Hs.176337 |
| EST | Hs.253167 | EST | Hs.176374 |
| EST | Hs.253168 | EST | Hs.176380 |
| EST | Hs.253169 | EST | Hs.176404 |
| interleukin 1 receptor, type II | <u>Hs.25333</u> | EST | Hs.176406 |
| | Hs.25361 | LCK | Hs.1765 |
| EST | Hs.253742 | LIG1 | Hs.1770 |
| EST | Hs.253743 | EST | Hs.177012 |
| EST, Weakly similar to AF161429_1 HSPC311 [H.sapiens] | Hs.253744 | PERB11 family member in MHC class I region | <u>Hs.17704</u> |
| EST | Hs.253747 | EST | Hs.177146 |
| EST | Hs.253748 | EST | Hs.177209 |
| EST | Hs.253753 | | Hs.177376 |
| EST, Moderately similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY□ [H.sapiens] | Hs.254108 | | Hs.177461 |
| ESTs | Hs.254948 | CD99 | Hs.177543 |
| ESTs | Hs.255011 | PMS2 | Hs.177548 |
| EST | Hs.255118 | human calmodulin | Hs.177656 |
| EST | Hs.255119 | | Hs.177712 |
| EST | Hs.255123 | Homo sapiens immunoglobulin lambda gene locus DNA, clone:288A10 | <u>Hs.178665</u> |
| EST | Hs.255129 | | Hs.178743 |
| EST | Hs.255134 | EST | Hs.179008 |
| EST | Hs.255135 | EST | Hs.179070 |
| EST | Hs.255139 | EST | Hs.179130 |

Table 2: Candidate genes, Database mining

| | | | |
|---|-----------|---|------------------|
| EST | Hs.255140 | EST | Hs.179132 |
| ESTs | Hs.255142 | | Hs.179149 |
| EST | Hs.255150 | EST | Hs.179490 |
| EST | Hs.255152 | EST | Hs.179492 |
| ESTs | Hs.255153 | promyelocytic leukemia cell mRNA, clones pHH58 and pHH81. | Hs.179735 |
| ESTs | Hs.255157 | | Hs.179817 |
| ESTs | Hs.255171 | major histocompatibility complex, class II, DO beta | <u>Hs.1802</u> |
| EST | Hs.255172 | HLA-DRB1 | <u>Hs.180255</u> |
| EST, Moderately similar to PGTA_HUMAN RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT [H.sapiens] | Hs.255174 | TNFRSF12 | Hs.180338 |
| EST | Hs.255177 | RAD23A (HR23A) | Hs.180455 |
| EST | Hs.255178 | MKK3 | Hs.180533 |
| EST | Hs.255245 | EST | Hs.180637 |
| EST | Hs.255246 | CD27 | <u>Hs.180841</u> |
| EST | Hs.255249 | STAT6 | Hs.181015 |
| EST | Hs.255251 | TNFSF4 | Hs.181097 |
| EST | Hs.255253 | immunoglobulin lambda locus | <u>Hs.181125</u> |
| EST | Hs.255254 | | Hs.181368 |
| EST | Hs.255255 | CD3 | <u>Hs.181392</u> |
| ESTs | Hs.255256 | EST | Hs.255745 |
| EST | Hs.255330 | EST | Hs.255746 |
| EST, Weakly similar to putative G protein-coupled Receptor [H.sapiens] | Hs.255333 | EST | Hs.255747 |
| EST | Hs.255336 | EST | Hs.255749 |
| EST | Hs.255337 | EST | Hs.255754 |
| EST | Hs.255339 | ESTs, Moderately similar to KIAA1271 protein [H.sapiens] | Hs.255759 |
| EST | Hs.255340 | EST | Hs.255762 |
| EST | Hs.255341 | EST | Hs.255763 |
| ESTs | Hs.255343 | EST | Hs.255764 |
| EST | Hs.255347 | EST | Hs.255766 |
| EST | Hs.255349 | EST | Hs.255767 |
| EST | Hs.255350 | EST | Hs.255768 |
| EST | Hs.255354 | EST | Hs.255769 |
| ESTs | Hs.255359 | EST | Hs.255770 |
| ESTs | Hs.255387 | EST | Hs.255772 |
| EST | Hs.255388 | EST | Hs.255777 |
| EST | Hs.255389 | EST | Hs.255778 |
| ESTs | Hs.255390 | EST | Hs.255779 |
| EST | Hs.255392 | EST | Hs.255782 |
| EST | Hs.255444 | EST | Hs.255783 |
| EST | Hs.255446 | EST | Hs.255784 |
| EST | Hs.255448 | EST | Hs.255785 |
| ESTs | Hs.255449 | EST, Weakly similar to Con1 [H.sapiens] | Hs.255788 |
| EST | Hs.255454 | EST | Hs.255791 |
| EST | Hs.255455 | EST | Hs.255794 |
| EST | Hs.255457 | EST | Hs.255796 |
| EST | Hs.255459 | EST | Hs.255797 |

Table 2: Candidate genes, Database mining

| | | | |
|--|-----------|---|-----------|
| EST | Hs.255462 | EST | Hs.255799 |
| EST | Hs.255464 | ESTs | Hs.255877 |
| EST | Hs.255492 | EST | Hs.255880 |
| EST | Hs.255494 | EST | Hs.255920 |
| EST | Hs.255495 | EST | Hs.255927 |
| EST | Hs.255497 | CD40 | Hs.25648 |
| EST | Hs.255498 | interleukin enhancer binding factor 3, 90kD | Hs.256583 |
| EST | Hs.255499 | ESTs | Hs.256810 |
| EST | Hs.255501 | EST | Hs.256956 |
| EST | Hs.255502 | EST | Hs.256957 |
| EST | Hs.255505 | EST | Hs.256959 |
| EST | Hs.255541 | EST | Hs.256961 |
| EST | Hs.255543 | EST | Hs.256970 |
| ESTs | Hs.255544 | EST | Hs.256971 |
| EST | Hs.255546 | ESTs | Hs.256979 |
| EST | Hs.255549 | ESTs | Hs.257572 |
| EST | Hs.255552 | EST | Hs.257579 |
| EST | Hs.255554 | EST | Hs.257581 |
| EST | Hs.255556 | EST | Hs.257582 |
| EST | Hs.255558 | EST | Hs.257630 |
| EST | Hs.255559 | EST | Hs.257632 |
| EST | Hs.255560 | EST | Hs.257633 |
| EST | Hs.255561 | EST | Hs.257636 |
| EST | Hs.255569 | EST | Hs.257640 |
| EST | Hs.255572 | ESTs | Hs.257641 |
| EST | Hs.255573 | EST | Hs.257644 |
| EST | Hs.255575 | EST | Hs.257645 |
| EST | Hs.255577 | EST | Hs.257646 |
| EST | Hs.255578 | EST | Hs.257647 |
| EST | Hs.255579 | EST | Hs.257667 |
| EST | Hs.255580 | EST | Hs.257668 |
| EST | Hs.255590 | EST | Hs.257677 |
| EST | Hs.255591 | EST | Hs.257679 |
| EST | Hs.255598 | EST | Hs.257680 |
| TNFRSF17 | Hs.2556 | ESTs | Hs.257682 |
| EST | Hs.255600 | ESTs | Hs.257684 |
| EST | Hs.255601 | EST | Hs.257687 |
| ESTs, Highly similar to KIAA1039 protein [H.sapiens] | Hs.255603 | EST | Hs.257688 |
| EST | Hs.255614 | EST | Hs.257690 |
| EST | Hs.255615 | EST | Hs.257695 |
| ESTs | Hs.255617 | EST | Hs.257697 |
| EST | Hs.255618 | EST | Hs.257705 |
| EST | Hs.255621 | EST | Hs.257706 |
| EST | Hs.255622 | EST | Hs.257709 |
| ESTs | Hs.255625 | ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY□ [H.sapiens] | Hs.257711 |
| EST | Hs.255626 | EST | Hs.257713 |
| ESTs | Hs.255627 | EST | Hs.257716 |
| ESTs | Hs.255630 | EST | Hs.257719 |
| EST | Hs.255632 | EST | Hs.257720 |
| EST | Hs.255633 | EST | Hs.257727 |

Table 2: Candidate genes, Database mining

| | | | |
|------|-----------|--|------------------|
| EST | Hs.255634 | EST | Hs.257730 |
| EST | Hs.255635 | EST | Hs.257738 |
| EST | Hs.255637 | EST | Hs.257743 |
| ESTs | Hs.255639 | ESTs | Hs.258513 |
| EST | Hs.255641 | EST | Hs.258820 |
| EST | Hs.255644 | EST | Hs.258864 |
| EST | Hs.255645 | sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F | <u>Hs.25887</u> |
| EST | Hs.255646 | EST | Hs.258898 |
| EST | Hs.255647 | EST | Hs.258933 |
| EST | Hs.255648 | interleukin 13 receptor, alpha 2 | <u>Hs.25954</u> |
| EST | Hs.255649 | Homo sapiens HSPC101 mRNA, partial cds | Hs.259683 |
| EST | Hs.255650 | EST | Hs.263695 |
| EST | Hs.255653 | ESTs | Hs.263784 |
| EST | Hs.255657 | TNFSF12 | Hs.26401 |
| EST | Hs.255661 | EST | Hs.264154 |
| ESTs | Hs.255664 | EST | Hs.264654 |
| EST | Hs.255665 | CDw116b | <u>Hs.265262</u> |
| EST | Hs.255666 | MHC binding factor, beta | <u>Hs.2654</u> |
| EST | Hs.255668 | EST | Hs.265634 |
| EST | Hs.255671 | EST | Hs.266387 |
| EST | Hs.255672 | ESTs | Hs.268027 |
| EST | Hs.255673 | ATHS (LDLR?) | Hs.268571 |
| EST | Hs.255674 | ESTs, Highly similar to AAD18086 BAT2 [H.sapiens] | <u>Hs.270193</u> |
| EST | Hs.255675 | ESTs | Hs.270198 |
| EST | Hs.255677 | ESTs | Hs.270294 |
| EST | Hs.255679 | ESTs, Weakly similar to alternatively spliced product using exon 13A [H.sapiens] | Hs.270542 |
| EST | Hs.255681 | ESTs, Moderately similar to ALU2_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY□ [H.sapiens] | Hs.270561 |
| EST | Hs.255682 | ESTs, Weakly similar to pro alpha 1(I) collagen [H.sapiens] | Hs.270564 |
| EST | Hs.255686 | ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY□ [H.sapiens] | Hs.270578 |
| ESTs | Hs.255687 | ESTs, Moderately similar to brain-derived immunoglobulin superfamily molecule [M.musculus] | <u>Hs.270588</u> |
| EST | Hs.255688 | TALL1 | Hs.270737 |
| ESTs | Hs.255689 | ESTs | Hs.271206 |
| EST | Hs.255691 | MYH | Hs.271353 |
| EST | Hs.255692 | POLI (RAD30B) | Hs.271699 |
| ESTs | Hs.255693 | ADPRTL3 | Hs.271742 |

Table 2: Candidate genes, Database mining

| | | | |
|---|-----------|--|---------------------------|
| EST | Hs.255695 | ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens] | Hs.272075 |
| EST, Highly similar to transmembrane chloride conductor protein [H.sapiens] | Hs.255697 | Human DNA sequence from clone RP5-1170K4 on chromosome 22q12.2-13.1 Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen), a | Hs.272271 |
| EST | Hs.255698 | interleukin 1 receptor accessory protein-like 2 | Hs.272354 |
| EST | Hs.255699 | Homo sapiens partial IGVH3 V3-20 gene for immunoglobulin heavy chain V region, case 1, clone 2 | Hs.272355 |
| EST | Hs.255705 | Homo sapiens partial IGVH3 gene for immunoglobulin heavy chain V region, case 1, clone 16 | Hs.272356 |
| EST | Hs.255706 | Homo sapiens partial IGVH3 gene for immunoglobulin heavy chain V region, case 1, clone 19 | Hs.272357 |
| EST | Hs.255708 | Homo sapiens partial IGVH3 gene for immunoglobulin heavy chain V region, case 1, cell Mo IV 72 | Hs.272358 |
| EST | Hs.255710 | Homo sapiens partial IGVH1 gene for immunoglobulin heavy chain V region, case 1, cell Mo V 94 | Hs.272359 |
| EST | Hs.255713 | Homo sapiens partial IGVH2 gene for immunoglobulin lambda light chain V region, case 1, cell Mo V 94 | Hs.272360 |
| EST | Hs.255717 | Homo sapiens partial IGVH3 gene for immunoglobulin heavy chain V region, case 1, cell Mo VI 7 | Hs.272361 |
| EST | Hs.255718 | Homo sapiens partial IGVH1 gene for immunoglobulin lambda light chain V region, case 1, cell Mo VI 65 | Hs.272362 |
| EST | Hs.255721 | Homo sapiens partial IGVH3 gene for immunoglobulin heavy chain V region, case 1, cell Mo VI 162 | Hs.272363 |
| ESTs | Hs.255723 | Homo sapiens partial IGVH3 DP29 gene for immunoglobulin heavy chain V region, case 1, cell Mo VII 116 | Hs.272364 |
| EST | Hs.255725 | Homo sapiens partial IGVH4 gene for immunoglobulin heavy chain V region, case 2, cell D 56 | Hs.272365 |
| EST | Hs.255726 | Homo sapiens partial IGVH3 gene for immunoglobulin heavy chain V region, case 2, cell E 172 | Hs.272366 |
| EST | Hs.255727 | interleukin 20 | Hs.272373 |

Table 2: Candidate genes, Database mining

| | | | |
|--|-----------------|--|------------------|
| EST | Hs.255736 | Human DNA sequence from clone RP1-149A16 on chromosome 22 Contains an IGLC (Immunoglobulin Lambda Chain C) pseudogene, the RFPL3 gene for Ret finger protein-like 3, the RFPL3S gene for Ret finger protein-like 3 antisense, the gene for a novel Immunoglobulin Lambda Chain V family protein, the gene for a novel protein similar to mouse RGDS (RALGDS, RALGEF, Guanine Nucleotide Dissociation Stimulator A) and rabbit oncogene RSC, the gene for a novel protein (ortholog of worm F16A11.2 and bacterial and archaea-bacterial predicted proteins), the gene for a novel protein similar to BPI (Bacterial Permeability-Increasing Protein) and rabbit LBP (Liposaccharide-Binding Protein) and the 5' part of a novel gene. Contains ESTs, STSs, GSSs and three putative CpG islands | <u>Hs.272521</u> |
| EST | Hs.255740 | TdT | Hs.272537 |
| EST | Hs.255742 | ret finger protein-like 3 antisense | <u>Hs.274285</u> |
| EST | Hs.255743 | PRKR | Hs.274382 |
| EST | Hs.7569 | H.sapiens immunoglobulin epsilon chain | Hs.274600 |
| SMAD4 | Hs.75862 | EST, Weakly similar to HLA-DQ alpha chain [H.sapiens] | <u>Hs.275720</u> |
| Homo sapiens splicing factor, arginine/serine-rich 4 (SFRS4) mRNA. | Hs.76122 | EST, Weakly similar to RL13_HUMAN 60S RIBOSOMAL PROTEIN L13 [H.sapiens] | Hs.276279 |
| thymosin beta-10 | Hs.76293 | EST | Hs.276341 |
| CD63 | <u>Hs.76294</u> | EST | Hs.276342 |
| AIF1 | Hs.76364 | EST, Weakly similar to RL13_HUMAN 60S RIBOSOMAL PROTEIN L13 [H.sapiens] | Hs.276353 |
| phospholipase A2, group IIA (platelets, synovial fluid), | Hs.76422 | EST | Hs.276774 |
| CES1 | Hs.76688 | EST | Hs.276819 |
| ubiquitin conjugating enzyme | Hs.76932 | EST | Hs.276871 |
| Homo sapiens KIAA0963 protein (KIAA0963), mRNA. | Hs.7724 | EST, Weakly similar to FBRL_HUMAN FIBRILLARIN [H.sapiens] | Hs.276872 |
| Homo sapiens fragile histidine triad gene (FHIT) mRNA. | Hs.77252 | EST | Hs.276887 |
| PAF-AH | Hs.77318 | EST | Hs.276902 |
| Mig | Hs.77367 | EST | Hs.276917 |
| DDB2 | Hs.77602 | EST | Hs.276918 |
| ATR | Hs.77613 | EST, Weakly similar to RL13_HUMAN 60S RIBOSOMAL PROTEIN L13 [H.sapiens] | Hs.276938 |
| XPB (ERCC3) | Hs.77929 | EST | Hs.277051 |
| PNKP | Hs.78016 | EST | Hs.277052 |
| C7 | <u>Hs.78065</u> | EST, Moderately similar to RL13_HUMAN 60S RIBOSOMAL PROTEIN L13 [H.sapiens] | Hs.277236 |

Table 2: Candidate genes, Database mining

| | | | |
|--|----------|---|-----------|
| Homo sapiens small nuclear RNA activating complex, polypeptide 2, 45kD (SNAPC2) mRNA. | Hs.78403 | EST, Moderately similar to DEAD Box Protein 5 [H.sapiens] | Hs.277237 |
| | Hs.78465 | EST | Hs.277238 |
| sphingolipid activator protein / cerebroside sulfate activator protein | Hs.78575 | EST | Hs.277286 |
| Homo sapiens aminolevulinate, delta-, synthase 1 (ALAS1), nuclear gene encoding mitochondrial protein, mRNA. | Hs.78712 | major histocompatibility complex, class I, C | Hs.277477 |
| tyrosine kinase with immunoglobulin and epidermal growth factor homology domains | Hs.78824 | EST, Weakly similar to AF150959 1 immunoglobulin G1 Fc fragment [H.sapiens] | Hs.277591 |
| Hsp72 | Hs.78846 | EST | Hs.277714 |
| UNG | Hs.78853 | EST | Hs.277715 |
| CX3CR1 | Hs.78913 | EST | Hs.277716 |
| MSH2 | Hs.78934 | EST | Hs.277717 |
| CRHR1 | Hs.79117 | EST | Hs.277718 |
| BCL2 | Hs.79241 | EST, Weakly similar to BAT3_HUMAN LARGE PROLINE-RICH PROTEIN BAT3 [H.sapiens] | Hs.277774 |
| P-selectin | Hs.79283 | EST | Hs.277975 |
| UBE2VE (MMS2) | Hs.79300 | EST | Hs.278060 |
| retinoid X receptor, beta | Hs.79372 | cytochrome P450, subfamily XXIA (steroid 21-hydroxylase, congenital adrenal hyperplasia), polypeptide 2 | Hs.278430 |
| MPG | Hs.79396 | KIAA0015 gene product | Hs.278441 |
| RPA2 | Hs.79411 | CD32B | Hs.278443 |
| heat shock 70kD protein-like 1 | Hs.80288 | KIR2DL1 | Hs.278453 |
| FANCG (XRCC9) | Hs.8047 | CD158a | Hs.278455 |
| CD43 | Hs.80738 | CD24 | Hs.278667 |
| POLG | Hs.80961 | HLA class II region expressed gene KE4 | Hs.278721 |
| Human CB-4 transcript of unrearranged immunoglobulin V(H)5 gene | Hs.81220 | IL-17C | Hs.278911 |
| Human L2-9 transcript of unrearranged immunoglobulin V(H)5 pseudogene | Hs.81221 | HSPC048 protein (HSPC048) | Hs.278944 |
| immunoglobulin superfamily, member 3 | Hs.81234 | HSPC054 protein (HSPC054) | Hs.278946 |
| UBL1 | Hs.81424 | HSPC073 protein (HSPC073) | Hs.278948 |
| PF4 | Hs.81564 | ESTs | Hs.279066 |
| palmitoyl-protein thioesterase 2 | Hs.81737 | ESTs | Hs.279067 |
| natural killer cell receptor, immunoglobulin superfamily member | Hs.81743 | ESTs | Hs.279068 |
| TNFRSF11B | Hs.81791 | ESTs | Hs.279069 |
| interleukin 6 signal transducer (gp130, oncostatin M receptor) | Hs.82065 | ESTs | Hs.279070 |
| CD138 | Hs.82109 | ESTs | Hs.279071 |
| Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds. | Hs.82210 | ESTs | Hs.279072 |
| sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B | Hs.82222 | ESTs, Weakly similar to KIAA0052 protein [H.sapiens] | Hs.279073 |
| HPRT | Hs.82314 | ESTs | Hs.279074 |
| Human RNA binding protein Etr-3 mRNA, complete cds. | Hs.82321 | ESTs | Hs.279075 |
| MNAT1 | Hs.82380 | ESTs | Hs.279076 |

Table 2: Candidate genes, Database mining

| | | | |
|---|-----------|--|-----------|
| SMAD2 | Hs.82483 | ESTs | Hs.279077 |
| CD47 | Hs.82685 | EST | Hs.279078 |
| CETN2 | Hs.82794 | EST | Hs.279079 |
| protein phosphatase 1, regulatory (inhibitor) subunit 11 | Hs.82887 | ESTs | Hs.279080 |
| MMP1 | Hs.83169 | EST | Hs.279081 |
| D3-type cyclin (CCND3) | Hs.83173 | ESTs | Hs.279082 |
| MMP3 | Hs.83326 | ESTs | Hs.279083 |
| TNFSF10 | Hs.83429 | ESTs | Hs.279084 |
| CD33 | Hs.83731 | ESTs | Hs.279085 |
| CD102 | Hs.83733 | ESTs | Hs.279086 |
| | Hs.84153 | ESTs, Weakly similar to AF201422_1 splicing coactivator subunit SRm300 [H.sapiens] | Hs.279087 |
| interleukin 8 receptor, beta | Hs.846 | ESTs | Hs.279088 |
| titin immunoglobulin domain protein (myotilin) | Hs.84665 | ESTs | Hs.279089 |
| KU80 (XRCC5) | Hs.84981 | | Hs.86437 |
| Raf-1 | Hs.85181 | | Hs.86761 |
| major histocompatibility complex, class I, J (pseudogene) | Hs.85242 | CD118 = IFNAR-2 | Hs.86958 |
| RELB | Hs.858 | | Hs.87113 |
| | Hs.85923 | PGHS-1 | Hs.88474 |
| ERK1 | Hs.861 | | Hs.8882 |
| FADD | Hs.86131 | LT-b | Hs.890 |
| MHC class I polypeptide-related sequence A | Hs.90598 | EST | Hs.92440 |
| TNF receptor-associated factor 6 | Hs.90957 | | Hs.92460 |
| Topo3A | Hs.91175 | myosin-binding protein H | Hs.927 |
| PARG | Hs.91390 | IFN-b | Hs.93177 |
| HLA-DPA1 | Hs.914 | C8A | Hs.93210 |
| SEEK1 | Hs.91600 | pre-B-cell leukemia transcription factor 2 | Hs.93728 |
| POLD1 | Hs.99890 | Tachykinin Receptor 3 | Hs.942 |
| ALK4 | Hs.99954 | Homo sapiens cDNA FLJ12242 fis, clone MAMMA1001292 | Hs.94810 |
| XPD (ERCC2) | Hs.99987 | CD29 | Hs.287797 |
| SCYA25 (CCL25) | Hs.50404 | LIF | Hs.2250 |
| SCYA19 (CCL19) | Hs.50002 | Human IP-10 | Hs.2248 |
| TCIRG1 | Hs.46465 | IL-5 | Hs.2247 |
| PAF-Receptor | Hs.46 | G-CSF | Hs.2233 |
| CD26 | Hs.44926 | TGF-bR | Hs.220 |
| | Hs.44865 | G-CSFR | Hs.2175 |
| REL | Hs.44313 | CD15 | Hs.2173 |
| IL-17 | Hs.41724 | STAT1 | Hs.21486 |
| CD49d | Hs.40034 | CD85 | Hs.204040 |
| CCR2 | Hs.395 | HCC-1 | Hs.20144 |
| | Hs.3688 | Fas ligand | Hs.2007 |
| TNF-b | Hs.36 | CD28 | Hs.1987 |
| lactoferrin | Hs.347 | HLA-DQA1 | Hs.198253 |
| MCP-1 | Hs.340 | Ku70 (G22P1) | Hs.197345 |
| CD150 | Hs.32970 | PGHS-2 | Hs.196384 |
| IL-10Ra | Hs.327 | CDw128 | Hs.194778 |
| EGR1 | Hs.326035 | IL-10 | Hs.193717 |

Table 2: Candidate genes, Database mining

| | | | |
|---|-----------|---|-----------|
| SCYC1 (XCL1) | Hs.3195 | CD126 | Hs.193400 |
| HLA-DR | Hs.318720 | | Hs.1880 |
| Topo I (TOP1) | Hs.317 | CD98 | Hs.184601 |
| SCYA2 (MCP1) | Hs.303649 | | Hs.184542 |
| HuRNPd | Hs.303627 | MHC class I region ORF | Hs.1845 |
| Human C mu gene for IgM heavy chain exons CH1-4, secretory | Hs.302063 | CDw116a | Hs.182378 |
| P1 | Hs.297681 | HLA-DRB5 | Hs.181366 |
| immunoglobulin lambda joining 3 | Hs.289110 | major histocompatibility complex, class I, A | Hs.181244 |
| major histocompatibility complex, class II, DQ alpha 2 | Hs.289095 | elongation factor 1-alpha (clone CEF4) | Hs.181165 |
| HSPCA | Hs.289088 | CD119 | Hs.180866 |
| interleukin 22 | Hs.287369 | | Hs.180804 |
| ribosomal protein L4 | Hs.286 | | Hs.180532 |
| IgM | Hs.285823 | POLB | Hs.180107 |
| EST | Hs.283267 | CD1d | Hs.1799 |
| TREM1 | Hs.283022 | CD87 | Hs.179657 |
| HLA-DRB3 | Hs.279930 | minichromosome maintenance deficient (S. cerevisiae) 3 | Hs.179565 |
| LIFR | Hs.2798 | RAD23B (HR23B) | Hs.178658 |
| C4B | Hs.278625 | | Hs.178391 |
| EST | Hs.276907 | | Hs.177781 |
| CDw52 | Hs.276770 | ADPRT | Hs.177766 |
| CD16 b | Hs.274467 | IFNGR2 | Hs.177559 |
| heat shock 70kD protein 1B | Hs.274402 | CD16 a | Hs.176663 |
| Th1 | Hs.273385 | CD4 | Hs.17483 |
| MIP-5/HCC-2 | Hs.272493 | SCYC2 (XCL2) | Hs.174228 |
| TBX21 | Hs.272409 | CD115 | Hs.174142 |
| Homo sapiens mRNA; cDNA DKFZp434O2417 (from clone DKFZp434O2417); partial cds | Hs.272307 | CD11a | Hs.174103 |
| Human DNA sequence from clone RP1- 108C2 on chromosome 6p12.1-21.1. Contains the MCM3 gene for minichromosome maintenance deficient (S. cerevisiae) 3 (DNA replication licensing factor, DNA polymerase alpha holoenzyme- associated protein P1, RLF beta subunit), a CACT (carnitine/acylcarnitine translocase) pseudogene, part of the gene for a PUTATIVE novel protein similar to IL17 (interleukin 17 (cytotoxic T-lymphocyte- associated serine esterase 8)) (cytotoxic T lymphocyte-associated antigen 8, CTLA8), ESTs, STSs, GSSs and a putative CpG island | Hs.272295 | IL-10Rb | Hs.173936 |

Table 2: Candidate genes, Database mining

| | | | |
|---|---------------------------|---|---------------------------|
| CD49b | Hs.271986 | MSCF | Hs.173894 |
| MCP-2 | Hs.271387 | TDG | Hs.173824 |
| CD49c | Hs.265829 | RAC1 | Hs.173737 |
| NBS1 | Hs.25812 | integrin cytoplasmic domain-associated protein 1 | Hs.173274 |
| CD120b = TNFRSF1B | Hs.256278 | IL2R | Hs.1724 |
| CDw75 | Hs.2554 | IL-1a | Hs.1722 |
| CD82 | Hs.25409 | | Hs.171872 |
| MCP-3 | Hs.251526 | | Hs.171118 |
| xanthine oxidase | Hs.250 | EST | Hs.171009 |
| Human Ig rearranged lambda-chain mRNA, subgroup VL3, V-J region, partial cds | Hs.247947 | EST | Hs.170934 |
| Eotaxin-2/MPIF-2 | Hs.247838 | EST | Hs.170587 |
| CTLA-4 | Hs.247824 | IL-9R | Hs.1702 |
| immunoglobulin kappa variable 1-9 | Hs.247792 | CD45 | Hs.170121 |
| CD68 | Hs.246381 | TGF-a | Hs.170009 |
| OSMR | Hs.238648 | CD44 | Hs.169610 |
| CDw127 | Hs.237868 | Fyn | Hs.169370 |
| transcription factor 8 (represses interleukin 2 expression) | Hs.232068 | MPIF-1 | Hs.169191 |
| CD8b | Hs.2299 | ICAM-1 | Hs.168383 |
| EST | Hs.229374 | IL-15 | Hs.168132 |
| TRF4-1 | Hs.225951 | STAT5A | Hs.167503 |
| CD3g | Hs.2259 | ESTs | Hs.167208 |
| C2 | Hs.2253 | ESTs | Hs.165693 |
| | Hs.116834 | | Hs.135750 |
| | Hs.117741 | DINB1 (POLK) | Hs.135756 |
| Human MHC Class I region proline rich protein mRNA, complete cds | Hs.118354 | Human DNA sequence from clone RP1-238O23 on chromosome 6. Contains part of the gene for a novel protein similar to PIGR (polymeric immunoglobulin receptor), part of the gene for a novel protein similar to rat SAC (soluble adenylyl cyclase), ESTs, STSs and GSS | Hs.136141 |
| ESTs, Weakly similar to FCE2 MOUSE LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR [M.musculus] | Hs.118392 | | Hs.136254 |
| MKK6 | Hs.118825 | | Hs.13646 |
| | Hs.118895 | | Hs.136537 |
| H.sapiens mRNA for ITBA4 gene. | Hs.119018 | Histone H1 (F3) | Hs.136857 |
| | Hs.119057 | MGMT | Hs.1384 |
| TNFRSF10c | Hs.119684 | | Hs.138563 |
| | Hs.12064 | IgG | Hs.140 |
| | Hs.120907 | | Hs.140478 |
| acid phosphatase 5, tartrate resistant | Hs.1211 | | Hs.14070 |
| | Hs.121297 | | Hs.141153 |

Table 2: Candidate genes, Database mining

| | | | |
|---|---------------------------|--|---------------------------|
| Human immunoglobulin (mAb59) light chain V region mRNA, partial sequence | Hs.121508 | | Hs.143954 |
| IL12Rb1 | Hs.121544 | ESTs, Moderately similar to I1BC_HUMAN INTERLEUKIN-1 BETA CONVERTASE PRECURSOR [H.sapiens] | Hs.144814 |
| Human MHC class II DO-alpha mRNA, partial cds | Hs.123041 | CHK2 (Rad53) | Hs.146329 |
| Histone H4 (H4F2) | Hs.123053 | EST | Hs.146591 |
| TSHR | Hs.123078 | | Hs.147040 |
| | Hs.123445 | CD42b | Hs.1472 |
| regulatory factor X, 1 (influences HLA class II expression) | Hs.123638 | | Hs.149235 |
| CD13 | Hs.1239 | AICD | Hs.149342 |
| IL-15R | Hs.12503 | Homo sapiens putative tumor suppressor protein (101F6) mRNA, complete cds. | Hs.149443 |
| RAD51L3 (RAD51D) | Hs.125244 | CD49e | Hs.149609 |
| CDw90 | Hs.125359 | heparan sulfate proteoglycan (HSPG) core protein | Hs.1501 |
| LYPLA1 | Hs.12540 | CD107a | Hs.150101 |
| ESTs, Weakly similar to AF201951 1 high affinity immunoglobulin epsilon receptor beta subunit [H.sapiens] | Hs.126580 | ESTs, Weakly similar to I57587 MHC HLA-SX-alpha [H.sapiens] | Hs.150175 |
| | Hs.127128 | ALK2 | Hs.150402 |
| | Hs.127444 | WRN | Hs.150477 |
| C5 | Hs.1281 | EST | Hs.150708 |
| C8G | Hs.1285 | XRCC4 | Hs.150930 |
| RAD54B | Hs.128501 | IFN-a | Hs.1510 |
| | Hs.129020 | MAPK | Hs.151051 |
| | Hs.129268 | | Hs.15200 |
| | Hs.129332 | immunoglobulin mu binding protein 2 | Hs.1521 |
| XRCC2 | Hs.129727 | 4-1BBL | Hs.1524 |
| potassium voltage-gated channel, Shaw-related subfamily, member 3 (KCNC3) | Hs.129738 | | Hs.152818 |
| interleukin 17 receptor | Hs.129751 | HUS1 | Hs.152983 |
| CD134 | Hs.129780 | SWAP70 | Hs.153026 |
| TNFRSF10d | Hs.129844 | DOM-3 (C. elegans) homolog Z | Hs.153299 |
| POLL | Hs.129903 | | Hs.153551 |
| GADD153=growth arrest and DNA-damage-inducible gene / fus-chop fusion protein | Hs.129913 | | Hs.15370 |

Table 2: Candidate genes, Database mining

| | | | |
|---|------------------|--|------------------|
| solute carrier family 5 (neutral amino acid transporters, system A), member 4 | <u>Hs.130101</u> | SMAD6 | Hs.153863 |
| | Hs.130232 | APEXL2 | Hs.154149 |
| | Hs.13034 | | Hs.154198 |
| CD30L | <u>Hs.1313</u> | | Hs.154366 |
| SCYA26 (CCL26) | Hs.131342 | BCL6 | Hs.155024 |
| CD30 | <u>Hs.1314</u> | | Hs.155150 |
| | Hs.131885 | | Hs.155402 |
| | Hs.131887 | RAIDD | Hs.155566 |
| | Hs.13256 | POLH | Hs.155573 |
| ESTs | Hs.132775 | | Hs.15589 |
| Homo sapiens (clone 3.8-1) MHC class I mRNA fragment | <u>Hs.132807</u> | Homo sapiens mRNA for KIAA0695 protein, complete cds. | Hs.155976 |
| | Hs.13288 | SNM1 (PS02) | Hs.1560 |
| | Hs.132943 | Topo2A | Hs.156346 |
| EST | Hs.133261 | ESTs, Highly similar to MHC class II antigen [H.sapiens] | <u>Hs.156811</u> |
| | Hs.133388 | Histamine H1 receptor | <u>Hs.1570</u> |
| EST | Hs.133393 | | Hs.157118 |
| EST | Hs.133930 | | Hs.157267 |
| ESTs | Hs.133947 | EST | Hs.157279 |
| ESTs | Hs.133949 | EST | Hs.157280 |
| EST | Hs.134017 | EST | Hs.157308 |
| EST | Hs.134018 | EST | Hs.157309 |
| EST | Hs.134590 | EST | Hs.157310 |
| | Hs.135135 | EST | Hs.157311 |
| immunoglobulin superfamily, member 6 | <u>Hs.135194</u> | ESTs | Hs.157344 |
| | Hs.135570 | ret finger protein-like 2 | <u>Hs.157427</u> |
| Homo sapiens arrestin, beta 2 (ARRB2) mRNA. | Hs.18142 | | Hs.214956 |
| myeloperoxidase | Hs.1817 | WASP | Hs.2157 |
| APO-1 | Hs.182359 | CD88 | <u>Hs.2161</u> |
| TRAP1 | Hs.182366 | | Hs.21618 |
| | Hs.182594 | ring finger protein 5 | <u>Hs.216354</u> |
| TNFRSF16 | Hs.1827 | class II cytokine receptor ZCYTOR7 | <u>Hs.21814</u> |
| | Hs.182817 | | Hs.219149 |
| regulatory factor X, 4 (influences HLA class II expression) | <u>Hs.183009</u> | cyclophilin-related protein | Hs.219153 |
| Homo sapiens killer cell lectin-like receptor F1 (KLRF1), mRNA. | Hs.183125 | Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT2) mRNA. | Hs.219479 |
| | Hs.183171 | perforin | <u>Hs.2200</u> |
| EST | Hs.183386 | | Hs.220154 |
| | Hs.183656 | ESTs, Weakly similar to FCE2 MOUSE LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR [M.musculus] | <u>Hs.220649</u> |
| | Hs.18368 | | Hs.220868 |

Table 2: Candidate genes, Database mining

| | | | |
|---|------------------|--|------------------|
| advanced glycosylation end product-specific receptor | <u>Hs.184</u> | | |
| CDK7 | Hs.184298 | immunoglobulin superfamily, member 1 | <u>Hs.22111</u> |
| | Hs.184376 | | Hs.221539 |
| CCR4 | <u>Hs.184926</u> | ESTs | Hs.221694 |
| EST, Weakly similar to A27307 proline-rich phosphoprotein [H.sapiens] | Hs.185463 | | Hs.222921 |
| EST | Hs.185498 | | Hs.222942 |
| EST, Weakly similar to B39066 proline-rich protein 15 - rat [R.norvegicus] | Hs.186243 | EST | Hs.223520 |
| EST, Weakly similar to salivary proline-rich protein [R.norvegicus] | Hs.186265 | EST | Hs.223935 |
| EST | Hs.187200 | EST, Moderately similar to SMO_HUMAN SMOOTHENED HOMOLOG PRECURSOR [H.sapiens] | Hs.224178 |
| | Hs.188048 | Blk | Hs.2243 |
| EST | Hs.188075 | EST | Hs.224344 |
| EST | Hs.188194 | EST | Hs.224408 |
| EST | Hs.188300 | EST | Hs.224409 |
| | Hs.190251 | CPN1 | Hs.2246 |
| | Hs.19056 | MMP7 | Hs.2256 |
| EST | Hs.190831 | MMP10 | Hs.2258 |
| MAPK8 | Hs.190913 | CCR9 | <u>Hs.225946</u> |
| EST | Hs.190921 | toll-like receptor 6 (TLR6) | Hs.227105 |
| EST, Weakly similar to S39206 hypothetical protein 1 - rat [R.norvegicus] | Hs.190924 | XPR1 | Hs.227656 |
| GTF2H2 | Hs.191356 | CD49f | <u>Hs.227730</u> |
| | Hs.191367 | | Hs.22790 |
| | Hs.191914 | EST | Hs.228337 |
| ESTs, Weakly similar to immunoglobulin superfamily member [D.melanogaster] | <u>Hs.192078</u> | EST, Highly similar to 1409218A elastase [H.sapiens] | Hs.228525 |
| XPA | Hs.192803 | EST | Hs.228528 |
| CD89 | <u>Hs.193122</u> | EST, Moderately similar to R37A_HUMAN 60S RIBOSOMAL PROTEIN L37A [H.sapiens] | Hs.228874 |
| DFFRY | Hs.193145 | EST | Hs.228891 |
| CD35 | <u>Hs.193716</u> | EST | Hs.228926 |
| REV7 (MAD2L2) | Hs.19400 | EST | Hs.229071 |
| | Hs.194082 | EST | Hs.229405 |
| | Hs.194110 | EST | Hs.229494 |
| BRCA1 | Hs.194143 | EST, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens] | Hs.229560 |
| ESTs, Moderately similar to MHC Class I region proline rich protein [H.sapiens] | <u>Hs.194249</u> | EST, Moderately similar to AAD18086 BAT2 [H.sapiens] | Hs.229901 |
| | Hs.194534 | EST | Hs.229902 |
| Topo3B | Hs.194685 | EST, Highly similar to 1409218A elastase [H.sapiens] | Hs.230053 |

Table 2: Candidate genes, Database mining

| | | | |
|--|---------------------------|--|---------------------------|
| Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs | Hs.194750 | RAD51 | Hs.23044 |
| major histocompatibility complex, class II, DP alpha 2 (pseudogene) | Hs.194764 | EST, Moderately similar to A54746 adhalin precursor - human <input type="checkbox"/> [H.sapiens] | Hs.230485 |
| Human DNA sequence from clone RP11-367J7 on chromosome 1. Contains (part of) two or more genes for novel Immunoglobulin domains containing proteins, a SON DNA binding protein (SON) pseudogene, a voltage-dependent anion channel 1 (VDAC1) (plasmalemmal porin) pseudogene, ESTs, STSs and GSSs | Hs.194976 | EST | Hs.230691 |
| | Hs.195447 | EST | Hs.230775 |
| PDGF-B | Hs.1976 | EST | Hs.230805 |
| CXCR3 | Hs.198252 | EST | Hs.230848 |
| | Hs.198694 | EST | Hs.230862 |
| | Hs.198738 | EST | Hs.230874 |
| MAR/SAR DNA binding protein (SATB1) | Hs.198822 | EST | Hs.230931 |
| CHUK | Hs.198998 | EST | Hs.231031 |
| hemochromatosis | Hs.20019 | EST | Hs.231261 |
| T-cell receptor active beta-chain | Hs.2003 | EST | Hs.231284 |
| APO-1 | Hs.2007 , | EST | Hs.231285 |
| RXRA | Hs.20084 | EST | Hs.231292 |
| EST | Hs.200876 | EST, Weakly similar to putative mitochondrial outer membrane protein import receptor [H.sapiens] | Hs.231512 |
| | Hs.201194 | Homo sapiens mRNA for KIAA0529 protein, partial cds. | Hs.23168 |
| TCRd | Hs.2014 | EST | Hs.235042 |
| ESTs, Highly similar to TNF-alpha converting enzyme [H.sapiens] | Hs.202407 | EST | Hs.235826 |
| | Hs.202608 | TREX1 (Dnase III) | Hs.23595 |
| Integrin b1 = CD29 | Hs.202661 | EST | Hs.237126 |
| thrombomodulin | Hs.2030 | | Hs.23860 |
| | Hs.203064 | RAD9 | Hs.240457 |
| | Hs.203184 | 1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) | Hs.240534 |
| | Hs.203584 | EST | Hs.240635 |
| EST | Hs.204477 | EST, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY <input type="checkbox"/> [H.sapiens] | Hs.241136 |

Table 2: Candidate genes, Database mining

| | | | |
|---|------------------|---|------------------|
| EST | Hs.204480 | TNFSF15 | Hs.241382 |
| EST, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens] | Hs.204483 | interleukin 1 receptor accessory protein-like 1 | <u>Hs.241385</u> |
| ESTs | Hs.204588 | RANTES | <u>Hs.241392</u> |
| EST, Weakly similar to salivary proline-rich protein 1 [H.sapiens] | Hs.204598 | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A | <u>Hs.2414</u> |
| EST | Hs.204610 | POLQ | Hs.241517 |
| ESTs | Hs.204703 | TNF-a | <u>Hs.241570</u> |
| ESTs | Hs.204751 | Homo sapiens genes encoding RNCC protein, DDAH protein, Ly6-C protein, Ly6- D protein and immunoglobulin receptor | <u>Hs.241586</u> |
| EST | Hs.204760 | megakaryocyte-enhanced gene transcript 1 protein | <u>Hs.241587</u> |
| EST | Hs.204771 | EST, Moderately similar to 1409218A elastase [H.sapiens] | Hs.241981 |
| ESTs | Hs.204873 | EST | Hs.241982 |
| ESTs | Hs.204932 | EST | Hs.241983 |
| EST | Hs.204954 | EST | Hs.242605 |
| EST | Hs.205158 | ADPRT2 | <u>Hs.24284</u> |
| ESTs | Hs.205159 | EST | Hs.243284 |
| ESTs | Hs.205327 | EST | Hs.243286 |
| CD39 | <u>Hs.205353</u> | ESTs | Hs.243288 |
| ESTs | Hs.205435 | SCYB14 | Hs.24395 |
| EST | Hs.205438 | EST | Hs.244046 |
| EST, Highly similar to elastic titin [H.sapiens] | Hs.205452 | EST | Hs.244048 |
| EST | Hs.205456 | EST | Hs.244049 |
| MRE11A | Hs.20555 | EST | Hs.244050 |
| HLA class II region expressed gene KE2 | <u>Hs.205736</u> | RFXAP | Hs.24422 |
| EST | Hs.205788 | | Hs.24435 |
| ESTs | Hs.205789 | STAT5B | Hs.244613 |
| EST | Hs.205803 | EST | Hs.244666 |
| EST | Hs.205815 | EST | Hs.245586 |
| ESTs | Hs.206160 | CDw108 | <u>Hs.24640</u> |
| | Hs.206654 | ESTs | Hs.246796 |
| EST | Hs.207060 | dimethylarginine dimethylaminohydrolase 2 | <u>Hs.247362</u> |
| EST | Hs.207062 | Homo sapiens clone mcg53-54 immunoglobulin lambda light chain variable region 4a mRNA, partial cds | <u>Hs.247721</u> |
| EST | Hs.207063 | Homo sapiens ELK1 pseudogene (ELK2) and immunoglobulin heavy chain gamma pseudogene (IGHGP) | <u>Hs.247775</u> |
| EST | Hs.207473 | immunoglobulin kappa variable 1/OR2-108 | <u>Hs.247804</u> |
| ESTs | Hs.207474 | butyrophilin-like 2 (MHC class II associated) | <u>Hs.247808</u> |

Table 2: Candidate genes, Database mining

| | | | |
|---|---------------------------|---|---------------------------|
| ESTs | Hs.207971 | Homo sapiens genes encoding RNCC protein, DDAH protein, Ly6-C protein, Ly6-D protein and immunoglobulin receptor | Hs.247879 |
| EST | Hs.207993 | Histamine H2 receptor | Hs.247885 |
| EST | Hs.208153 | Human anti-streptococcal/anti-myosin immunoglobulin lambda light chain variable region mRNA, partial cds | Hs.247898 |
| EST, Weakly similar to S10889 proline-rich protein - human [H.sapiens] | Hs.208667 | Homo sapiens isolate donor Z clone Z55K immunoglobulin kappa light chain variable region mRNA, partial cds | Hs.247907 |
| ESTs | Hs.209142 | Homo sapiens isolate donor D clone D103L immunoglobulin lambda light chain variable region mRNA, partial cds | Hs.247908 |
| EST | Hs.209261 | Homo sapiens isolate 459 immunoglobulin lambda light chain variable region (IGL) gene, partial cds | Hs.247909 |
| ESTs | Hs.209306 | Homo sapiens isolate donor N clone N88K immunoglobulin kappa light chain variable region mRNA, partial cds | Hs.247910 |
| | Hs.209362 | Homo sapiens isolate donor N clone N8K immunoglobulin kappa light chain variable region mRNA, partial cds | Hs.247911 |
| EST, Weakly similar to FCEB MOUSE HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT [M.musculus] | Hs.209540 | Human Ig rearranged mu-chain V-region gene, subgroup VH-III, exon 1 and 2 | Hs.247923 |
| EST | Hs.209913 | Epsilon , IgE=membrane-bound IgE, epsilon m/s isoform {alternative splicing} [human, mRNA Partial, 216 nt] | Hs.247930 |
| EST | Hs.209989 | H.sapiens (T1.1) mRNA for IG lambda light chain | Hs.247949 |
| EST | Hs.210049 | H.sapiens mRNA for Ig light chain, variable region (ID:CLL001VL) | Hs.247950 |
| EST, Moderately similar to probable sodium potassium ATPase gamma chain [H.sapiens] | Hs.210276 | Human interleukin 2 gene, clone pATtacIL-2C/2TT, complete cds, clone pATtacIL-2C/2TT | Hs.247956 |
| EST, Weakly similar to N-WASP [H.sapiens] | Hs.210306 | pre-B lymphocyte gene 1 | Hs.247979 |
| EST | Hs.210307 | Human immunoglobulin heavy chain variable region (V4-31) gene, partial cds | Hs.247987 |
| EST | Hs.210385 | Human immunoglobulin heavy chain variable region (V4-30.2) gene, partial cds | Hs.247989 |
| interleukin 21 receptor | Hs.210546 | Human DNA sequence from phage LAW2 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains Interleukin 9 receptor pseudogene | Hs.247991 |
| EST | Hs.210727 | Homo sapiens HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds | Hs.247993 |

Table 2: Candidate genes, Database mining

| | | | |
|--|-----------|---|-----------|
| | Hs.211266 | Homo sapiens immunoglobulin lambda gene locus DNA, clone:61D6 | Hs.248010 |
| SMAD3 | Hs.211578 | immunoglobulin lambda variable 9-49 | Hs.248011 |
| MHC class I polypeptide-related sequence B | Hs.211580 | immunoglobulin lambda variable 4-3 | Hs.248012 |
| ESTs, Weakly similar to CA1B_MOUSE COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR [M.musculus] | Hs.211744 | H.sapiens mRNA for IgG lambda light chain V-J-C region (clone Tgl11) | Hs.248030 |
| sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E | Hs.212414 | Human immunoglobulin (mAb56) light chain V region mRNA, partial sequence | Hs.248043 |
| TNFRSF18 | Hs.212680 | Homo sapiens lymphocyte-predominant Hodgkin's disease case #4 immunoglobulin heavy chain gene, variable region, partial cds | Hs.248077 |
| Homo sapiens general transcription factor 2-I pseudogene 1 (GTF2IP1) mRNA. | Hs.212939 | Homo sapiens lymphocyte-predominant Hodgkin's disease case #7 immunoglobulin heavy chain gene, variable region, partial cds | Hs.248078 |
| RAD18 | Hs.21320 | Homo sapiens clone ASMneg1-b3 immunoglobulin lambda chain VJ region, (IGL) mRNA, partial cds | Hs.248083 |
| | Hs.213226 | OSM | Hs.248156 |
| ESTs | Hs.279090 | | Hs.29128 |
| ESTs | Hs.279091 | Homo sapiens clone 24659 mRNA sequence. | Hs.29206 |
| ESTs | Hs.279092 | EST | Hs.292235 |
| EST | Hs.279093 | EST | Hs.292450 |
| ESTs | Hs.279094 | EST, Moderately similar to Ewing sarcoma breakpoint region 1, isoform EWS [H.sapiens] | Hs.292455 |
| ESTs | Hs.279095 | EST | Hs.292461 |
| ESTs, Weakly similar to AF279265_1 putative anion transporter 1 [H.sapiens] | Hs.279096 | ESTs | Hs.292501 |
| ESTs | Hs.279097 | EST | Hs.292516 |
| EST | Hs.279098 | EST | Hs.292517 |
| ESTs | Hs.279099 | EST | Hs.292520 |
| ESTs | Hs.279100 | EST, Moderately similar to RL13_HUMAN 60S RIBOSOMAL PROTEIN L13 [H.sapiens] | Hs.292540 |
| ESTs | Hs.279101 | EST | Hs.292545 |
| ESTs | Hs.279102 | EST, Weakly similar to ORFII [H.sapiens] | Hs.292704 |
| ESTs | Hs.279103 | EST | Hs.292761 |
| ESTs | Hs.279104 | ESTs | Hs.292803 |
| ESTs | Hs.279105 | ESTs | Hs.293183 |
| ESTs | Hs.279106 | ESTs | Hs.293280 |
| EST | Hs.279107 | ESTs | Hs.293281 |
| ESTs | Hs.279108 | ESTs, Moderately similar to 0501254A protein Tro alpha1 H,myeloma [H.sapiens] | Hs.293441 |
| EST | Hs.279109 | MMP13 | Hs.2936 |
| ESTs | Hs.279110 | major histocompatibility complex, class II, DR beta 4 | Hs.293934 |

Table 2: Candidate genes, Database mining

| | | | |
|--|-----------|---|---------------------------|
| ESTs | Hs.279111 | Human MHC class III serum complement factor B, mRNA | Hs.294163 |
| ESTs | Hs.279112 | EST | Hs.294315 |
| EST | Hs.279113 | EST | Hs.294316 |
| ESTs | Hs.279114 | EST, Highly similar to Y196_HUMAN HYPOTHETICAL PROTEIN KIAA0196□ [H.sapiens] | Hs.295582 |
| ESTs | Hs.279115 | EST | Hs.295583 |
| ESTs | Hs.279116 | EST, Highly similar to ZN07_HUMAN ZINC FINGER PROTEIN 7 [H.sapiens] | Hs.295584 |
| ESTs | Hs.279117 | EST | Hs.295585 |
| ESTs | Hs.279118 | EST | Hs.295586 |
| ESTs | Hs.279119 | EST, Moderately similar to angiotensin converting enzyme [H.sapiens] | Hs.295595 |
| ESTs | Hs.279120 | EST | Hs.295621 |
| ESTs | Hs.279121 | EST | Hs.295622 |
| ESTs | Hs.279122 | EST, Moderately similar to RL13_HUMAN 60S RIBOSOMAL PROTEIN L13 [H.sapiens] | Hs.295629 |
| ESTs | Hs.279123 | EST | Hs.295724 |
| ESTs | Hs.279124 | EST | Hs.296064 |
| ESTs | Hs.279125 | EST, Moderately similar to IDS_HUMAN IDURONATE 2-SULFATASE PRECURSOR□ [H.sapiens] | Hs.296070 |
| ESTs | Hs.279126 | EST | Hs.296073 |
| ESTs | Hs.279127 | interleukin enhancer binding factor 1 | Hs.296281 |
| EST | Hs.279128 | similar to rat integral membrane glycoprotein POM121 | Hs.296429 |
| ESTs, Weakly similar to aconitase [H.sapiens] | Hs.279129 | Human histocompatibility antigen mrna clone phla-1 | Hs.296476 |
| ESTs | Hs.279130 | immunoglobulin lambda-like polypeptide 3 | Hs.296552 |
| ESTs | Hs.279131 | RFXANK | Hs.296776 |
| ESTs | Hs.279132 | | Hs.29826 |
| ESTs | Hs.279133 | | Hs.29871 |
| ESTs, Weakly similar to PYRG_HUMAN CTP SYNTHASE [H.sapiens] | Hs.279134 | MEKK1 | Hs.298727 |
| ESTs, Weakly similar to RIR1_HUMAN RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M1 CHAIN [H.sapiens] | Hs.279135 | | Hs.30029 |
| ESTs | Hs.279136 | CD3e | Hs.3003 |
| ESTs | Hs.279137 | ESTs, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens] | Hs.300697 |
| ESTs | Hs.279138 | Homo sapiens clone BCSynL38 immunoglobulin lambda light chain variable region mRNA, partial cds | Hs.300865 |
| ESTs | Hs.279139 | FCGR3A | Hs.300983 |
| ESTs | Hs.279140 | Homo sapiens DP47 gene for immunoglobulin heavy chain, partial cds | Hs.301365 |
| ESTs | Hs.279141 | PMS2L9 | Hs.301862 |

Table 2: Candidate genes, Database mining

| | | | |
|--|------------------|---|------------------|
| EST | Hs.279142 | CCR1 | Hs.301921 |
| ESTs | Hs.279143 | FANCE | Hs.302003 |
| ESTs | Hs.279144 | interleukin 21 | <u>Hs.302014</u> |
| ESTs | Hs.279145 | interleukin 17E | <u>Hs.302036</u> |
| ESTs | Hs.279146 | | Hs.30446 |
| EST | Hs.279147 | EST | Hs.30709 |
| ESTs | Hs.279148 | EST | Hs.30731 |
| ESTs | Hs.279149 | MHC class II transactivator | Hs.3076 |
| ESTs | Hs.279150 | EST | Hs.30766 |
| ESTs, Weakly similar to PUR2_HUMAN TRIFUNCTIONAL PURINE BIOSYNTHETIC PROTEIN ADENOSINE- 3 [H.sapiens] | Hs.279151 | EST | Hs.30793 |
| ESTs | Hs.279152 | | Hs.30818 |
| ESTs | Hs.279153 | CD97 | <u>Hs.3107</u> |
| ESTs | Hs.279154 | RAR-beta2 | Hs.31408 |
| ESTs | Hs.279155 | RECQL4 | Hs.31442 |
| ESTs | Hs.279156 | XPC | Hs.320 |
| ESTs | Hs.279157 | ERK2 | Hs.324473 |
| ESTs | Hs.279158 | | Hs.32456 |
| ESTs | Hs.279159 | MSH6 | Hs.3248 |
| ESTs | Hs.279160 | ribosomal protein L23-related | Hs.3254 |
| ESTs, Weakly similar to IDHA_HUMAN ISOCITRATE DEHYDROGENASE [H.sapiens] | Hs.279161 | PI3CG | Hs.32942 |
| ESTs | Hs.279162 | CSA (CKN1) | Hs.32967 |
| ESTs | Hs.279163 | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F | <u>Hs.32981</u> |
| ESTs | Hs.279164 | BRCA2 | Hs.34012 |
| ESTs | Hs.279165 | MEK1 | Hs.3446 |
| ESTs | Hs.279166 | STRL33 (CXCR6) | Hs.34526 |
| ESTs | Hs.279167 | MBD4 | Hs.35947 |
| ESTs | Hs.279168 | immunoglobulin (CD79A) binding protein 1 | <u>Hs.3631</u> |
| EST | Hs.279169 | CD7 | <u>Hs.36972</u> |
| ESTs | Hs.279170 | IFNA1 | Hs.37026 |
| ESTs | Hs.279171 | PDGF-A | <u>Hs.37040</u> |
| EST | Hs.279172 | immunoglobulin kappa variable 1-13 | <u>Hs.37089</u> |
| ESTs | Hs.279174 | DMC1 | Hs.37181 |
| ESTs | Hs.279175 | | Hs.37892 |
| CD86 | <u>Hs.27954</u> | Homo sapiens suppressor of variegation 3-9 (Drosophila) homolog (SUV39H) mRNA, and translated products. | Hs.37936 |
| CGI-81 protein | <u>Hs.279583</u> | C8B | <u>Hs.38069</u> |
| ESTs | Hs.279821 | MTH1 (NUDT1) | Hs.388 |
| ESTs | Hs.279823 | Adrenomedullin | Hs.394 |
| ESTs, Weakly similar to IRE1_HUMAN IRON-RESPONSIVE ELEMENT BINDING PROTEIN 1 [H.sapiens] | Hs.279824 | | Hs.39441 |
| ESTs | Hs.279825 | CD66b | <u>Hs.41</u> |
| ESTs | Hs.279826 | RAD50 | Hs.41587 |

Table 2: Candidate genes, Database mining

| | | | |
|--|-----------|---|-----------------|
| MLH3 | Hs.279843 | CD94 | <u>Hs.41682</u> |
| TNFRSF14 | Hs.279899 | HLJ1 | Hs.41693 |
| RPA4 | Hs.283018 | ESM1 | Hs.41716 |
| EST | Hs.283165 | MSH3 | Hs.42674 |
| EST | Hs.283166 | cAMP responsive element binding protein-like 1 | <u>Hs.42853</u> |
| EST | Hs.283167 | IKBKG | Hs.43505 |
| EST | Hs.283168 | Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA. | Hs.43543 |
| ESTs | Hs.283169 | LEU2 | Hs.43628 |
| EST | Hs.283245 | Homo sapiens immunoglobulin lambda gene locus DNA, clone:288A10 | <u>Hs.43834</u> |
| EST | Hs.283247 | SIRT2 | Hs.44017 |
| ESTs | Hs.283248 | | Hs.44087 |
| EST | Hs.283249 | TREM2 | Hs.44234 |
| EST | Hs.283250 | serine/threonine kinase 19 | <u>Hs.444</u> |
| EST | Hs.283251 | | Hs.44512 |
| EST | Hs.283252 | | Hs.44628 |
| EST | Hs.283253 | | Hs.45063 |
| EST | Hs.283254 | LTC4 synthase | <u>Hs.456</u> |
| EST | Hs.283255 | FUT2 | Hs.46328 |
| EST | Hs.283256 | CCR6 | Hs.46468 |
| EST | Hs.283257 | POLM | Hs.46964 |
| EST | Hs.283258 | EXO1 (HEX1) | Hs.47504 |
| ESTs | Hs.283259 | FEN1 (Dnase IV) | Hs.4756 |
| EST | Hs.283261 | | Hs.4863 |
| EST | Hs.283262 | golgin-165 | Hs.4953 |
| EST | Hs.283263 | | Hs.50102 |
| EST | Hs.283264 | ATP-binding cassette, sub-family B (MDR/TAP), member 3 | <u>Hs.502</u> |
| EST | Hs.283266 | | Hs.5057 |
| ESTs | Hs.283268 | corneodesmosin | <u>Hs.507</u> |
| EST | Hs.283269 | Histone H2 (H2AFP) | Hs.51011 |
| EST, Weakly similar to AF189011_1 ribonuclease III [H.sapiens] | Hs.283270 | CCNH | Hs.514 |
| EST | Hs.283271 | EST | Hs.5146 |
| EST | Hs.283272 | SMUG1 | Hs.5212 |
| EST | Hs.283274 | ABH (ALKB) | Hs.54418 |
| EST | Hs.283275 | CCR5 | <u>Hs.54443</u> |
| EST | Hs.283276 | CD81 | <u>Hs.54457</u> |
| ESTs, Weakly similar to S32605 collagen alpha 3(VI) chain - mouse [M.musculus] | Hs.283392 | TNFSF13 | Hs.54673 |
| ESTs | Hs.283433 | PRPS1 | Hs.56 |
| ESTs | Hs.283434 | | Hs.56156 |
| ESTs | Hs.283438 | | Hs.56265 |
| ESTs | Hs.283442 | killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2 | <u>Hs.56328</u> |
| ESTs | Hs.283443 | EST | Hs.5656 |
| ESTs | Hs.283456 | | Hs.56845 |
| ESTs | Hs.283457 | MLH1 | Hs.57301 |
| ESTs, Weakly similar to similar to collagen [C.elegans] | Hs.283458 | testis specific basic protein | <u>Hs.57692</u> |

Table 2: Candidate genes, Database mining

| | | | |
|--|-----------|---|----------|
| ESTs | Hs.283459 | ESTs | Hs.57841 |
| ESTs | Hs.283460 | Human 6Ckine | Hs.57907 |
| ESTs | Hs.283462 | EST | Hs.5816 |
| ESTs | Hs.283463 | Homo sapiens cell growth regulatory with ring finger domain (CGR19) mRNA. | Hs.59106 |
| ESTs | Hs.283496 | ERCC1 | Hs.59544 |
| ESTs | Hs.283497 | | Hs.61558 |
| ESTs | Hs.283499 | Homo sapiens GPI transamidase mRNA, complete cds. | Hs.62187 |
| ESTs | Hs.283500 | | Hs.62699 |
| ESTs, Weakly similar to ORF YDL014w [S.cerevisiae] | Hs.283504 | | Hs.63913 |
| ESTs, Weakly similar to S09646 collagen alpha 2(VI) chain precursor, medium splice form - human [H.sapiens] | Hs.283505 | Homo sapiens chloride intracellular channel 3 (CLIC3), mRNA. | Hs.64746 |
| ESTs | Hs.283608 | FANCF | Hs.65328 |
| CD42c | Hs.283743 | | Hs.6544 |
| tenascin XA | Hs.283750 | interleukin 1 receptor-like 1 | Hs.66 |
| immunoglobulin kappa variable 1D-8 | Hs.283770 | CD38 | Hs.66052 |
| protocadherin gamma subfamily A, 2 (PCDHGA2) | Hs.283801 | | Hs.6607 |
| Homo sapiens mRNA; cDNA DKFZp762F0616 (from clone DKFZp762F0616) | Hs.283849 | RAD54L | Hs.66718 |
| Homo sapiens clone bsmneg3-t7 immunoglobulin lambda light chain VJ region, (IGL) mRNA, partial cds | Hs.283876 | SCYA17 (CCL17) | Hs.66742 |
| Homo sapiens transgenic-JHD mouse #2357 immunoglobulin heavy chain variable region (IgG VH251) mRNA, partial cds | Hs.283878 | IL-12 | Hs.673 |
| Homo sapiens clone N97 immunoglobulin heavy chain variable region mRNA, partial cds | Hs.283882 | Human IL-12 p40 | Hs.674 |
| Homo sapiens clone case06H1 immunoglobulin heavy chain variable region gene, partial cds | Hs.283924 | LILRB4 | Hs.67846 |
| Homo sapiens HSPC077 mRNA, partial cds | Hs.283929 | interleukin 5 receptor, alpha | Hs.68876 |
| Homo sapiens HSPC088 mRNA, partial cds | Hs.283931 | | Hs.6891 |
| Homo sapiens HSPC097 mRNA, partial cds | Hs.283933 | | Hs.69233 |
| Homo sapiens HSPC102 mRNA, partial cds | Hs.283934 | FUT1 | Hs.69747 |
| Homo sapiens HSPC107 mRNA, partial cds | Hs.283935 | B-factor, properdin | Hs.69771 |
| CMKRL1 | Hs.28408 | | Hs.70333 |
| FANCA | Hs.284153 | | Hs.71618 |
| Homo sapiens immunoglobulin mu chain antibody MO30 (IgM) mRNA, complete cds | Hs.284277 | RAD1 | Hs.7179 |
| gamma-glutamyltransferase 1 | Hs.284380 | interleukin 19 | Hs.71979 |

Table 2: Candidate genes, Database mining

| | | | |
|--|---------------------------|---|--------------------------|
| putative human HLA class II associated protein I | Hs.285013 | MEK2 | Hs.72241 |
| interleukin 13 receptor, alpha 1 | Hs.285115 | IL-7 | Hs.72927 |
| CDw131 | Hs.285401 | STAT2 | Hs.72988 |
| Homo sapiens VH2-D3.10-JH5b gene for immunoglobulin heavy chain variable region | Hs.287403 | CD42d | Hs.73734 |
| Homo sapiens cDNA: FLJ22546 fis, clone HSI00290 | Hs.287697 | MIF | Hs.73798 |
| Homo sapiens cDNA: FLJ23140 fis, clone LNG09065 | Hs.287728 | ECP | Hs.73839 |
| H.sapiens mRNA for HLA-C alpha chain (Cw*1701) | Hs.287811 | CPN2 | Hs.73858 |
| Homo sapiens clone ASMneg1-b1 immunoglobulin lambda chain VJ region, (IGL) mRNA, partial cds | Hs.287815 | MMP8 | Hs.73862 |
| Homo sapiens clone CPRF1-T2 immunoglobulin lambda chain VJ region, (IGL) mRNA, partial cds | Hs.287816 | HLA-G histocompatibility antigen, class I, G | Hs.73885 |
| EST | Hs.287817 | TNFRSF9 | Hs.73895 |
| myelin protein zero-like 1 | Hs.287832 | IL-4 | Hs.73917 |
| immunoglobulin lambda-like polypeptide 1 | Hs.288168 | HLA-DQB1 | Hs.73931 |
| cathepsinB | Hs.288181 | RAG1 | Hs.73958 |
| G18.2 protein | Hs.288316 | LAG-3 | Hs.74011 |
| ESTs | Hs.288403 | | Hs.7402 |
| EST | Hs.288431 | CD163 | Hs.74076 |
| Homo sapiens partial IGVH2 gene for immunoglobulin heavy chain V region, case 2, cell B 45 | Hs.288553 | immunoglobulin superfamily, member 2 | Hs.74115 |
| polymeric immunoglobulin receptor | Hs.288579 | CD158b | Hs.74134 |
| Human immunoglobulin heavy chain variable region (V4-4) gene, partial cds | Hs.288711 | | Hs.7434 |
| Human immunoglobulin heavy chain variable region (V4-4b) gene, partial cds | Hs.289036 | TCRa | Hs.74647 |
| | Hs.28921 | human immunodeficiency virus type I enhancer-binding protein 2 | Hs.75063 |
| EST | Hs.289577 | MLN50 | Hs.75080 |
| EST | Hs.289836 | lysyl hydroxylase (PLOD) | Hs.75093 |
| EST | Hs.289878 | TAK1 | Hs.7510 |
| GSN | Hs.290070 | Homo sapiens transcription factor 6-like 1 (mitochondrial transcription factor 1-like) (TCF6L1) mRNA. | Hs.75133 |
| EST, Weakly similar to unnamed protein product [H.sapiens] | Hs.290133 | UBE2N (UBC13, BTG1) | Hs.75355 |
| EST | Hs.290227 | | Hs.75450 |
| ESTs | Hs.290315 | HSPA2 | Hs.75452 |
| EST | Hs.290339 | CD151 | Hs.75564 |
| EST | Hs.290340 | RELA | Hs.75569 |
| | Hs.29055 | CD122 | Hs.75596 |
| EST | Hs.291125 | CD14 | Hs.75627 |
| EST | Hs.291126 | nuclear factor erythroid 2 isoform f=basil leucine zipper protein {alternatively spliced | Hs.75643 |
| CD91= LRP | Hs.89137 | CIQB | Hs.8986 |

Table 2: Candidate genes, Database mining

| | | | |
|--|----------|---|----------|
| XPF (ERCC4) | Hs.89296 | superkiller viralicidic activity 2 (S. cerevisiae homolog)-like | Hs.89864 |
| Carbonic anhydrase IV | Hs.89485 | EST | Hs.90165 |
| CETP | Hs.89538 | EST | Hs.90171 |
| RAD52 | Hs.89571 | GTF2H3 | Hs.90304 |
| GTF2H1 | Hs.89578 | protein tyrosine kinase related sequence | Hs.90314 |
| Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide | Hs.897 | | Hs.90463 |
| transcript ch138 | Hs.94881 | SGRF protein, Interleukin 23 p19 subunit | Hs.98309 |
| | Hs.9578 | XRCC1 | Hs.98493 |
| IL-9 | Hs.960 | Homo sapiens mRNA for KIAA0543 protein, partial cds. | Hs.98507 |
| NFATC1 | Hs.96149 | | Hs.9893 |
| OGG1 | Hs.96398 | DIR1 protein | Hs.99134 |
| | Hs.96499 | XRCC3 | Hs.99742 |
| NFKBIB | Hs.9731 | Elastase(leukocyte) | Hs.99863 |
| XAB2 (HCNP) | Hs.9822 | JAK3 | Hs.99877 |
| CD40 | Hs652 | | |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| Example Clone | Offset on Acc Start | End | Accession Number | UniGene | Signif | Number Clones | Genbank Description |
|---------------|---------------------|------|------------------|---------|-----------|---------------|--|
| 56D1 | 1521 | 1685 | D00022 | Hs.25 | 1.00E-84 | 1 | for F1 beta subunit, complete |
| 586E3 | 1227 | 1448 | NM_001686 | Hs.25 | 1.00E-89 | 1 | ATP synthase, H ⁺ transporting, mitochondrial |
| 459F4 | 1484 | 2522 | NM_002832 | Hs.35 | 0 | 3 | protein tyrosine phosphatase, non-receptor t |
| 41A11 | 885 | 1128 | D12614 | Hs.36 | 1.00E-125 | 1 | lymphotoxin (TNF-beta), complete |
| 41G12 | 442 | 1149 | D10202 | Hs.46 | 0 | 1 | for platelet-activating factor receptor, |
| 98E12 | 1928 | 2652 | NM_002835 | Hs.62 | 0 | 1 | protein tyrosine phosphatase, non-receptor t |
| 170E1 | 473 | 1071 | U13044 | Hs.78 | 0 | 1 | nuclear respiratory factor-2 subunit alpha mRNA, com |
| 40C6 | 939 | 1357 | D11086 | Hs.84 | 0 | 1 | interleukin 2 receptor gamma chain |
| 521F9 | 283 | 1176 | NM_000206 | Hs.84 | 0 | 8 | interleukin 2 receptor, gamma (severe combined |
| 60A11 | 989 | 1399 | L08069 | Hs.94 | 0 | 2 | heat shock protein, E. coli DnaJ homologue complete cd |
| 520B9 | 545 | 1438 | NM_001539 | Hs.94 | 0 | 3 | heat shock protein, DNAJ-like 2 (HSJ2), mRNA / |
| 460H9 | 626 | 1104 | NM_021127 | Hs.96 | 0 | 1 | phorbol-12-myristate-13-acetate-induced p |
| 127G12 | 651 | 1223 | NM_004906 | Hs.119 | 0 | 2 | Wilms' tumour 1-associating protein (KIAA0105 |
| 586A7 | 438 | 808 | NM_000971 | Hs.153 | 0 | 3 | ribosomal protein L7 (RPL7), mRNA /cds=(10,756 |
| 99H12 | 2447 | 4044 | NM_002600 | Hs.188 | 0 | 2 | phosphodiesterase 4B, cAMP-specific (dunce (|
| 464D4 | 2317 | 2910 | NM_002344 | Hs.210 | 0 | 1 | leukocyte tyrosine kinase (LTK), mRNA /cds=(17 |
| 464B3 | 10 | 385 | NM_002515 | Hs.214 | 1.00E-164 | 1 | neuro-oncological ventral antigen 1 (NOVA1), |
| 40A12 | 296 | 1153 | L11695 | Hs.220 | 0 | 1 | activin receptor-like kinase (ALK-5) mRNA, complete |
| 129A2 | 4138 | 4413 | NM_000379 | Hs.250 | 1.00E-155 | 1 | xanthene dehydrogenase (XDH), mRNA |
| 36B10 | 80 | 1475 | AF068836 | Hs.270 | 0 | 3 | cytohesin binding protein HE mRNA, complete cd |
| 45C11 | 58 | 1759 | NM_004288 | Hs.270 | 0 | 2 | pleckstrin homology, Sec7 and coiled/coiled dom |
| 128C12 | 2555 | 3215 | NM_000153 | Hs.273 | 0 | 4 | galactosylceramidase (Krabbe disease) (GALC) |
| 67H2 | 259 | 1418 | D23660 | Hs.286 | 0 | 8 | ribosomal protein, complete cds |
| 151E6 | 624 | 1170 | AF052124 | Hs.313 | 0 | 1 | clone 23810 osteopontin mRNA, complete cds /c |
| 45A7 | 4 | 262 | NM_000582 | Hs.313 | 1.00E-136 | 1 | secreted phosphoprotein 1 (osteopontin, bone |
| 44C10 | 2288 | 2737 | J03250 | Hs.317 | 0 | 1 | topoisomerase I mRNA, complete cds /cds=(211,2508) / |
| 99H9 | 2867 | 3246 | NM_001558 | Hs.327 | 0 | 2 | interleukin 10 receptor, alpha (IL10RA), mRNA |
| 41B4 | 2867 | 3315 | U00672 | Hs.327 | 0 | 6 | interleukin-10 receptor mRNA, complete |
| 144E1 | 283 | 989 | M26683 | Hs.340 | 0 | 36 | interferon gamma treatment inducible /cds=(14,1 |
| 41A12 | 1854 | 2590 | X53961 | Hs.347 | 0 | 1 | lactoferrin /cds=(294,2429) /gb=X53961 /gi= |
| 40F1 | 1377 | 1734 | U95626 | Hs.395 | 0 | 1 | ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and cc |
| 463H4 | 55 | 434 | NM_001459 | Hs.428 | 0 | 1 | fms-related tyrosine kinase 3 ligand (FLT3LG) |
| 127E1 | 552 | 1048 | NM_005180 | Hs.431 | 0 | 1 | murine leukemia viral (bmi-1) oncogene homolo |
| 73G12 | 189 | 1963 | NM_004024 | Hs.460 | 0 | 17 | activating transcription factor 3 (ATF3), ATF |
| 524A4 | 1361 | 2136 | NM_004168 | Hs.469 | 0 | 2 | succinate dehydrogenase complex, subunit A, |
| 41C7 | 1554 | 2097 | D10925 | Hs.516 | 0 | 1 | HM145 /cds=(22,1089) /gb=D10925 /gi=219862 |
| 588A2 | 48 | 163 | NM_001032 | Hs.539 | 1.00E-59 | 1 | ribosomal protein S29 (RPS29), mRNA /cds=(30,2 |
| 177B4 | 1 | 1674 | AF076465 | Hs.550 | 2.00E-37 | 2 | PhLOP2 mRNA, complete cds /cds=(5,358) /gb=AF |
| 68G5 | 2 | 1454 | M26383 | Hs.624 | 0 | 17 | monocyte-derived neutrophil-activating protein (M |
| 45F10 | 1 | 1454 | NM_000584 | Hs.624 | 0 | 11 | interleukin 8 (IL8), mRNA /cds=(74,373) /gb=N |
| 59F11 | 59 | 1822 | X68550 | Hs.652 | 0 | 14 | TRAP mRNA for ligand of CD40 /cds=(56,841) /gb=X6 |
| 471C9 | 3115 | 3776 | NM_000492 | Hs.663 | 0 | 1 | cystic fibrosis transmembrane conductance re |
| 68D1 | 228 | 866 | M20137 | Hs.694 | 0 | 3 | interleukin 3 (IL-3) mRNA, complete cds, clone pcD-SR |
| 49H3 | 42 | 665 | NM_000588 | Hs.694 | 0 | 1 | interleukin 3 (colony-stimulating factor, mu |
| 147H3 | 110 | 340 | BF690338 | Hs.695 | 1.00E-102 | 1 | 602186730T1 cDNA, 3' end /clone=IMAGE:4299006 |
| 483E4 | 310 | 846 | NM_000942 | Hs.699 | 0 | 1 | peptidylprolyl isomerase B (cyclophilin B) (|
| 522B12 | 349 | 755 | NM_000788 | Hs.709 | 0 | 2 | deoxycytidine kinase (DCK), mRNA /cds=(159,94 |
| 331E5 | 1293 | 1470 | J03634 | Hs.727 | 9.00E-75 | 1 | erythroid differentiation protein mRNA (EDF), comple |
| 514D12 | 1164 | 1579 | NM_004907 | Hs.737 | 1.00E-169 | 3 | immediate early protein (ETR101), mRNA /cds=(|
| 73H7 | 1953 | 3017 | AJ243425 | Hs.738 | 0 | 8 | EGR1 gene for early growth response protein 1 / |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|---------|-----------|-----|--|
| 592A8 | 10 | 454 | NM_003973 | Hs.738 | 0 | 5 | ribosomal protein L14 (RPL14), mRNA |
| 519A1 | 116 | 1527 | NM_000801 | Hs.752 | 1.00E-163 | 2 | FK506-binding protein 1A (12kD) (FKBP1A), mRN |
| 109H11 | 1 | 1206 | M60626 | Hs.753 | 0 | 10 | N-formylpeptide receptor (fMLP-R98) mRNA, complete |
| 99C5 | 1 | 1175 | NM_002029 | Hs.753 | 0 | 25 | formyl peptide receptor 1 (FPR1), mRNA |
| 103C1 | 2285 | 2890 | NM_002890 | Hs.758 | 0 | 1 | RAS p21 protein activator (GTPase activating p |
| 41H4 | 3142 | 3332 | NM_000419 | Hs.785 | 1.00E-84 | 1 | integrin, alpha 2b (platelet glycoprotein IIb |
| 171D2 | 198 | 748 | X54489 | Hs.789 | 1.00E-132 | 2 | melanoma growth stimulatory activity (MGSA) |
| 458H7 | 2165 | 2818 | NM_001656 | Hs.792 | 0 | 1 | ADP-ribosylation factor domain protein 1, 64 |
| 62B3 | 833 | 1241 | M60278 | Hs.799 | 0 | 2 | heparin-binding EGF-like growth factor mRNA, complet |
| 53G4 | 1299 | 2166 | AK001364 | Hs.808 | 0 | 6 | FLJ10502 fis, clone NT2RP2000414, highly |
| 597F3 | 1136 | 1797 | NM_004966 | Hs.808 | 0 | 2 | heterogeneous nuclear ribonucleoprotein F (|
| 143F7 | 575 | 985 | M74525 | Hs.811 | 0 | 3 | HHR6B (yeast RAD 6 homologue) mRNA, complete |
| 518H8 | 580 | 974 | NM_003337 | Hs.811 | 0 | 1 | ubiquitin-conjugating enzyme E2B (RAD6 homol |
| 45G8 | 277 | 833 | NM_002121 | Hs.814 | 0 | 1 | major histocompatibility complex, class II, |
| 41H11 | 719 | 1534 | NM_005191 | Hs.838 | 0 | 1 | CD80 antigen (CD28 antigen ligand 1, B7-1 antig |
| 41G1 | 117 | 557 | U31120 | Hs.845 | 0 | 1 | interleukin-13 (IL-13) precursor gene, complete cds |
| 75E1 | 693 | 862 | J05272 | Hs.850 | 2.00E-58 | 4 | IMP dehydrogenase type 1 mRNA complete |
| 129B11 | 3361 | 3883 | L25851 | Hs.851 | 0 | 1 | integrin alpha E precursor, mRNA, complete cds |
| 481E9 | 3361 | 3742 | NM_002208 | Hs.851 | 1.00E-173 | 1 | integrin, alpha E (antigen CD103, human mucosa |
| 71G7 | 1 | 1193 | NM_000619 | Hs.856 | 0 | 111 | interferon, gamma (IFNG), mRNA /cds=(108,608) |
| 75H5 | 1 | 1193 | X13274 | Hs.856 | 0 | 314 | interferon IFN-gamma /cds=(108,608) /gb=X13 |
| 525B12 | 672 | 894 | NM_002341 | Hs.890 | 1.00E-121 | 1 | lymphotoxin beta (TNF superfamily, member 3) |
| 40E8 | 75 | 999 | AL121985 | Hs.901 | 0 | 6 | DNA sequence RP11-404F10 on chromosome 1q2 |
| 48H4 | 680 | 933 | NM_001778 | Hs.901 | 1.00E-130 | 2 | CD48 antigen (B-cell membrane protein) (CD48) |
| 179G8 | 1652 | 2181 | AL163285 | Hs.926 | 0 | 1 | chromosome 21 segment HS21C085 |
| 48G11 | 1049 | 2092 | NM_002463 | Hs.926 | 0 | 3 | myxovirus (influenza) resistance 2, homolog o |
| 110B12 | 209 | 1734 | M32011 | Hs.949 | 0 | 8 | neutrophil oxidase factor (p67-phox) mRNA, complete |
| 99C9 | 207 | 1733 | NM_000433 | Hs.949 | 0 | 11 | neutrophil cytosolic factor 2 (65kD, chronic g |
| 125D2 | 958 | 1645 | NM_004645 | Hs.966 | 0 | 1 | coilin (COIL), mRNA /cds=(22,1752) /gb=N |
| 458C1 | 1649 | 2285 | NM_006025 | Hs.997 | 0 | 1 | protease, serine, 22 (P11), mRNA /cds=(154,126 |
| 40H11 | 621 | 864 | L26953 | Hs.1010 | 1.00E-135 | 1 | chromosomal protein mRNA, complete cds /cds=(7 |
| 116D10 | 513 | 858 | NM_002932 | Hs.1010 | 0 | 1 | regulator of mitotic spindle assembly 1 (RMSA |
| 40G11 | 1565 | 2151 | M31452 | Hs.1012 | 0 | 1 | proline-rich protein (PRP) mRNA, complete |
| 192A6 | 321 | 908 | NM_000284 | Hs.1023 | 0 | 1 | pyruvate dehydrogenase (lipoamide) alpha 1 (|
| 460H11 | 2158 | 2402 | NM_004762 | Hs.1050 | 2.00E-91 | 1 | pleckstrin homology, Sec7 and coiled/coil dom |
| 41F12 | 291 | 565 | M57888 | Hs.1051 | 1.00E-112 | 1 | (clone lambda B34) cytotoxic T-lymphocyte-associate |
| 41A5 | 1311 | 1852 | M55654 | Hs.1100 | 0 | 1 | TATA-binding protein mRNA, complete |
| 461D7 | 999 | 1277 | NM_002698 | Hs.1101 | 1.00E-92 | 1 | POU domain, class 2, transcription factor 2 (P |
| 597H9 | 1083 | 1224 | NM_000660 | Hs.1103 | 3.00E-75 | 1 | transforming growth factor, beta 1 (TGFB1), mR |
| 40B5 | 1433 | 2010 | X02812 | Hs.1103 | 0 | 1 | transforming growth factor-beta (TGF-beta) |
| 106A10 | 1977 | 2294 | M73047 | Hs.1117 | 1.00E-176 | 1 | tripeptidyl peptidase II mRNA, complete cds /c |
| 165E8 | 4273 | 4582 | NM_003291 | Hs.1117 | 1.00E-173 | 1 | tripeptidyl peptidase II (TPP2), mRNA /cds=(23 |
| 63G12 | 1114 | 2339 | D49728 | Hs.1119 | 0 | 7 | NAK1 mRNA for DNA binding protein, complete |
| 45B10 | 1317 | 1857 | NM_002135 | Hs.1119 | 0 | 1 | nuclear receptor subfamily 4, group A, member |
| 37H3 | 568 | 783 | M24069 | Hs.1139 | 1.00E-119 | 1 | DNA-binding protein A (dbpA) gene, 3' end |
| 476F9 | 209 | 608 | NM_000174 | Hs.1144 | 0 | 1 | glycoprotein IX (platelet) (GP9), mRNA /cds=(|
| 43A10 | 1105 | 1357 | U15085 | Hs.1162 | 3.00E-41 | 1 | HLA-DMB mRNA, complete cds |
| 139D6 | 1345 | 1680 | L11329 | Hs.1183 | 1.00E-102 | 1 | protein tyrosine phosphatase (PAC-1) mRNA, co |
| 134B12 | 1233 | 1675 | NM_004418 | Hs.1183 | 0 | 1 | dual specificity phosphatase 2 (DUSP2), mRNA |
| 58F1 | 17 | 341 | NM_002157 | Hs.1197 | 0 | 1 | heat shock 10kD protein 1 (chaperonin 10) (HSP |
| 158G5 | 20 | 341 | U07550 | Hs.1197 | 1.00E-180 | 2 | chaperonin 10 mRNA, complete cds |
| 167C8 | 813 | 1453 | NM_000022 | Hs.1217 | 0 | 4 | adenosine deaminase (ADA), mRNA /cds=(95,1186 |
| 179H1 | 730 | 1452 | X02994 | Hs.1217 | 0 | 6 | adenosine deaminase (adenosine aminohydrola |
| 40E10 | 594 | 792 | M38690 | Hs.1244 | 1.00E-109 | 1 | CD9 antigen mRNA, complete cds |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|---------|-----------|----|---|
| 41C5 | 1280 | 1438 | AK024951 | Hs.1279 | 2.00E-80 | 1 | FLJ21298 fis, clone COL02040, highly sim |
| 40E3 | 1002 | 1735 | NM_000065 | Hs.1282 | 0 | 1 | complement component 6 (C6) mRNA /cd |
| 40A11 | 1638 | 1821 | K02766 | Hs.1290 | 3.00E-98 | 1 | complement component C9 mRNA, complete |
| 40B12 | 4639 | 5215 | NM_007289 | Hs.1298 | 0 | 1 | membrane metallo-endopeptidase (neutral end |
| 41G2 | 1576 | 1870 | M28825 | Hs.1309 | 1.00E-115 | 1 | thymocyte antigen CD1a mRNA, complete cds |
| 41F8 | 1171 | 1551 | AX023365 | Hs.1349 | 0 | 1 | Sequence 36 from Patent WO0006605 |
| 40E1 | 673 | 1147 | M30142 | Hs.1369 | 0 | 1 | decay-accelerating factor mRNA, complete cds |
| 118B12 | 1129 | 1719 | NM_000574 | Hs.1369 | 0 | 1 | decay accelerating factor for complement (CD5 |
| 75F8 | 830 | 2979 | NM_000399 | Hs.1395 | 0 | 48 | early growth response 2 (Krox-20 (Drosophila) |
| 41F11 | 973 | 1428 | M15059 | Hs.1416 | 0 | 1 | Fc-epsilon receptor (IgE receptor) mRNA, complete cd |
| 110G12 | 1931 | 2071 | AL031729 | Hs.1422 | 2.00E-70 | 1 | DNA seq RP1-159A19 on chromosome 1p36 |
| 113D10 | 1718 | 2066 | NM_005248 | Hs.1422 | 6.00E-76 | 2 | Gardner-Rasheed feline sarcoma viral (v-fgr) |
| 477C2 | 3292 | 3842 | NM_000152 | Hs.1437 | 0 | 1 | glucosidase, alpha; acid (Pompe disease, glyc |
| 124D1 | 795 | 1127 | NM_000167 | Hs.1466 | 0 | 1 | glycerol kinase (GK), mRNA /cds=(66,1640) /gb |
| 41B9 | 2231 | 2447 | J03171 | Hs.1513 | 1.00E-108 | 1 | interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, |
| 99F7 | 927 | 1889 | NM_014882 | Hs.1528 | 0 | 2 | KIAA0053 gene product (KIAA0053), mRNA /cds=(|
| 469G9 | 1220 | 1507 | NM_005082 | Hs.1579 | 1.00E-117 | 1 | zinc finger protein 147 (estrogen-responsive |
| 195B7 | 190 | 1801 | BC002971 | Hs.1600 | 0 | 3 | clone IMAGE:3543711, mRNA, partial cds /cds= |
| 195F10 | 3676 | 3856 | NM_000110 | Hs.1602 | 1.00E-85 | 1 | dihydropyrimidine dehydrogenase (DPYD), mRN |
| 129E7 | 648 | 1827 | L08176 | Hs.1652 | 0 | 2 | Epstein-Barr virus induced G-protein coupled recepto |
| 478H5 | 1839 | 2050 | NM_002056 | Hs.1674 | 7.00E-79 | 1 | glutamine-fructose-6-phosphate transaminas |
| 39H1 | 436 | 865 | L35249 | Hs.1697 | 0 | 1 | vacuolar H ⁺ -ATPase Mr 56,000 subunit (HO57) mR |
| 183H8 | 972 | 1183 | NM_001693 | Hs.1697 | 1.00E-106 | 1 | ATPase, H ⁺ transporting, lysosomal (vacuolar |
| 481A4 | 1594 | 1785 | NM_001420 | Hs.1701 | 2.00E-79 | 1 | ELAV (embryonic lethal, abnormal vision, Dros |
| 40B3 | 3846 | 4009 | L39064 | Hs.1702 | 4.00E-70 | 1 | interleukin 9 receptor precursor (IL9R) gene, |
| 176G8 | 1033 | 1400 | NM_006084 | Hs.1706 | 0 | 1 | interferon-stimulated transcription factor |
| 589C11 | 1 | 1347 | NM_005998 | Hs.1708 | 0 | 2 | chaperonin containing TCP1, subunit 3 (gamma) |
| 70H5 | 1 | 494 | X74801 | Hs.1708 | 0 | 1 | Cctg mRNA for chaperonin /cds=(0,1634) /gb=X7480 |
| 460C12 | 3310 | 3809 | NM_012089 | Hs.1710 | 0 | 1 | ATP-binding cassette, sub-family B (MDR/TAP), |
| 41D5 | 484 | 1862 | M28983 | Hs.1722 | 0 | 3 | interleukin 1 alpha (IL 1) mRNA, complete cds / |
| 119E8 | 493 | 904 | NM_000575 | Hs.1722 | 1.00E-151 | 2 | interleukin 1, alpha (IL1A), mRNA /cds=(36,851 |
| 479E11 | 5 | 268 | NM_000417 | Hs.1724 | 1.00E-145 | 1 | interleukin 2 receptor, alpha (IL2RA), mRNA / |
| 62C8 | 85 | 1887 | X01057 | Hs.1724 | 0 | 2 | interleukin-2 receptor /cds=(180,998) /gb=X |
| 466A3 | 2166 | 2675 | NM_000889 | Hs.1741 | 0 | 1 | integrin, beta 7 (ITGB7), mRNA /cds=(151,2547) |
| 107A4 | 4960 | 5610 | L33075 | Hs.1742 | 0 | 1 | ras GTPase-activating-like protein (IQGAP1) |
| 189A5 | 4318 | 7450 | NM_003870 | Hs.1742 | 0 | 3 | IQ motif containing GTPase activating protein |
| 597D1 | 1230 | 1737 | NM_005356 | Hs.1765 | 1.00E-127 | 5 | lymphocyte-specific protein tyrosine kinase |
| 41C10 | 1057 | 1602 | J04142 | Hs.1799 | 0 | 1 | (lambda-gt11ht-5) MHC class I antigen-like gl |
| 104H1 | 1854 | 2023 | L06175 | Hs.1845 | 4.00E-54 | 1 | P5-1 mRNA, complete cds /cds=(304,735) /gb=L06 |
| 98F7 | 34 | 2041 | NM_006674 | Hs.1845 | 4.00E-63 | 5 | MHC class I region ORF (P5-1), /cds=(304,735) / |
| 104F1 | 1390 | 1756 | NM_002436 | Hs.1861 | 0 | 2 | membrane protein, palmitoylated 1 (55kD) (MPP |
| 171F7 | 1760 | 2192 | M55284 | Hs.1880 | 0 | 1 | protein kinase C-L (PRKCL) mRNA, complete cds |
| 134B2 | 123 | 1182 | NM_002727 | Hs.1908 | 0 | 10 | proteoglycan 1, secretory granule (PRG1), mRN |
| 61C11 | 126 | 902 | X17042 | Hs.1908 | 0 | 11 | hematopoietic proteoglycan core protein /cds |
| 458G1 | 1 | 475 | NM_001885 | Hs.1940 | 0 | 1 | crystallin, alpha B (CRYAB), mRNA |
| 520E10 | 71 | 343 | NM_001024 | Hs.1948 | 1.00E-142 | 3 | ribosomal protein S21 (RPS21), mRNA |
| 459D6 | 2435 | 3055 | NM_001761 | Hs.1973 | 0 | 1 | cyclin F (CCNF), mRNA /cds=(43,2403) |
| 41H3 | 184 | 1620 | NM_006139 | Hs.1987 | 0 | 2 | CD28 antigen (Tp44) (CD28), mRNA /cds=(222,884 |
| 71C5 | 721 | 1329 | NM_000639 | Hs.2007 | 0 | 2 | tumor necrosis factor (ligand) superfamily, m |
| 73C1 | 721 | 1603 | X89102 | Hs.2007 | 0 | 8 | fasligand /cds=(157,1002) |
| 135G3 | 940 | 1352 | NM_002852 | Hs.2050 | 6.00E-96 | 1 | pentaxin-related gene, rapidly induced by IL |
| 44A10 | 1562 | 1748 | M58028 | Hs.2055 | 7.00E-69 | 1 | ubiquitin-activating enzyme E1 (UBE1) mRNA, complete |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|---------|-----------|----|---|
| 155G5 | 973 | 2207 | AL133415 | Hs.2064 | 0 | 7 | DNA sequence from clone RP11-124N14 on chromosome 10. |
| 599H7 | 48 | 3022 | AK025306 | Hs.2083 | 0 | 12 | cDNA: FLJ21653 fis, clone COL08586, |
| 71H1 | 1598 | 2163 | NM_004419 | Hs.2128 | 0 | 5 | dual specificity phosphatase 5 (DUSP5), mRNA |
| 69H7 | 1595 | 2161 | U15932 | Hs.2128 | 0 | 11 | dual-specificity protein phosphatase mRNA, complete |
| 458C4 | 1928 | 2356 | NM_005658 | Hs.2134 | 0 | 1 | TNF receptor-associated factor 1 (TRAF1), mRN |
| 192E11 | 6 | 414 | NM_002704 | Hs.2164 | 0 | 1 | pro-platelet basic protein (includes platele |
| 40D12 | 1935 | 2645 | M58597 | Hs.2173 | 0 | 2 | ELAM-1 ligand fucosyltransferase (ELFT) mRNA, comple |
| 40E5 | 2834 | 3024 | M59820 | Hs.2175 | 1.00E-104 | 1 | granulocyte colony-stimulating factor receptor (CSF |
| 482D8 | 2521 | 2943 | NM_000760 | Hs.2175 | 0 | 2 | colony stimulating factor 3 receptor (granuloc |
| 60H6 | 918 | 1723 | AF119850 | Hs.2186 | 0 | 6 | PRO1608 mRNA, complete cds /cds=(1221,2174) / |
| 597F11 | 99 | 1267 | NM_001404 | Hs.2186 | 0 | 29 | eukaryotic translation elongation factor 1 g |
| 595G4 | 6 | 570 | L40410 | Hs.2210 | 0 | 1 | thyroid receptor interactor (TRIP3) mRNA, 3' |
| 41H12 | 970 | 1353 | X03656 | Hs.2233 | 0 | 1 | granulocyte colony-stimulating factor (G-C |
| 461A9 | 287 | 730 | Z29067 | Hs.2236 | 0 | 1 | H.sapiens nek3 mRNA for protein kinase |
| 493E11 | 212 | 608 | NM_000879 | Hs.2247 | 1.00E-141 | 2 | interleukin 5 (colony-stimulating factor, eo |
| 150B5 | 363 | 815 | X04688 | Hs.2247 | 0 | 1 | T-cell replacing factor (interleukin-5) /cd |
| 461E12 | 255 | 342 | NM_001565 | Hs.2248 | 8.00E-34 | 1 | small inducible cytokine subfamily B (Cys-X-C |
| 129A8 | 1790 | 1970 | NM_002309 | Hs.2250 | 2.00E-94 | 1 | leukemia inhibitory factor (cholinergic diff |
| 40G10 | 2152 | 2560 | X04481 | Hs.2253 | 0 | 1 | complement component C2 /cds=(36,2294) /gb=X |
| 479A2 | 95 | 610 | NM_000073 | Hs.2259 | 0 | 2 | CD3G antigen, gamma polypeptide (TIT3 complex |
| 592G6 | 783 | 1163 | NM_002950 | Hs.2280 | 0 | 2 | ribophorin I (RPN1), mRNA /cds=(137,1960) /gb |
| 459G11 | 673 | 1316 | NM_004931 | Hs.2299 | 0 | 1 | CD8 antigen, beta polypeptide 1 (p37) (CD8B1), |
| 129B8 | 1159 | 1316 | X13444 | Hs.2299 | 1.00E-74 | 1 | CD8 beta-chain glycoprotein (CD8 beta.1) /cd |
| 467F12 | 2928 | 3239 | NM_000346 | Hs.2316 | 3.00E-85 | 1 | SRY (sex determining region Y)-box 9 (campomeli |
| 44A6 | 1506 | 1629 | U23028 | Hs.2437 | 7.00E-62 | 1 | eukaryotic initiation factor 2B-epsilon mRNA, partia |
| 127B8 | 1814 | 2405 | NM_003816 | Hs.2442 | 0 | 1 | a disintegrin and metalloproteinase domain 9 |
| 36G6 | 1361 | 2019 | D13645 | Hs.2471 | 0 | 2 | KIAA0020 gene, complete cds /cds=(418,1944) |
| 458D6 | 396 | 961 | NM_021966 | Hs.2484 | 0 | 1 | T-cell leukemia/lymphoma 1A (TCL1A), mRNA /c |
| 124G1 | 966 | 1473 | NM_005565 | Hs.2488 | 0 | 1 | lymphocyte cytosolic protein 2 (SH2 domain-con |
| 107A6 | 1962 | 2031 | U20158 | Hs.2488 | 2.00E-22 | 1 | 76 kDa tyrosine phosphoprotein SLP-76 mRNA, complete |
| 592E12 | 2175 | 2458 | NM_002741 | Hs.2499 | 1.00E-158 | 1 | protein kinase C-like 1 (PRKCL1), mRNA /cds=(8 |
| 106A11 | 1455 | 2219 | U34252 | Hs.2533 | 0 | 2 | gamma-aminobutyraldehyde dehydrogenase mRNA, compl |
| 40F8 | 2201 | 2694 | NM_003032 | Hs.2554 | 0 | 1 | sialyltransferase 1 (beta-galactoside alpha- |
| 460G6 | 565 | 2052 | NM_002094 | Hs.2707 | 0 | 2 | G1 to S phase transition 1 mRNA |
| 60G5 | 35 | 184 | X92518 | Hs.2726 | 7.00E-27 | 2 | HMG1-C protein /cds=UNKNOWN |
| 461F10 | 1034 | 1520 | NM_002145 | Hs.2733 | 0 | 2 | homeo box B2 (HOXB2), mRNA |
| 69G2 | 408 | 1369 | AK026515 | Hs.2795 | 0 | 4 | FLJ22862 fis, clone KAT01966, highly sim |
| 71D8 | 13 | 541 | NM_005566 | Hs.2795 | 0 | 1 | lactate dehydrogenase A (LDHA), mRNA /cds=(97 |
| 40H12 | 4119 | 4807 | NM_002310 | Hs.2798 | 0 | 1 | leukemia inhibitory factor receptor (LIFR) mR |
| 189C12 | 696 | 1287 | NM_006196 | Hs.2853 | 0 | 2 | poly(rC)-binding protein 1 (PCBP1), mRNA /cds |
| 111E8 | 1298 | 1938 | NM_003566 | Hs.2864 | 0 | 1 | early endosome antigen 1, 162kD (EEA1), mRNA / |
| 127F12 | 34 | 248 | NM_001033 | Hs.2934 | 1.00E-109 | 1 | ribonucleotide reductase M1 polypeptide (RRM |
| 74G6 | 11 | 241 | AK023088 | Hs.2953 | 1.00E-128 | 38 | FLJ13026 fis, clone NT2RP3000968, modera |
| 128D8 | 178 | 518 | NM_000117 | Hs.2985 | 1.00E-173 | 1 | emerin (Emery-Dreifuss muscular dystrophy) (|
| 169G7 | 2406 | 3112 | AL136593 | Hs.3059 | 0 | 1 | DKFZp761K102 (from clone DKFZp761K1 |
| 193A3 | 2405 | 3017 | NM_016451 | Hs.3059 | 0 | 5 | coatamer protein complex, subunit beta (COPB) |
| 53F12 | 486 | 1007 | L11066 | Hs.3069 | 0 | 3 | sequence /cds=UNKNOWN /gb=L11066 /gi=307322 /u |
| 71E8 | 1623 | 2131 | NM_004134 | Hs.3069 | 0 | 2 | heat shock 70kD protein 9B (mortalin-2) (HSPA9 |
| 458A5 | 2236 | 2874 | NM_014877 | Hs.3085 | 0 | 1 | KIAA0054 gene product; Helicase (KIAA0054), m |
| 69E8 | 1752 | 1916 | D31884 | Hs.3094 | 7.00E-68 | 1 | KIAA0063 gene, complete cds /cds=(279,887) / |
| 66B3 | 251 | 1590 | D32053 | Hs.3100 | 0 | 2 | for Lysyl tRNA Synthetase, complete cds / |
| 458E1 | 1645 | 1964 | NM_001666 | Hs.3109 | 1.00E-178 | 1 | Rho GTPase activating protein 4 (ARHGAP4), mRN |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|---------|-----------|----|---|
| 331D8 | 2882 | 3585 | U26710 | Hs.3144 | 0 | 1 | cbl-b mRNA, complete cds /cds=(322,3270) /gb=U26710 |
| 73D9 | 1 | 613 | AL031736 | Hs.3195 | 0 | 18 | DNA sequence clone 738P11 on chromosome 1q24.1-2 |
| 58B1 | 1 | 607 | NM_002995 | Hs.3195 | 0 | 17 | small inducible cytokine subfamily C, member |
| 98F11 | 145 | 588 | NM_003172 | Hs.3196 | 0 | 1 | surfeit 1 (SURF1), mRNA /cds=(14,916) /gb=NM_ |
| 124E9 | 1258 | 2414 | NM_007318 | Hs.3260 | 0 | 2 | presenilin 1 (Alzheimer disease 3) (PSEN1), tr |
| 64G7 | 1040 | 1569 | NM_002155 | Hs.3268 | 0 | 1 | heat shock 70kD protein 6 (HSP70B') (HSPA6), mR |
| 36D4 | 1116 | 1917 | X51757 | Hs.3268 | 0 | 4 | heat-shock protein HSP70B' gene /cds=(0,1931) /gb=X5 |
| 39H11 | 1 | 507 | BE895166 | Hs.3297 | 1.00E-152 | 4 | 601436095F1 cDNA, 5' end /clone=IMAGE:3921239 |
| 103G4 | 16 | 540 | NM_002954 | Hs.3297 | 0 | 4 | ribosomal protein S27a (RPS27A), mRNA /cds=(3 |
| 127H7 | 1391 | 1806 | AB037752 | Hs.3355 | 0 | 1 | mRNA for KIAA1331 protein, partial cds /cds=(0 |
| 107D3 | 1932 | 2517 | AK027064 | Hs.3382 | 0 | 1 | FLJ23411 fis, clone HEP20452, highly sim |
| 121B3 | 1270 | 3667 | NM_005134 | Hs.3382 | 0 | 4 | protein phosphatase 4, regulatory subunit 1 (|
| 58H1 | 104 | 573 | NM_001122 | Hs.3416 | 0 | 6 | adipose differentiation-related protein (AD |
| 75G1 | 104 | 1314 | X97324 | Hs.3416 | 0 | 16 | adipophilin /cds=(0,1313) /gb=X97324 / |
| 182A4 | 147 | 334 | NM_001867 | Hs.3462 | 1.00E-102 | 1 | cytochrome c oxidase subunit VIIc (COX7C), mRN |
| 134D7 | 36 | 270 | NM_001025 | Hs.3463 | 1.00E-127 | 3 | ribosomal protein S23 (RPS23), mRNA /cds=(13,4 |
| 192B10 | 129 | 1135 | AL357536 | Hs.3576 | 0 | 3 | mRNA full length insert cDNA clone EUROIMAGE 37 |
| 112G12 | 56 | 687 | NM_003001 | Hs.3577 | 0 | 1 | succinate dehydrogenase complex, subunit C, |
| 526H6 | 143 | 537 | BF666961 | Hs.3585 | 0 | 1 | 602121608F1 cDNA, 5' end /clone=IMAGE:4278768 |
| 599F10 | 2098 | 2351 | NM_004834 | Hs.3628 | 1.00E-118 | 2 | mitogen-activated protein kinase kinase kina |
| 594F1 | 239 | 1321 | NM_001551 | Hs.3631 | 0 | 4 | immunoglobulin (CD79A) binding protein 1 (IG |
| 463E7 | 911 | 1033 | AL359940 | Hs.3640 | 1.00E-63 | 1 | mRNA; cDNA DKFZp762P1915 (from clone DKFZp762P |
| 182A9 | 657 | 1179 | AL050268 | Hs.3642 | 0 | 2 | mRNA; cDNA DKFZp564B163 (from clone DKFZp564B1 |
| 38B4 | 257 | 568 | AB034205 | Hs.3688 | 1.00E-151 | 3 | for cisplatin resistance-associated ove |
| 185H6 | 769 | 995 | NM_006003 | Hs.3712 | 2.00E-88 | 1 | ubiquinol-cytochrome c reductase, Rieske iro |
| 587A1 | 716 | 1609 | NM_006007 | Hs.3776 | 0 | 2 | zinc finger protein 216 (ZNF216), mRNA /cds=(2 |
| 473B5 | 46 | 531 | NM_021633 | Hs.3826 | 0 | 1 | kelch-like protein C3IP1 (C3IP1), mRNA /cds=(|
| 194G5 | 2456 | 2984 | AB002366 | Hs.3852 | 0 | 1 | mRNA for KIAA0368 gene, partial cds /cds=(0,4327) /gb |
| 589B4 | 526 | 1337 | NM_000310 | Hs.3873 | 0 | 3 | palmitoyl-protein thioesterase 1 (ceroid-lip |
| 515A10 | 1618 | 2130 | NM_002267 | Hs.3886 | 0 | 1 | karyopherin alpha 3 (importin alpha 4) (KPNA3) |
| 186A8 | 1160 | 1632 | NM_002807 | Hs.3887 | 0 | 1 | proteasome (prosome, macropain) 26S subunit, |
| 102F7 | 4226 | 4531 | AB023163 | Hs.4014 | 1.00E-158 | 1 | for KIAA0946 protein, partial cds /cds=(0 |
| 50B8 | 1 | 166 | AL117595 | Hs.4055 | 3.00E-89 | 2 | cDNA DKFZp564C2063 (from clone DKFZp564 |
| 473A10 | 1064 | 1709 | NM_006582 | Hs.4069 | 0 | 1 | glucocorticoid modulatory element binding pr |
| 524A12 | 2863 | 3386 | AL136105 | Hs.4082 | 0 | 1 | DNA sequence from clone RP4-670F13 on chromosome 1q42 |
| 525E1 | 521 | 974 | BC002435 | Hs.4096 | 0 | 1 | clone IMAGE:3346451, mRNA, partial cds /cds= |
| 163G12 | 1130 | 1630 | X52882 | Hs.4112 | 0 | 6 | t-complex polypeptide 1 gene /cds=(21,1691) /gb=X528 |
| 176A7 | 515 | 892 | BC000687 | Hs.4147 | 0 | 1 | translocating chain-associating membrane p |
| 185B5 | 3480 | 3707 | AB023216 | Hs.4278 | 1.00E-86 | 1 | mRNA for KIAA0999 protein, partial cds /cds=(0 |
| 154E12 | 1731 | 2531 | AF079566 | Hs.4311 | 0 | 2 | ubiquitin-like protein activating enzyme (UB |
| 331C9 | 1595 | 1966 | AF067008 | Hs.4747 | 0 | 1 | dyskerin (DKC1) mRNA, complete cds /cds=(60,16 |
| 182C8 | 1676 | 1966 | NM_001363 | Hs.4747 | 1.00E-148 | 2 | dyskeratosis congenita 1, dyskerin (DKC1), mR |
| 178C4 | 1623 | 2162 | AL136610 | Hs.4750 | 0 | 3 | mRNA; cDNA DKFZp564K0822 (from clone DKFZp564K |
| 107F9 | 3857 | 4266 | AB032976 | Hs.4779 | 0 | 1 | for KIAA1150 protein, partial cds /cds=(0 |
| 191C11 | 1945 | 2618 | AF240468 | Hs.4788 | 0 | 3 | nicastrin mRNA, complete cds /cds=(142,2271) |
| 143G11 | 869 | 2076 | AK022974 | Hs.4859 | 0 | 2 | FLJ12912 fis, clone NT2RP2004476, highly |
| 127H11 | 977 | 1666 | NM_020307 | Hs.4859 | 0 | 1 | cyclin L ania-6a (LOC57018), mRNA /cds=(54,163 |
| 479A11 | 215 | 544 | AK001942 | Hs.4863 | 1.00E-173 | 1 | cDNA FLJ11080 fis, clone PLACE1005181 /cds=UN |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|---------|-----------|----|---|
| 73C5 | 2314 | 2851 | AF105366 | Hs.4876 | 0 | 1 | K-CI cotransporter KCC3a mRNA, alternatively |
| 525F9 | 1059 | 1764 | NM_006513 | Hs.4888 | 0 | 3 | seryl-tRNA synthetase (SARS), mRNA /cds=(75,1 |
| 114D8 | 931 | 1061 | Z24724 | Hs.4934 | 4.00E-52 | 1 | H.sapiens polyA site DNA /cds=UNKNOWN /gb=Z24724 /gi=50503 |
| 587C10 | 1104 | 1343 | NM_006787 | Hs.4943 | 3.00E-94 | 1 | hepatocellular carcinoma associated protein; |
| 174F12 | 1749 | 2291 | NM_018107 | Hs.4997 | 0 | 3 | hypothetical protein FLJ10482 (FLJ10482), mR |
| 514C11 | 899 | 1489 | AK021776 | Hs.5019 | 0 | 1 | cDNA FLJ11714 fis, clone HEMBA1005219, weakly |
| 126H9 | 25 | 397 | BE379724 | Hs.5027 | 1.00E-118 | 1 | 601159415T1 cDNA, 3' end /clone=IMAGE:3511107 |
| 599B5 | 801 | 970 | NM_017840 | Hs.5080 | 5.00E-73 | 1 | hypothetical protein FLJ20484 (FLJ20484), mR |
| 47E5 | 4 | 720 | AL034553 | Hs.5085 | 0 | 2 | DNA sequence from clone 914P20 on chromosome 20q13.13 |
| 122C11 | 492 | 860 | NM_003859 | Hs.5085 | 0 | 1 | dolichyl-phosphate mannosyltransferase pol |
| 116H6 | 1644 | 2902 | NM_014868 | Hs.5094 | 1.00E-102 | 2 | ring finger protein 10 (RNF10), mRNA /cds=(698, |
| 187G7 | 700 | 1268 | NM_004710 | Hs.5097 | 0 | 1 | synaptogyrin 2 (SYNGR2), mRNA /cds=(29,703) / |
| 174G3 | 240 | 500 | NM_003746 | Hs.5120 | 1.00E-144 | 4 | dynein, cytoplasmic, light polypeptide (PIN) |
| 145B6 | 199 | 695 | BE539096 | Hs.5122 | 1.00E-165 | 2 | 601061641F1 cDNA, 5' end /clone=IMAGE:3447850 |
| 486C1 | 1 | 529 | BG028906 | Hs.5122 | 0 | 2 | 602293015F1 cDNA, 5' end /clone=IMAGE:4387778 |
| 69F6 | 62 | 455 | BF307213 | Hs.5174 | 0 | 1 | 601891365F1 cDNA, 5' end /clone=IMAGE:4136752 |
| 583F4 | 82 | 477 | NM_001021 | Hs.5174 | 0 | 1 | ribosomal protein S17 (RPS17), mRNA /cds=(25,4 |
| 74C4 | 1955 | 2373 | AK025367 | Hs.5181 | 1.00E-179 | 1 | FLJ21714 fis, clone COL10256, highly sim |
| 73E12 | 702 | 987 | AL109840 | Hs.5184 | 1.00E-161 | 1 | DNA sequence from clone RP4-543J19 on chromosome 20 C |
| 180G4 | 26 | 639 | NM_002212 | Hs.5215 | 0 | 2 | integrin beta 4 binding protein (ITGB4BP), mRN |
| 98F1 | 17 | 636 | NM_014165 | Hs.5232 | 0 | 5 | HSPC125 protein (HSPC125), mRNA /cds=(79,606) |
| 525A8 | 479 | 992 | NM_006698 | Hs.5300 | 0 | 1 | bladder cancer associated protein (BLCAP), mR |
| 99C1 | 19 | 507 | NM_003333 | Hs.5308 | 0 | 3 | ubiquitin A-52 residue ribosomal protein fusi |
| 172D11 | 714 | 1805 | NM_005721 | Hs.5321 | 0 | 3 | ARP3 (actin-related protein 3, yeast) homolog |
| 591F6 | 475 | 970 | NM_015702 | Hs.5324 | 0 | 1 | hypothetical protein (CL25022), mRNA /cds=(1 |
| 68H8 | 724 | 1190 | NM_014106 | Hs.5327 | 0 | 2 | PRO1914 protein (PRO1914), mRNA /cds=(1222,14 |
| 194D12 | 2128 | 2499 | AB018305 | Hs.5378 | 0 | 1 | mRNA for KIAA0762 protein, partial cds /cds=(0 |
| 501G11 | 823 | 1322 | NM_020122 | Hs.5392 | 0 | 3 | potassium channel modulatory factor (DKFZP434 |
| 74B4 | 502 | 1257 | AF008442 | Hs.5409 | 0 | 7 | RNA polymerase I subunit hRPA39 mRNA, complete |
| 134H7 | 543 | 916 | NM_004875 | Hs.5409 | 0 | 1 | RNA polymerase I subunit (RPA40), mRNA /cds=(2 |
| 168A3 | 1909 | 2379 | AF090891 | Hs.5437 | 0 | 1 | clone HQ0105 PRO0105 mRNA, complete cds /cds=(|
| 145C10 | 2375 | 2564 | AF016270 | Hs.5464 | 1.00E-104 | 2 | thyroid hormone receptor coactivating protein |
| 587H7 | 1857 | 2563 | NM_006696 | Hs.5464 | 0 | 4 | thyroid hormone receptor coactivating protein |
| 183D10 | 1199 | 1347 | NM_006495 | Hs.5509 | 9.00E-40 | 1 | ecotropic viral integration site 2B (EVI2B), m |
| 181D7 | 1385 | 1752 | AK002173 | Hs.5518 | 0 | 1 | cDNA FLJ11311 fis, clone PLACE1010102 /cds=UNK |
| 173B1 | 1 | 642 | NM_003315 | Hs.5542 | 0 | 2 | tetratricopeptide repeat domain 2 (TTC2), mRN |
| 120F8 | 1782 | 2430 | AF157323 | Hs.5548 | 0 | 2 | p45SKP2-like protein mRNA, complete cds /cds= |
| 464H2 | 46 | 357 | NM_000998 | Hs.5566 | 1.00E-163 | 2 | ribosomal protein L37a (RPL37A), mRNA /cds=(1 |
| 75F5 | 1252 | 2194 | AK027192 | Hs.5615 | 0 | 9 | FLJ23539 fis, clone LNG08101, highly sim |
| 56E8 | 27 | 205 | A1570531 | Hs.5637 | 2.00E-95 | 1 | tm77g04.x1 cDNA, 3' end /clone=IMAGE:2164182 |
| 524G2 | 2 | 926 | NM_006098 | Hs.5662 | 0 | 9 | guanine nucleotide binding protein (G protein |
| 39F6 | 2311 | 2902 | AB014579 | Hs.5734 | 0 | 1 | for KIAA0679 protein, partial cds /cds=(0 |
| 587G2 | 2883 | 4606 | NM_012215 | Hs.5734 | 0 | 11 | meningioma expressed antigen 5 (hyaluronidase |
| 469E5 | 5041 | 5393 | NM_014864 | Hs.5737 | 3.00E-75 | 2 | KIAA0475 gene product (KIAA0475), mRNA /cds=(|
| 120H3 | 1022 | 1553 | NM_016230 | Hs.5741 | 0 | 1 | flavohepatoxin b5+b5R (LOC51167), mRNA /cd |
| 63H8 | 1049 | 1507 | AK025729 | Hs.5798 | 0 | 1 | FLJ22076 fis, clone HEP12479, highly sim |
| 590D9 | 1015 | 1470 | NM_015946 | Hs.5798 | 0 | 1 | pelota (Drosophila) homolog (PELO), mRNA /cds |
| 102E3 | 665 | 1027 | AK000474 | Hs.5811 | 0 | 1 | FLJ20467 fis, clone KAT06638 /cds=(360,77 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|---------|-----------|----|--|
| 187E5 | 665 | 1028 | NM_017835 | Hs.5811 | 0 | 1 | chromosome 21 open reading frame 59 (C21ORF59), |
| 39F9 | 1402 | 1728 | AK025773 | Hs.5822 | 0 | 3 | FLJ22120 fis, clone HEP18874 /cds=UNKNOWN |
| 39E12 | 1064 | 1843 | AF208844 | Hs.5862 | 0 | 1 | BM-002 mRNA, complete cds /cds=(39,296) /gb=A |
| 173H9 | 906 | 1684 | NM_016090 | Hs.5887 | 0 | 2 | RNA binding motif protein 7 (LOC51120), mRNA / |
| 120E8 | 1702 | 2055 | NM_012179 | Hs.5912 | 1.00E-146 | 1 | F-box only protein 7 (FBXO7), mRNA /cds=(205,17 |
| 195D1 | 1309 | 2656 | AK025620 | Hs.5985 | 0 | 8 | cDNA: FLJ21967 fis, clone HEP05652, highly sim |
| 116A6 | 1451 | 2073 | AK024941 | Hs.6019 | 0 | 1 | cDNA: FLJ21288 fis, clone COL01927 /cds=UNKNOWN |
| 113F9 | 1232 | 1598 | NM_002896 | Hs.6106 | 1.00E-126 | 1 | RNA binding motif protein 4 (RBM4), mRNA /cds=(|
| 520H1 | 563 | 1007 | NM_018285 | Hs.6118 | 0 | 2 | hypothetical protein FLJ10968 (FLJ10968), mR |
| 180H12 | 5224 | 5568 | AF315591 | Hs.6151 | 1.00E-135 | 1 | Pumilio 2 (PUMH2) mRNA, complete cds /cds=(23,3 |
| 185A7 | 612 | 1558 | NM_016001 | Hs.6153 | 0 | 6 | CGI-48 protein (LOC51096), mRNA /cds=(107,167 |
| 595G2 | 3207 | 4752 | Z97056 | Hs.6179 | 0 | 10 | DNA seq from clone RP3-434P1 on chromosome 22 |
| 592B11 | 234 | 4611 | AI745230 | Hs.6187 | 1.00E-130 | 6 | wg10e05.x1 cDNA, 3' end /clone=IMAGE:2364704 |
| 590F2 | 994 | 1625 | NM_004517 | Hs.6196 | 0 | 3 | integrin-linked kinase (ILK), mRNA /cds=(156, |
| 188A3 | 1550 | 2929 | M61906 | Hs.6241 | 0 | 3 | P13-kinase associated p85 mRNA sequence |
| 103C12 | 502 | 1129 | AF246238 | Hs.6289 | 0 | 1 | HT027 mRNA, complete cds /cds=(260,784) /gb=A |
| 100C2 | 804 | 1111 | AK024539 | Hs.6289 | 1.00E-122 | 1 | FLJ20886 fis, clone ADKA03257 /cds=(359, |
| 480A11 | 1149 | 1242 | AB032977 | Hs.6298 | 1.00E-46 | 1 | mRNA for KIAA1151 protein, partial cds /cds=(0 |
| 473C8 | 3944 | 4149 | NM_014859 | Hs.6336 | 1.00E-106 | 1 | KIAA0672 gene product (KIAA0672), mRNA /cds=(|
| 125A10 | 1293 | 1766 | NM_006791 | Hs.6353 | 0 | 1 | MORF-related gene 15 (MRG15), mRNA /cds=(131,1 |
| 182F5 | 143 | 2118 | NM_018471 | Hs.6375 | 0 | 3 | uncharacterized hypothalamus protein HT010 |
| 587E8 | 398 | 2287 | NM_016289 | Hs.6406 | 0 | 7 | MO25 protein (LOC51719), mRNA /cds=(53,1078) |
| 135C3 | 2519 | 3084 | AF130110 | Hs.6456 | 0 | 2 | clone FLB6303 PRO1633 mRNA, complete cds /cds= |
| 178B5 | 1744 | 2425 | AL117352 | Hs.6523 | 0 | 2 | DNA seq from clone RP5-876B10 on chromosome |
| 522F10 | 2392 | 2591 | NM_001183 | Hs.6551 | 1.00E-110 | 2 | 1q42 |
| 595C4 | 1676 | 2197 | NM_021008 | Hs.6574 | 0 | 4 | ATPase, H ⁺ transporting, lysosomal (vacuolar |
| 481F3 | 745 | 904 | AL117565 | Hs.6607 | 9.00E-82 | 1 | suppressin (nuclear deformed epidermal autor |
| 124A3 | 1046 | 1575 | NM_017792 | Hs.6631 | 0 | 1 | mRNA; cDNA DKFZp566F164 (from clone |
| 177F11 | 1966 | 2281 | AB046844 | Hs.6639 | 1.00E-152 | 1 | DKFZp566F1 |
| 521G7 | 4600 | 5210 | NM_014856 | Hs.6684 | 0 | 2 | hypothetical protein FLJ20373 (FLJ20373), mR |
| 54C6 | 265 | 756 | AB037801 | Hs.6685 | 0 | 1 | for KIAA1624 protein, partial cds /cds=(0 |
| 75F7 | 95 | 3507 | AB014560 | Hs.6727 | 0 | 4 | for KIAA0660 protein, complete cds /cds=(|
| 477H12 | 2 | 457 | BF976590 | Hs.6749 | 0 | 1 | 602244267F1 cDNA, 5' end /clone=IMAGE:4335353 |
| 60A1 | 1028 | 1307 | AB026908 | Hs.6790 | 1.00E-155 | 1 | for microvascular endothelial differenti |
| 100G9 | 341 | 454 | BE875609 | Hs.6820 | 2.00E-58 | 1 | 601487048F1 cDNA, 5' end /clone=IMAGE:3889762 |
| 184F7 | 1259 | 1633 | AF056717 | Hs.6856 | 0 | 5 | ash2l2 (ASH2L2) mRNA, complete cds /cds=(295,1 |
| 195E7 | 1250 | 1711 | NM_004674 | Hs.6856 | 0 | 3 | ash2 (absent, small, or homeotic, Drosophila, |
| 135F11 | 328 | 600 | NM_020188 | Hs.6879 | 1.00E-151 | 1 | DC13 protein (DC13), mRNA /cds=(175,414) /gb= |
| 172G2 | 1477 | 1782 | NM_015530 | Hs.6880 | 1.00E-169 | 1 | DKFZP434D156 protein (DKFZP434D156), mRNA /c |
| 483G5 | 3712 | 3947 | AL031681 | Hs.6891 | 3.00E-72 | 1 | DNA sequence from clone 862K6 on chromosome |
| 184B1 | 1 | 622 | AF006086 | Hs.6895 | 0 | 3 | 20q12-13.1 |
| 599C12 | 1 | 622 | NM_005719 | Hs.6895 | 0 | 24 | Arp2/3 protein complex subunit p21-Arc (ARC21 |
| 43A1 | 2111 | 2312 | AF037204 | Hs.6900 | 9.00E-78 | 1 | actin related protein 2/3 complex, subunit 3 (|
| 105F6 | 638 | 1209 | AK026850 | Hs.6906 | 0 | 1 | RING zinc finger protein (RZF) mRNA, complete c |
| 178G10 | 5939 | 6469 | AJ238403 | Hs.6947 | 0 | 1 | FLJ23197 fis, clone REC00917 /cds=UNKNOWN |
| 72A2 | 178 | 2992 | AF001542 | Hs.6975 | 0 | 9 | mRNA for huntingtin interacting protein 1 /cd |
| 37F2 | 1757 | 2397 | AK022568 | Hs.7010 | 0 | 1 | AF001542 /clone=alpha_est218/52C1 /gb= |
| | | | | | | | FLJ12506 fis, clone NT2RM2001700, weakly |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|---------|-----------|---|--|
| 598D3 | 1153 | 1299 | NM_004637 | Hs.7016 | 8.00E-56 | 1 | RAB7, member RAS oncogene family (RAB7), mRNA |
| 524C11 | 5542 | 5678 | AB033034 | Hs.7041 | 3.00E-72 | 1 | mRNA for KIAA1208 protein, partial cds /cds=(2 |
| 109E10 | 452 | 1093 | AF104921 | Hs.7043 | 0 | 1 | succinyl-CoA synthetase alpha subunit (SUCLA1 |
| 595F7 | 449 | 1150 | NM_003849 | Hs.7043 | 0 | 2 | succinate-CoA ligase, GDP-forming, alpha sub |
| 104H2 | 644 | 992 | NM_020194 | Hs.7045 | 1.00E-156 | 1 | GL004 protein (GL004), mRNA /cds=(72,728) /gb |
| 155C1 | 3322 | 3779 | AK024478 | Hs.7049 | 0 | 2 | FLJ00071 protein, partial cds /cds=(3 |
| 473B1 | 3029 | 3439 | AB051492 | Hs.7076 | 1.00E-152 | 1 | mRNA for KIAA1705 protein, partial cds /cds=(1 |
| 125E3 | 3612 | 3948 | AL390127 | Hs.7104 | 0 | 1 | mRNA; cDNA DKFZp761P06121 (from clone DKFZp761 |
| 499B11 | 1451 | 1852 | NM_021188 | Hs.7137 | 0 | 2 | clones 23667 and 23775 zinc finger protein (LOC |
| 52B12 | 1850 | 2178 | U90919 | Hs.7137 | 1.00E-174 | 1 | clones 23667 and 23775 zinc finger protein mRNA, compl |
| 486A11 | 855 | 1186 | NM_003904 | Hs.7165 | 1.00E-132 | 1 | zinc finger protein 259 (ZNF259), mRNA /cds=(2 |
| 460B6 | 2514 | 3182 | NM_021931 | Hs.7174 | 0 | 1 | hypothetical protein FLJ22759 (FLJ22759), mR |
| 592H8 | 3999 | 4524 | AB051544 | Hs.7187 | 0 | 2 | mRNA for KIAA1757 protein, partial cds /cds=(3 |
| 180A10 | 102 | 468 | AL117502 | Hs.7200 | 1.00E-141 | 3 | mRNA; cDNA DKFZp434D0935 (from clone DKFZp434 |
| 127A12 | 1503 | 2688 | AL035661 | Hs.7218 | 0 | 2 | DNA sequence from clone RP4-568C11 on chromosome 20p1 |
| 592G9 | 12 | 263 | NM_015953 | Hs.7236 | 1.00E-138 | 2 | CGI-25 protein (LOC51070), mRNA /cds=(44,949) |
| 127E3 | 2624 | 4554 | AB028980 | Hs.7243 | 0 | 3 | mRNA for KIAA1057 protein, partial cds /cds=(0 |
| 135F2 | 5029 | 5175 | AB033050 | Hs.7252 | 3.00E-78 | 1 | mRNA for KIAA1224 protein, partial cds /cds=(0 |
| 57G1 | 2299 | 2723 | NM_014319 | Hs.7256 | 0 | 1 | integral inner nuclear membrane protein (MAN1 |
| 122D11 | 2920 | 3123 | AB014558 | Hs.7278 | 5.00E-74 | 1 | mRNA for KIAA0658 protein, partial cds /cds=(0 |
| 471H6 | 1 | 449 | AV702692 | Hs.7312 | 0 | 1 | AV702692 cDNA, 5' end /clone=ADBBQC12 /clone_ |
| 104G12 | 4314 | 4797 | AF084555 | Hs.7351 | 0 | 2 | okadaic acid-inducible and cAMP-regulated ph |
| 590G7 | 771 | 1259 | NM_005662 | Hs.7381 | 0 | 5 | voltage-dependent anion channel 3 (VDAC3), mR |
| 159H2 | 355 | 1252 | AL137423 | Hs.7392 | 0 | 3 | mRNA; cDNA DKFZp761E0323 (from clone DKFZp761E |
| 161F3 | 1708 | 2371 | NM_024045 | Hs.7392 | 0 | 1 | hypothetical protein MGC3199 (MGC3199), mRNA |
| 195E1 | 1107 | 1362 | NM_022736 | Hs.7503 | 1.00E-129 | 1 | hypothetical protein FLJ14153 (FLJ14153), mR |
| 137F5 | 59 | 666 | NM_018491 | Hs.7535 | 0 | 2 | COBW-like protein (LOC55871), mRNA /cds=(64,9 |
| 597E1 | 2302 | 2893 | AF126028 | Hs.7540 | 0 | 2 | unknown mRNA /cds=(0,1261) /gb=AF126028 /gi= |
| 473B6 | 3006 | 3302 | AK025615 | Hs.7567 | 1.00E-158 | 1 | cDNA: FLJ21962 fis, clone HEP05564 /cds=UNKNOWN |
| 519H1 | 232 | 720 | BG112505 | Hs.7589 | 0 | 2 | 602282107F1 cDNA, 5' end /clone=IMAGE:4369729 |
| 73A9 | 106 | 3912 | M20681 | Hs.7594 | 0 | 8 | glucose transporter-like protein-III (GLUT3), compl |
| 51D3 | 106 | 3200 | NM_006931 | Hs.7594 | 0 | 2 | solute carrier family 2 (facilitated glucose t |
| 596E8 | 1512 | 1748 | M94046 | Hs.7647 | 1.00E-129 | 2 | zinc finger protein (MAZ) mRNA /cds=UNKNOWN /gb=M9404 |
| 472A8 | 1575 | 1983 | NM_004576 | Hs.7688 | 0 | 1 | protein phosphatase 2 (formerly 2A), regulator |
| 191A10 | 386 | 889 | NM_007278 | Hs.7719 | 0 | 3 | GABA(A) receptor-associated protein (GABARAP |
| 459C4 | 5636 | 5897 | AB002323 | Hs.7720 | 2.00E-87 | 1 | mRNA for KIAA0325 gene, partial cds /cds=(0,6265) /gb |
| 99A12 | 606 | 1253 | NM_018453 | Hs.7731 | 0 | 1 | uncharacterized bone marrow protein BM036 (BM |
| 72G8 | 5806 | 6409 | AB007938 | Hs.7764 | 0 | 5 | for KIAA0469 protein, complete cds /cds=(|
| 45G2 | 6168 | 6404 | NM_014851 | Hs.7764 | 1.00E-132 | 1 | KIAA0469 gene product (KIAA0469), mRNA /cds=(|
| 172A4 | 371 | 588 | NM_007273 | Hs.7771 | 1.00E-107 | 1 | B-cell associated protein (REA), mRNA /cds=(9 |
| 177B8 | 2055 | 2431 | AK023166 | Hs.7797 | 0 | 1 | FLJ13104 fis, clone NT2RP3002343 /cds=(28 |
| 99B6 | 865 | 1244 | NM_012461 | Hs.7797 | 0 | 1 | TERF1 (TRF1)-interacting nuclear factor 2 (T |
| 160G8 | 727 | 860 | U94855 | Hs.7811 | 5.00E-66 | 1 | translation initiation factor 3 47 kDa subunit |
| 54G6 | 1 | 1007 | AK001319 | Hs.7837 | 1.00E-148 | 3 | FLJ10457 fis, clone NT2RP1001424 /cds=UN |
| 594A7 | 1295 | 1793 | NM_013446 | Hs.7838 | 0 | 4 | makorin, ring finger protein, 1 (MKRN1), mRNA |
| 188A12 | 1 | 2013 | NM_017761 | Hs.7862 | 0 | 3 | hypothetical protein FLJ20312 (FLJ20312), mR |
| 594A2 | 3060 | 3588 | AK023813 | Hs.7871 | 0 | 2 | cDNA FLJ13751 fis, clone PLACE3000339, weakly |
| 124C12 | 472 | 1251 | NM_001550 | Hs.7879 | 0 | 1 | interferon-related developmental regulator |
| 147A8 | 1381 | 1711 | Y10313 | Hs.7879 | 1.00E-134 | 1 | for PC4 protein (IFRD1 gene) /cds=(219,158 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|---------|-----------|----|---|
| 74H3 | 4430 | 4978 | AF302505 | Hs.7886 | 0 | 2 | pellino 1 (PELI1) mRNA, complete cds /cds=(4038 |
| 71G3 | 473 | 1112 | NM_016224 | Hs.7905 | 0 | 2 | SH3 and PX domain-containing protein SH3PX1 (S |
| 52C7 | 1637 | 2231 | AB029551 | Hs.7910 | 0 | 1 | YEAFF1 mRNA for YY1 and E4TF1 associated factor |
| 177H5 | 5411 | 6045 | AB002321 | Hs.7911 | 0 | 1 | KIAA0323 gene, partial cds /cds=(0,2175) /gb |
| 114C8 | 1678 | 3078 | NM_017657 | Hs.7942 | 1.00E-149 | 2 | hypothetical protein FLJ20080 (FLJ20080), mR |
| 169D8 | 1453 | 2158 | AK001437 | Hs.7943 | 0 | 1 | FLJ10575 fis, clone NT2RP2003295, highly |
| 599G8 | 618 | 1204 | NM_003796 | Hs.7943 | 0 | 1 | RPB5-mediating protein (RMP), mRNA /cds=(465, |
| 127E11 | 107 | 796 | NM_016099 | Hs.7953 | 0 | 3 | HSPC041 protein (LOC51125), mRNA /cds=(141,45 |
| 98D6 | 4769 | 6506 | NM_001111 | Hs.7957 | 0 | 20 | adenosine deaminase, RNA-specific (ADAR), tr |
| 37H10 | 2479 | 6594 | X79448 | Hs.7957 | 0 | 8 | IFI-4 mRNA for type I protein /cds=(1165,3960) /g |
| 178G4 | 4209 | 5132 | AB028981 | Hs.8021 | 0 | 4 | mRNA for KIAA1058 protein, partial cds /cds=(0 |
| 118E9 | 630 | 1688 | NM_006083 | Hs.8024 | 0 | 2 | IK cytokine, down-regulator of HLA II (IK), mRN |
| 171A8 | 1658 | 1973 | AK002026 | Hs.8033 | 1.00E-151 | 1 | FLJ11164 fis, clone PLACE1007226, weakly |
| 103G5 | 1504 | 1977 | NM_018346 | Hs.8033 | 0 | 1 | hypothetical protein FLJ11164 (FLJ11164), mR |
| 179G7 | 2860 | 3032 | AK022497 | Hs.8068 | 6.00E-46 | 1 | FLJ12435 fis, clone NT2RM1000059 /cds=(88 |
| 594A11 | 2327 | 2658 | NM_018210 | Hs.8083 | 1.00E-167 | 1 | hypothetical protein FLJ10769 (FLJ10769), mR |
| 103B5 | 1968 | 2448 | AF267856 | Hs.8084 | 0 | 1 | HT033 mRNA, complete cds /cds=(203,931) /gb=A |
| 98E4 | 1367 | 1808 | AF113008 | Hs.8102 | 0 | 7 | clone FLB0708 mRNA sequence /cds=UNKNOWN |
| 191H10 | 4581 | 5819 | NM_018695 | Hs.8117 | 0 | 3 | /gb= |
| 99F1 | 550 | 2672 | AB014550 | Hs.8118 | 0 | 4 | erbB2-interacting protein ERBIN (LOC55914), |
| 165H11 | 488 | 663 | NM_024408 | Hs.8121 | 3.00E-93 | 1 | mRNA for KIAA0650 protein, partial cds /cds=(0 |
| 515C7 | 2188 | 2514 | AL050371 | Hs.8128 | 1.00E-114 | 1 | Notch (Drosophila) homolog 2 (NOTCH2), mRNA / |
| 166A12 | 234 | 1196 | AF131856 | Hs.8148 | 1.00E-155 | 2 | mRNA; cDNA DKFZp566G2246 (from clone |
| 520H8 | 512 | 712 | NM_016275 | Hs.8148 | 1.00E-110 | 1 | DKFZp566G |
| 592D4 | 1 | 735 | NM_014886 | Hs.8170 | 1.00E-152 | 3 | clone 24856 mRNA sequence, complete cds /cds=(|
| 105F12 | 349 | 760 | AK001665 | Hs.8173 | 0 | 1 | selenoprotein T (LOC51714), mRNA /cds=(138,62 |
| 75A7 | 737 | 1458 | AF000652 | Hs.8180 | 0 | 1 | hypothetical protein (YR-29), mRNA /cds=(82,8 |
| 64H5 | 105 | 618 | NM_005625 | Hs.8180 | 0 | 3 | FLJ10803 fis, clone NT2RP4000833 /cds=(1 |
| 61G9 | 3147 | 3660 | AB018339 | Hs.8182 | 0 | 2 | syntenin (synt) mRNA, complete cds /cds=(148,1 |
| 39G2 | 255 | 1675 | AF042284 | Hs.8185 | 0 | 4 | syndecan binding protein (syntenin) (SDCBP), |
| 192G5 | 1054 | 1580 | NM_021199 | Hs.8185 | 0 | 8 | for KIAA0796 protein, partial cds /cds=(0 |
| 109D3 | 1463 | 2503 | AF269150 | Hs.8203 | 0 | 2 | unknown mRNA /cds=(76,1428) /gb=AF042284 /gi |
| 115H4 | 1251 | 3187 | NM_020123 | Hs.8203 | 0 | 12 | CGI-44 protein; sulfide dehydrogenase like (y |
| 113F12 | 2349 | 3576 | AL355476 | Hs.8217 | 4.00E-35 | 2 | transmembrane protein TM9SF3 (TM9SF3) mRNA, c |
| 125D5 | 582 | 1050 | NM_005006 | Hs.8248 | 0 | 1 | endomembrane protein emp70 precursor isolog (|
| 460D3 | 4851 | 5043 | AF035947 | Hs.8257 | 7.00E-76 | 1 | DNA sequence from clone RP11-517O1 on |
| 111E7 | 729 | 3182 | NM_013995 | Hs.8262 | 0 | 2 | chromosome X Co |
| 590F10 | 3012 | 4133 | AK022790 | Hs.8309 | 0 | 6 | NADH dehydrogenase (ubiquinone) Fe-S protein |
| 109B1 | 138 | 476 | AW973507 | Hs.8360 | 1.00E-161 | 1 | cytokine-inducible inhibitor of signalling t |
| 61A3 | 1137 | 1649 | AB033017 | Hs.8594 | 0 | 1 | lysosomal-associated membrane protein 2 (LAM |
| 523E12 | 905 | 2998 | NM_007271 | Hs.8724 | 0 | 4 | cDNA FLJ12728 fis, clone NT2RP2000040, highly |
| 590G2 | 3618 | 3932 | NM_018031 | Hs.8737 | 1.00E-166 | 3 | EST385607 /gb=AW973507 /gi=8164686 /ug= |
| 464C3 | 2299 | 2494 | NM_018255 | Hs.8739 | 1.00E-107 | 1 | for KIAA1191 protein, partial cds /cds=(0 |
| 128H8 | 1580 | 1711 | NM_018450 | Hs.8740 | 2.00E-64 | 1 | serine threonine protein kinase (NDR), mRNA / |
| 179D3 | 921 | 1457 | AF083255 | Hs.8765 | 0 | 1 | WD repeat domain 6 (WDR6), mRNA /cds=(39,3404) |
| 195H11 | 1247 | 1481 | NM_007269 | Hs.8813 | 1.00E-100 | 1 | hypothetical protein FLJ10879 (FLJ10879), mR |
| 460F1 | 68 | 308 | AA454036 | Hs.8832 | 1.00E-105 | 1 | uncharacterized bone marrow protein BM029 (BM |
| 110E10 | 3672 | 5371 | AB032252 | Hs.8858 | 0 | 3 | RNA helicase-related protein complete c |
| 113D1 | 4814 | 5890 | NM_013448 | Hs.8858 | 0 | 2 | syntaxin binding protein 3 (STXBP3), mRNA /cds |
| 120H7 | 373 | 633 | NM_017748 | Hs.8928 | 1.00E-143 | 1 | zx48b04.r1 cDNA, 5' end /clone=IMAGE:795439 / |
| 470F10 | 1670 | 2260 | NM_003917 | Hs.8991 | 0 | 2 | BAZ1A mRNA for bromodomain adjacent to zinc fi |
| 72H11 | 1785 | 2418 | M11717 | Hs.8997 | 1.00E-147 | 23 | bromodomain adjacent to zinc finger domain, 1A |
| | | | | | | | hypothetical protein FLJ20291 (FLJ20291), mR |
| | | | | | | | adaptor-related protein complex 1, gamma 2 su |
| | | | | | | | heat shock protein (hsp 70) gene, complete cds |
| | | | | | | | /cds=(2 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|---|
| 49H4 | 1769 | 2243 | NM_005345 | Hs.8997 | 1.00E-145 | 12 | heat shock 70kD protein 1A (HSPA1A), mRNA /cds= |
| 519E7 | 270 | 729 | NM_003574 | Hs.9006 | 0 | 1 | VAMP (vesicle-associated membrane protein)-a |
| 142E2 | 1265 | 1518 | AK022215 | Hs.9043 | 1.00E-107 | 1 | FLJ12153 fis, clone MAMMA1000458 /cds=UNK |
| 108B9 | 1160 | 1823 | AJ002030 | Hs.9071 | 0 | 1 | for putative progesterone binding protein |
| 47C7 | 452 | 795 | AB011420 | Hs.9075 | 0 | 1 | for DRAK1, complete cds /cds=(117,1361) / |
| 590A4 | 791 | 1377 | NM_004760 | Hs.9075 | 0 | 4 | serine/threonine kinase 17a (apoptosis-induc |
| 168D11 | 1000 | 1641 | NM_017426 | Hs.9082 | 0 | 1 | nucleoporin p54 (NUP54), mRNA /cds=(25,1542) |
| 63H9 | 799 | 1163 | Y17829 | Hs.9192 | 0 | 1 | for Homer-related protein Syn47 /cds=(75, |
| 167B11 | 1466 | 1863 | NM_006251 | Hs.9247 | 0 | 1 | protein kinase, AMP-activated, alpha 1 cataly |
| 196D5 | 1021 | 1492 | AK024327 | Hs.9343 | 0 | 1 | cDNA FLJ14265 fis, clone PLACE1002256 /cds=UNK |
| 192F3 | 245 | 790 | NM_017983 | Hs.9398 | 0 | 1 | hypothetical protein FLJ10055 (FLJ10055), mR |
| 121C3 | 3381 | 3567 | AF217190 | Hs.9414 | 3.00E-90 | 1 | MLEL1 protein (MLEL1) mRNA, complete cds /cds= |
| 196B6 | 959 | 1551 | NM_003601 | Hs.9456 | 0 | 1 | SWI/SNF related, matrix associated, actin dep |
| 331B5 | 2624 | 2950 | AF027302 | Hs.9573 | 1.00E-179 | 1 | TNF-alpha stimulated ABC protein (ABC50) mRNA |
| 592E11 | 1 | 479 | NM_002520 | Hs.9614 | 1.00E-139 | 7 | nucleophosmin (nucleolar phosphoprotein B23 |
| 515D6 | 1739 | 2091 | AB037796 | Hs.9663 | 1.00E-160 | 1 | mRNA for KIAA1375 protein, partial cds /cds=(0 |
| 124A5 | 1387 | 1762 | NM_012068 | Hs.9754 | 0 | 2 | activating transcription factor 5 (ATF5), mRN |
| 122A7 | 1484 | 1928 | AB028963 | Hs.9846 | 1.00E-154 | 1 | mRNA for KIAA1040 protein, partial cds /cds=(0 |
| 591E2 | 1626 | 2194 | AF123073 | Hs.9851 | 0 | 5 | C/EBP-induced protein mRNA, complete cds /cds |
| 111G2 | 4208 | 5361 | AB033076 | Hs.9873 | 0 | 2 | mRNA for KIAA1250 protein, partial cds /cds=(0 |
| 469D5 | 932 | 3551 | AK022758 | Hs.9908 | 1.00E-178 | 6 | cDNA FLJ12696 fis, clone NT2RP1000513, highly |
| 590D5 | 172 | 742 | NM_001425 | Hs.9999 | 2.00E-94 | 2 | epithelial membrane protein 3 (EMP3), mRNA /c |
| 112E7 | 1065 | 1753 | NM_001814 | Hs.10029 | 0 | 1 | cathepsin C (CTSC), mRNA /cds=(33,1424) /gb=N |
| 106C7 | 1066 | 1641 | X87212 | Hs.10029 | 0 | 1 | cathepsin C /cds=(33,1424) /gb=X87212 / |
| 127B1 | 1003 | 1429 | NM_014959 | Hs.10031 | 0 | 1 | KIAA0955 protein (KIAA0955), mRNA /cds=(313,1 |
| 462E5 | 332 | 487 | AW293461 | Hs.10041 | 3.00E-46 | 1 | UI-H-BI2-ahm-e-02-0-UI.s1 cDNA, 3' end /clon |
| 190E3 | 101 | 356 | NM_016551 | Hs.10071 | 6.00E-98 | 1 | seven transmembrane protein TM7SF3 (TM7SF3), |
| 61B6 | 2571 | 2764 | AL163249 | Hs.10175 | 7.00E-94 | 1 | chromosome 21 segment HS21C049 /cds=(128,2599 |
| 110F6 | 5310 | 5808 | D87432 | Hs.10315 | 0 | 1 | KIAA0245 gene, complete cds /cds=(261,1808) |
| 196E10 | 5312 | 5753 | NM_003983 | Hs.10315 | 0 | 1 | solute carrier family 7 (cationic amino acid t |
| 49D8 | 315 | 2207 | AK024597 | Hs.10362 | 0 | 3 | cDNA: FLJ20944 fis, clone ADSE01780 /cds=UNKNO |
| 129C7 | 1000 | 1364 | AB018249 | Hs.10458 | 0 | 1 | CC chemokine LEC, complete cds /cds=(1 |
| 62F11 | 1239 | 2034 | AL031685 | Hs.10590 | 0 | 2 | DNA sequence from clone RP5-963K23 on |
| 460D5 | 86 | 815 | AL357374 | Hs.10600 | 0 | 4 | chromosome 20q1 |
| 179C12 | 3765 | 4300 | AK000005 | Hs.10647 | 0 | 2 | DNA sequence from clone RP11-353C18 on |
| 482D12 | 1753 | 2359 | NM_004848 | Hs.10649 | 0 | 1 | chromosome 20 |
| 184F4 | 2686 | 3194 | AL137721 | Hs.10702 | 0 | 1 | FLJ00005 protein, partial cds /cds=(0 |
| 186F10 | 2688 | 3084 | NM_017601 | Hs.10702 | 1.00E-137 | 2 | basement membrane-induced gene (ICB-1), mRNA |
| 461E3 | 593 | 1110 | NM_021821 | Hs.10724 | 0 | 1 | mRNA; cDNA DKFZp761H221 (from clone |
| 598D5 | 660 | 1191 | NM_014306 | Hs.10729 | 0 | 2 | DKFZp761H2 |
| 125D9 | 104 | 397 | NM_002495 | Hs.10758 | 1.00E-165 | 1 | hypothetical protein DKFZp761H221 (DKFZp761H |
| 36A7 | 172 | 1114 | NM_006325 | Hs.10842 | 0 | 11 | MDS023 protein (MDS023), mRNA /cds=(335,1018) |
| 54H1 | 240 | 1467 | NM_012257 | Hs.10882 | 0 | 2 | hypothetical protein (HSPC117), mRNA /cds=(75 |
| 596B8 | 1186 | 1895 | AK025212 | Hs.10888 | 0 | 17 | NADH dehydrogenase (ubiquinone) Fe-S protein |
| 458G7 | 989 | 1492 | Z78330 | Hs.10927 | 0 | 1 | RAN, member RAS oncogene family RAN, member |
| 115D2 | 308 | 638 | BF793378 | Hs.10957 | 1.00E-102 | 1 | RAS |
| 148H9 | 226 | 863 | AF021819 | Hs.10958 | 0 | 1 | HMG-box containing protein 1 (HBP1), mRNA /cds |
| 173D5 | 356 | 816 | NM_007262 | Hs.10958 | 0 | 1 | cDNA: FLJ21559 fis, clone COL06406 /cds=UNKNOW |
| 39B7 | 1553 | 2256 | AF063605 | Hs.11000 | 0 | 1 | HSZ78330 cDNA /clone=2.49-(CEPH) /gb=Z78330 |
| 592H5 | 1553 | 2257 | NM_015344 | Hs.11000 | 0 | 3 | 602254823F1 cDNA, 5' end /clone=IMAGE:4347076 |
| | | | | | | | RNA-binding protein regulatory subunit mRNA, |
| | | | | | | | RNA-binding protein regulatory subunit (DJ-1 |
| | | | | | | | brain my047 protein mRNA, complete cds /cds=(8 |
| | | | | | | | MY047 protein (MY047), mRNA /cds=(84,479) /gb |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|---|---|
| 112G3 | 2591 | 3180 | AB046813 | Hs.11123 | 0 | 1 | mRNA for KIAA1593 protein, partial cds /cds=(4 |
| 592E8 | 251 | 725 | NM_014041 | Hs.11125 | 0 | 2 | HSPC033 protein (HSPC033), mRNA /cds=(168,443 |
| 477A2 | 1610 | 1697 | NM_003100 | Hs.11183 | 8.00E-43 | 2 | sorting nexin 2 (SNX2), mRNA /cds=(29,1588) /g |
| 41G4 | 6498 | 6751 | AB014522 | Hs.11238 | 1.00E-142 | 1 | for KIAA0622 protein, partial cds /cds=(0 |
| 519A3 | 759 | 987 | NM_018371 | Hs.11260 | 1.00E-127 | 1 | hypothetical protein FLJ11264 (FLJ11264), mR |
| 175B4 | 404 | 688 | BE788546 | Hs.11355 | 4.00E-75 | 1 | 601476186F1 cDNA, 5' end /clone=IMAGE:3878948 |
| 114F11 | 245 | 401 | BF665055 | Hs.11356 | 4.00E-55 | 1 | 602119656F1 cDNA, 5' end /clone=IMAGE:4276860 |
| 40D2 | 96 | 824 | U59808 | Hs.11383 | 0 | 1 | monocyte chemotactic protein-4 precursor (MCP-4) |
| 109C3 | 767 | 2345 | M74002 | Hs.11482 | 0 | 2 | mR arginine-rich nuclear protein mRNA, complete cds /cds |
| 117G9 | 408 | 2345 | NM_004768 | Hs.11482 | 0 | 8 | splicing factor, arginine/serine-rich 11 (SF |
| 458G6 | 2053 | 2164 | AK022628 | Hs.11556 | 1.00E-54 | 1 | cDNA FLJ12566 fis, clone NT2RM4000852 /cds=UNK |
| 181E7 | 644 | 1004 | AK021632 | Hs.11571 | 1.00E-167 | 1 | cDNA FLJ11570 fis, clone HEMBA1003309 /cds=UNK |
| 458B3 | 85 | 522 | R12665 | Hs.11594 | 1.00E-137 | 1 | yf40a04.s1 cDNA, 3' end /clone=IMAGE:129294 / |
| 146B6 | 498 | 677 | BE794595 | Hs.11607 | 5.00E-82 | 1 | 601590368F1 5' end /clone=IMAGE:3944489 |
| 516F12 | 388 | 711 | BG288429 | Hs.11637 | 1.00E-132 | 1 | 602388093F1 cDNA, 5' end /clone=IMAGE:4517086 |
| 60B1 | 1291 | 1882 | NM_005121 | Hs.11861 | 0 | 1 | thyroid hormone receptor-associated protein, |
| 44C6 | 2613 | 2834 | NM_000859 | Hs.11899 | 9.00E-72 | 1 | 3-hydroxy-3-methylglutaryl-Coenzyme A reduct |
| 39F10 | 1 | 221 | BF668230 | Hs.12035 | 1.00E-120 | 2 | 602122419F1 cDNA, 5' end /clone=IMAGE:4279300 |
| 596D8 | 234 | 849 | U72514 | Hs.12045 | 0 | 2 | C2f mRNA, complete cds |
| 481E7 | 1902 | 2190 | AB028986 | Hs.12064 | 1.00E-151 | 1 | mRNA for KIAA1063 protein, partial cds /cds=(0 |
| 465D9 | 2529 | 2699 | NM_004003 | Hs.12068 | 8.00E-91 | 1 | carnitine acetyltransferase (CRAT), nuclear |
| 116H8 | 283 | 738 | NM_003321 | Hs.12084 | 0 | 1 | Tu translation elongation factor, mitochondri |
| 44A4 | 319 | 836 | S75463 | Hs.12084 | 0 | 1 | P43=mitochondrial elongation factor homolog [human, |
| 114F7 | 4254 | 4495 | AL137753 | Hs.12144 | 1.00E-115 | 1 | live mRNA; cDNA DKFZp434K1412 (from clone |
| 123F12 | 1 | 219 | NM_021203 | Hs.12152 | 1.00E-114 | 1 | DKFZp434K |
| 519H7 | 166 | 753 | AK025775 | Hs.12245 | 0 | 1 | APMCF1 protein (APMCF1), mRNA /cds=(82,225) / |
| 70E3 | 953 | 4720 | AB014530 | Hs.12259 | 0 | 3 | cDNA: FLJ22122 fis, clone HEP19214 /cds=UNKNOWN |
| 107H1 | 680 | 1078 | AK024756 | Hs.12293 | 0 | 1 | for KIAA0630 protein, partial cds /cds=(0 |
| 71E5 | 4750 | 5283 | NM_003170 | Hs.12303 | 0 | 1 | FLJ21103 fis, clone CAS04883 /cds=(107,1 |
| 106F3 | 977 | 1490 | AL050272 | Hs.12305 | 0 | 1 | suppressor of Ty (S.cerevisiae) 6 homolog (SUP |
| 481F4 | 1859 | 2403 | NM_015509 | Hs.12305 | 0 | 1 | cDNA DKFZp566B183 (from clone DKFZp566B1 |
| 114D3 | 1271 | 1520 | AF038202 | Hs.12311 | 1.00E-118 | 1 | DKFZp566B183 protein (DKFZp566B183), mRNA /c |
| 463B9 | 1006 | 1224 | AK021670 | Hs.12315 | 1.00E-121 | 1 | clone 23570 mRNA sequence /cds=UNKNOWN |
| 167A8 | 71 | 723 | BG034192 | Hs.12396 | 0 | 2 | /gb=AF0 |
| 460E9 | 3808 | 4166 | D83776 | Hs.12413 | 1.00E-176 | 1 | cDNA FLJ11608 fis, clone HEMBA1003976 /cds=(56 |
| 157E1 | 1887 | 3154 | NM_020403 | Hs.12450 | 0 | 3 | 602302446F1 cDNA, 5' end /clone=IMAGE:4403866 |
| 69F11 | 2715 | 3447 | AK001676 | Hs.12457 | 0 | 1 | mRNA for KIAA0191 gene, partial cds /cds=(0,4552) |
| 118B8 | 5781 | 6374 | AB032973 | Hs.12461 | 0 | 1 | /gb |
| 193G12 | 2069 | 2368 | NM_005993 | Hs.12570 | 1.00E-169 | 1 | cadherin superfamily protein VR4-11 (LOC57123 |
| 459D11 | 2828 | 3122 | NM_021151 | Hs.12743 | 1.00E-147 | 1 | FLJ10814 fis, clone NT2RP4000984 /cds=(92 |
| 196H4 | 1 | 5439 | AB046785 | Hs.12772 | 0 | 2 | mRNA for KIAA1147 protein, partial cds /cds=(0 |
| 56G11 | 458 | 1088 | AL080156 | Hs.12813 | 0 | 1 | tubulin-specific chaperone d (TBCD), mRNA /cd |
| 476E6 | 1221 | 1638 | NM_006590 | Hs.12820 | 0 | 1 | carnitine octanoyltransferase (COT), mRNA /c |
| 109E7 | 1 | 180 | AF208855 | Hs.12830 | 3.00E-79 | 1 | mRNA for KIAA1565 protein, partial cds /cds=(0 |
| | | | | | | | cDNA DKFZp434J214 (from clone DKFZp434J2 |
| | | | | | | | SnRNP assembly defective 1 homolog (SAD1), mRN |
| | | | | | | | BM-013 mRNA, complete cds /cds=(67,459) /gb=A |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|--|
| 458A2 | 1818 | 2276 | AK026747 | Hs.12969 | 0 | 1 | cDNA: FLJ23094 fis, clone LNG07379, highly sim |
| 466D10 | 1469 | 1745 | AK001822 | Hs.12999 | 9.00E-39 | 1 | cDNA FLJ10960 fis, clone PLACE1000564 /cds=UNK |
| 187A11 | 1866 | 2555 | NM_003330 | Hs.13046 | 0 | 2 | thioredoxin reductase 1 (TXNRD1), mRNA /cds=(|
| 60D9 | 1757 | 3508 | X91247 | Hs.13046 | 0 | 3 | thioredoxin reductase /cds=(439,1932) |
| 75D7 | 2071 | 2550 | AF055581 | Hs.13131 | 0 | 1 | adaptor protein Lnk mRNA, complete cds /cds=(3 |
| 196C2 | 190 | 845 | AK026239 | Hs.13179 | 0 | 2 | cDNA: FLJ22586 fis, clone HSI02774 /cds=UNKNOWN |
| 480G6 | 11 | 380 | AL570416 | Hs.13256 | 1.00E-161 | 1 | AL570416 cDNA /clone=CS0DI020YK05-(3-prime) |
| 196H3 | 2814 | 3382 | AB020663 | Hs.13264 | 0 | 1 | mRNA for KIAA0856 protein, partial cds /cds=(0 |
| 460H3 | 127 | 431 | BF029796 | Hs.13268 | 1.00E-151 | 1 | 601556721F1 cDNA, 5' end /clone=IMAGE:3826637 |
| 170B2 | 1487 | 1635 | AB011164 | Hs.13273 | 1.00E-69 | 1 | for KIAA0592 protein, partial cds /cds=(0, |
| 115E6 | 2153 | 2376 | AK025707 | Hs.13277 | 1.00E-124 | 1 | cDNA: FLJ22054 fis, clone HEP09634 /cds=(144,9 |
| 110F10 | 119 | 648 | BE537908 | Hs.13328 | 0 | 1 | 601067373F1 cDNA, 5' end /clone=IMAGE:3453594 |
| 36C2 | 427 | 4137 | AF054284 | Hs.13453 | 0 | 5 | spliceosomal protein SAP 155 mRNA, complete cd |
| 594C3 | 5 | 4229 | NM_012433 | Hs.13453 | 0 | 10 | splicing factor 3b, subunit 1, 155kD (SF3B1), m |
| 110C6 | 4 | 1853 | AF131753 | Hs.13472 | 0 | 5 | clone 24859 mRNA sequence /cds=UNKNOWN /gb=AF |
| 173B6 | 1156 | 1672 | NM_013236 | Hs.13493 | 0 | 1 | like mouse brain protein E46 (E46L), mRNA /cds= |
| 462C4 | 794 | 1093 | BC001909 | Hs.13580 | 1.00E-115 | 1 | clone IMAGE:3537447, mRNA, partial cds /cds= |
| 597H11 | 412 | 936 | NM_014174 | Hs.13645 | 0 | 1 | HSPC144 protein (HSPC144), mRNA /cds=(446,112 |
| 107F8 | 429 | 821 | AK025767 | Hs.13755 | 0 | 1 | FLJ22114 fis, clone HEP18441 /cds=UNKNOWN |
| 102D12 | 3153 | 4764 | AF000993 | Hs.13980 | 0 | 2 | ubiquitous TPR motif, X isoform (UTX) mRNA, alt |
| 515G12 | 1710 | 2120 | AK025425 | Hs.14040 | 0 | 2 | cDNA: FLJ21772 fis, clone COLF7808 /cds=UNKNOWN |
| 480H5 | 1945 | 2259 | AK024228 | Hs.14070 | 1.00E-119 | 1 | cDNA FLJ14166 fis, clone NT2RP1000796 /cds=(20 |
| 61D1 | 73 | 499 | NM_014245 | Hs.14084 | 0 | 1 | ring finger protein 7 (RNF7), mRNA /cds=(53,394 |
| 122E4 | 2162 | 2685 | NM_014454 | Hs.14125 | 0 | 1 | p53 regulated PA26 nuclear protein (PA26), mRN |
| 123D9 | 22 | 722 | NM_001161 | Hs.14142 | 0 | 1 | nudix (nucleoside diphosphate linked moiety |
| 460F11 | 1084 | 1322 | NM_017827 | Hs.14220 | 4.00E-74 | 1 | hypothetical protein FLJ20450 (FLJ20450), mR |
| 458D2 | 127 | 536 | NM_018648 | Hs.14317 | 0 | 1 | nucleolar protein family A, member 3 (H1ACA sm |
| 167G1 | 30 | 198 | AK022939 | Hs.14347 | 3.00E-91 | 1 | cDNA FLJ12877 fis, clone NT2RP2003825 /cds=(3 |
| 117H10 | 975 | 1721 | NM_003022 | Hs.14368 | 0 | 1 | SH3 domain binding glutamic acid-rich protein |
| 591B12 | 1082 | 1801 | NM_001614 | Hs.14376 | 0 | 9 | actin, gamma 1 (ACTG1), mRNA /cds=(74,1201) /g |
| 179H3 | 1160 | 1791 | X04098 | Hs.14376 | 1.00E-178 | 5 | cytoskeletal gamma-actin /cds=(73,1200) /g |
| 116D9 | 5818 | 6073 | NM_012199 | Hs.14520 | 5.00E-84 | 1 | eukaryotic translation initiation factor 2C, |
| 64D11 | 1901 | 2506 | NM_003592 | Hs.14541 | 0 | 1 | cullin 1 (CUL1), mRNA /cds=(124,2382) /gb=Nm_0 |
| 516F4 | 750 | 1331 | AK025166 | Hs.14555 | 0 | 1 | cDNA: FLJ21513 fis, clone COL05778 /cds=UNKNOWN |
| 459G5 | 1 | 260 | AK025269 | Hs.14562 | 5.00E-88 | 1 | cDNA: FLJ21616 fis, clone COL07477 /cds=(119,1 |
| 521B7 | 7 | 1825 | NM_005335 | Hs.14601 | 0 | 8 | hematopoietic cell-specific Lyn substrate 1 |
| 110D7 | 7 | 1295 | X16663 | Hs.14601 | 0 | 3 | HS1 gene for hematopoietic lineage cell specific pro |
| 114D11 | 1460 | 1559 | NM_003584 | Hs.14611 | 1.00E-45 | 1 | dual specificity phosphatase 11 (RNA/RNP comp |
| 589A3 | 1665 | 2197 | NM_016293 | Hs.14770 | 0 | 2 | bridging integrator 2 (BIN2), mRNA /cds=(38,17 |
| 104C8 | 2113 | 2380 | AB031050 | Hs.14805 | 1.00E-135 | 2 | for organic anion transporter OATP-D, com |
| 481D10 | 2466 | 2694 | NM_013272 | Hs.14805 | 1.00E-68 | 1 | solute carrier family 21 (organic anion transp |
| 125B2 | 2704 | 3183 | NM_001455 | Hs.14845 | 0 | 1 | forkhead box O3A (FOXO3A), mRNA /cds=(924,2945 |
| 500D7 | 2174 | 2379 | AL050021 | Hs.14846 | 1.00E-100 | 1 | mRNA; cDNA DKFZp564D016 (from clone DKFZp564D0 |
| 123B5 | 1793 | 2195 | NM_016598 | Hs.14896 | 0 | 1 | DHHC1 protein (LOC51304), mRNA /cds=(214,1197 |
| 499E2 | 1266 | 1549 | AB020644 | Hs.14945 | 1.00E-155 | 3 | mRNA for KIAA0837 protein, partial cds /cds=(0 |
| 123H6 | 2980 | 3652 | NM_007192 | Hs.14963 | 0 | 3 | chromatin-specific transcription elongation |
| 61G10 | 264 | 528 | D13627 | Hs.15071 | 1.00E-144 | 1 | KIAA0002 gene, complete cds /cds=(28,1674) / |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|---|
| 460D10 | 2162 | 4305 | NM_014837 | Hs.15087 | 0 | 4 | KIAA0250 gene product (KIAA0250), mRNA /cds=(|
| 176E12 | 9289 | 9739 | NM_022473 | Hs.15220 | 0 | 1 | zinc finger protein 106 (ZFP106), mRNA /cds=(3 |
| 487E11 | 1561 | 1989 | NM_006170 | Hs.15243 | 0 | 1 | nucleolar protein 1 (120kD) (NOL1), mRNA /cds= |
| 75E11 | 1628 | 2201 | AF127139 | Hs.15259 | 0 | 20 | Bcl-2-binding protein BIS (BIS) mRNA, complete |
| 71H9 | 1656 | 2532 | NM_004281 | Hs.15259 | 0 | 12 | BCL2-associated athanogene 3 (BAG3), mRNA /cd |
| 484G9 | 465 | 1006 | NM_005826 | Hs.15265 | 0 | 1 | heterogeneous nuclear ribonucleoprotein R (|
| 480H8 | 2013 | 2635 | AB037828 | Hs.15370 | 0 | 1 | mRNA for KIAA1407 protein, partial cds /cds=(0 |
| 587G9 | 2436 | 2769 | AK024088 | Hs.15423 | 1.00E-167 | 1 | cDNA FLJ14026 fis, clone HEMBA1003679, weakly |
| 483D6 | 5239 | 5810 | NM_004774 | Hs.15589 | 0 | 1 | PPAR binding protein (PPARBP), mRNA /cds=(235, |
| 514A7 | 673 | 942 | NM_006833 | Hs.15591 | 1.00E-151 | 1 | COP9 subunit 6 (MOV34 homolog, 34 kD) (MOV34-34 |
| 125A2 | 522 | 746 | NM_024348 | Hs.15961 | 1.00E-112 | 1 | dynactin 3 (p22) (DCTN3), transcript variant |
| 591A5 | 295 | 704 | NM_005005 | Hs.15977 | 0 | 3 | NADH dehydrogenase (ubiquinone) 1 beta subcom |
| 39H12 | 1641 | 1993 | X74262 | Hs.16003 | 1.00E-180 | 1 | RbAp48 mRNA encoding retinoblastoma binding prot |
| 113A9 | 1328 | 1891 | NM_016334 | Hs.16085 | 0 | 1 | putative G-protein coupled receptor (SH120), |
| 45C2 | 765 | 1674 | NM_006461 | Hs.16244 | 0 | 2 | mitotic spindle coiled-coil related protein (|
| 494H10 | 113 | 2576 | NM_016312 | Hs.16420 | 0 | 3 | Npw38-binding protein NpwBP (LOC51729), mRNA |
| 40D8 | 52 | 246 | Y13710 | Hs.16530 | 1.00E-107 | 1 | for alternative activated macrophage spe |
| 597E7 | 244 | 524 | AL523085 | Hs.16648 | 1.00E-147 | 1 | AL523085 cDNA /clone=CS0DC001YF21-(5-prime) |
| 458D11 | 232 | 319 | AY007106 | Hs.16773 | 1.00E-42 | 1 | clone TCCCIA00427 mRNA sequence |
| 70F2 | 824 | 991 | AL021786 | Hs.17109 | 2.00E-90 | 2 | /cds=UNKNOWN |
| 167C5 | 5768 | 5905 | D86964 | Hs.17211 | 3.00E-62 | 1 | DNA sequence from PAC 696H22 on chromosome |
| 460H2 | 3424 | 3624 | AL162070 | Hs.17377 | 1.00E-103 | 1 | Xq21.1-21.2 |
| 70G11 | 1384 | 1885 | AK023680 | Hs.17448 | 0 | 2 | mRNA for KIAA0209 gene, partial cds /cds=(0,5530) |
| 129C11 | 2458 | 3044 | U47924 | Hs.17483 | 0 | 2 | /gb |
| 467H3 | 4713 | 4908 | NM_014521 | Hs.17667 | 1.00E-61 | 1 | mRNA; cDNA DKFZp762H186 (from clone |
| 71A11 | 100 | 370 | BG035218 | Hs.17719 | 1.00E-142 | 1 | DKFZp762H1 |
| 598C7 | 513 | 902 | NM_021622 | Hs.17757 | 1.00E-178 | 1 | FLJ13618 fis, clone PLACE1010925 /cds=UNK |
| 595A7 | 3296 | 5680 | AB046774 | Hs.17767 | 0 | 5 | chromosome 12p13 sequence /cds=(194,1570) |
| 58D12 | 5225 | 5857 | AB007861 | Hs.17803 | 0 | 1 | /gb=U4792 |
| 524G8 | 357 | 809 | NM_014350 | Hs.17839 | 0 | 1 | SH3-domain binding protein 4 (SH3BP4), mRNA / |
| 521B10 | 1008 | 1476 | NM_002707 | Hs.17883 | 0 | 2 | 602324727F1 cDNA, 5' end /clone=IMAGE:4412910 |
| 69B12 | 1014 | 1490 | Y13936 | Hs.17883 | 0 | 1 | pleckstrin homology domain-containing, fami |
| 178E6 | 1903 | 4365 | NM_014827 | Hs.17969 | 0 | 3 | mRNA for KIAA1554 protein, partial cds /cds=(0 |
| 173H3 | 481 | 2362 | AK001630 | Hs.18063 | 0 | 4 | KIAA0401 mRNA, partial cds /cds=(0,1036) /gb= |
| 113A8 | 1285 | 1393 | NM_005606 | Hs.18069 | 5.00E-48 | 1 | TNF-induced protein (GG2-1), mRNA /cds=(197,7 |
| 118H9 | 3709 | 3950 | AB020677 | Hs.18166 | 1.00E-125 | 1 | protein phosphatase 1G (formerly 2C), magnesiu |
| 513H7 | 2204 | 2757 | NM_005839 | Hs.18192 | 1.00E-112 | 3 | for protein phosphatase 2C gamma /cds=(24, |
| 523G9 | 507 | 768 | AB044661 | Hs.18259 | 1.00E-147 | 1 | KIAA0663 gene product (KIAA0663), mRNA /cds=(|
| 105B9 | 695 | 1115 | AJ010842 | Hs.18259 | 0 | 1 | cDNA FLJ10768 fis, clone NT2RP4000150 /cds=UN |
| 589D12 | 335 | 715 | NM_016565 | Hs.18552 | 0 | 2 | protease, cysteine, 1 (legumain) (PRSC1), mRN |
| 170C8 | 414 | 737 | AF072860 | Hs.18571 | 0 | 2 | mRNA for KIAA0870 protein, partial cds /cds=(0 |
| 189A12 | 414 | 736 | NM_003690 | Hs.18571 | 0 | 1 | Ser/Arg-related nuclear matrix protein (plen |
| 134B9 | 2751 | 3057 | AB046808 | Hs.18587 | 1.00E-165 | 1 | XAB1 mRNA for XPA binding protein 1, complete c |
| 519G5 | 1291 | 1581 | NM_012332 | Hs.18625 | 1.00E-157 | 2 | for putative ATP(GTP)-binding protein, p |
| 526H2 | 827 | 1205 | NM_004208 | Hs.18720 | 0 | 1 | E2IG2 protein (LOC51287), mRNA /cds=(131,421) |
| | | | | | | | protein activator of the interferon-induced p |
| | | | | | | | protein kinase, interferon-inducible double |
| | | | | | | | mRNA for KIAA1588 protein, partial cds /cds=(2 |
| | | | | | | | Mitochondrial Acyl-CoA Thioesterase (MT-ACT4 |
| | | | | | | | programmed cell death 8 (apoptosis-inducing f |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|---|
| 462F12 | 409 | 556 | NM_017899 | Hs.18791 | 2.00E-78 | 1 | hypothetical protein FLJ20607 (FLJ20607), mR |
| 138B2 | 388 | 995 | AF003938 | Hs.18792 | 0 | 1 | thioredoxin-like protein complete cds |
| 36G12 | 935 | 1272 | AJ250014 | Hs.18827 | 0 | 2 | for Familial Cylindromatosis cyld gene / |
| 194D3 | 924 | 2123 | NM_018253 | Hs.18851 | 0 | 2 | hypothetical protein FLJ10875 (FLJ10875), mR |
| 523E1 | 3653 | 4056 | NM_012290 | Hs.18895 | 0 | 1 | tousled-like kinase 1 (TLK1), mRNA /cds=(212,2 |
| 587G5 | 1 | 350 | NM_016302 | Hs.18925 | 1.00E-166 | 1 | protein x 0001 (LOC51185), mRNA /cds=(33,1043) |
| 595C10 | 161 | 1281 | AC006042 | Hs.18987 | 0 | 4 | BAC clone RP11-505D17 from 7p22-p21 /cds=(0,12 |
| 125G10 | 54 | 752 | NM_002492 | Hs.19236 | 0 | 3 | NADH dehydrogenase (ubiquinone) 1 beta subcom |
| 478G7 | 1 | 193 | NM_021603 | Hs.19520 | 9.00E-51 | 1 | FXFD domain-containing ion transport regulat |
| 595F11 | 3623 | 3736 | AB051481 | Hs.19597 | 3.00E-49 | 1 | mRNA for KIAA1694 protein, partial cds /cds=(0 |
| 177C6 | 284 | 671 | AF161339 | Hs.19807 | 0 | 2 | HSPC076 mRNA, partial cds /cds=(0,301) /gb=AF |
| 37E12 | 3485 | 3919 | AB018298 | Hs.19822 | 0 | 1 | for KIAA0755 protein, complete cds /cds=(|
| 64G8 | 962 | 1311 | NM_001902 | Hs.19904 | 0 | 1 | cystathionase (cystathionine gamma-lyase) (|
| 499D5 | 2829 | 3183 | AB011169 | Hs.20141 | 0 | 1 | mRNA for KIAA0597 protein, partial cds /cds=(0, |
| 40D11 | 62 | 684 | NM_004166 | Hs.20144 | 0 | 1 | small inducible cytokine subfamily A (Cys-Cys |
| 66C10 | 1240 | 2240 | U76248 | Hs.20191 | 0 | 12 | hSIAH2 mRNA, complete cds /cds=(526,1500) /gb=U76248 |
| 586B12 | 1686 | 4288 | AB040922 | Hs.20237 | 0 | 2 | mRNA for KIAA1489 protein, partial cds /cds=(1 |
| 173G8 | 2578 | 3197 | AL096776 | Hs.20252 | 0 | 1 | DNA sequence from clone RP4-646B12 on chromosome 1q42 |
| 98C6 | 3303 | 4699 | AB051487 | Hs.20281 | 0 | 6 | mRNA for KIAA1700 protein, partial cds /cds=(1 |
| 107H11 | 781 | 1380 | AK022103 | Hs.20281 | 0 | 1 | FLJ12041 fis, clone HEMBB1001945 /cds=UNK |
| 121B8 | 778 | 1264 | NM_001548 | Hs.20315 | 0 | 1 | interferon-induced protein with tetratricope |
| 110C4 | 1050 | 1431 | AF244137 | Hs.20597 | 0 | 1 | hepatocellular carcinoma-associated antigen |
| 99H6 | 899 | 1412 | NM_014315 | Hs.20597 | 0 | 2 | host cell factor homolog (LCP), mRNA /cds=(316, |
| 152B12 | 69 | 424 | AK025446 | Hs.20760 | 0 | 1 | FLJ21793 fis, clone HEP00466 /cds=UNKNOWN |
| 459A8 | 1858 | 2143 | AL021366 | Hs.20830 | 1.00E-155 | 1 | DNA sequence from cosmid ICK0721Q on chromosome |
| 587A11 | 720 | 1080 | AL137576 | Hs.21015 | 0 | 1 | mRNA; cDNA DKFZp564L0864 (from clone DKFZp564L |
| 191E12 | 1688 | 2235 | AK025019 | Hs.21056 | 0 | 2 | cDNA: FLJ21366 fis, clone COL03012, highly sim |
| 52G3 | 225 | 1652 | NM_005880 | Hs.21189 | 0 | 6 | HIRA interacting protein 4 (dnaJ-like) (HIRIP |
| 181B7 | 3176 | 3316 | AB018325 | Hs.21264 | 3.00E-72 | 1 | mRNA for KIAA0782 protein, partial cds /cds=(0 |
| 45E11 | 1378 | 1518 | NM_003115 | Hs.21293 | 1.00E-72 | 1 | UDP-N-acetylglucosamine pyrophosphorylase |
| 109G1 | 2989 | 3487 | AB032948 | Hs.21356 | 0 | 1 | for KIAA1122 protein, partial cds /cds=(0 |
| 116D4 | 5522 | 5741 | NM_016936 | Hs.21479 | 1.00E-107 | 1 | ubiquitin 1 (UBN1), mRNA /cds=(114,3518) /gb |
| 37G10 | 294 | 3960 | M97935 | Hs.21486 | 0 | 4 | transcription factor ISGF-3 mRNA, complete cd |
| 599E8 | 329 | 3568 | NM_007315 | Hs.21486 | 0 | 6 | signal transducer and activator of transcripti |
| 592D10 | 2223 | 3204 | NM_002709 | Hs.21537 | 0 | 3 | protein phosphatase 1, catalytic subunit, bet |
| 68A7 | 1327 | 1612 | AB028958 | Hs.21542 | 1.00E-161 | 1 | for KIAA1035 protein, partial cds /cds=(0 |
| 72B3 | 2519 | 2862 | L03426 | Hs.21595 | 1.00E-179 | 1 | XE7 mRNA, complete alternate coding regions /cds=(166 |
| 592E6 | 2520 | 2854 | NM_005088 | Hs.21595 | 1.00E-161 | 1 | DNA segment on chromosome X and (unique) 155 ex |
| 589G6 | 190 | 522 | AL573787 | Hs.21732 | 1.00E-141 | 1 | AL573787 cDNA /clone=CS0DI055YM17-(3-prime) |
| 593H1 | 452 | 899 | NM_005875 | Hs.21756 | 0 | 2 | translation factor sui1 homolog (GC20), mRNA |
| 59B8 | 2893 | 3273 | NM_012406 | Hs.21807 | 0 | 1 | PR domain containing 4 (PRDM4), mRNA /cds=(122, |
| 196A9 | 12 | 543 | AL562895 | Hs.21812 | 0 | 1 | AL562895 cDNA /clone=CS0DC021YO20-(3-prime) |
| 67D8 | 62 | 631 | AW512498 | Hs.21879 | 1.00E-150 | 3 | xx75e03.x1 cDNA, 3' end /clone=IMAGE:2849500 |
| 477B6 | 1969 | 2520 | D84454 | Hs.21899 | 0 | 1 | mRNA for UDP-galactose translocator, complete cds /c |
| 515D1 | 2232 | 2647 | NM_007067 | Hs.21907 | 0 | 2 | histone acetyltransferase (HBOA), mRNA /cds= |
| 100F8 | 1082 | 1508 | AK022554 | Hs.21938 | 0 | 1 | FLJ12492 fis, clone NT2RM2001632, weakly |
| 470E4 | 1135 | 1244 | NM_020239 | Hs.22065 | 4.00E-45 | 2 | small protein effector 1 of Cdc42 (SPEC1), mRNA |
| 68G4 | 1391 | 2013 | AK022057 | Hs.22265 | 0 | 2 | FLJ11995 fis, clone HEMBB1001443, highly |
| 193H6 | 922 | 1328 | NM_022494 | Hs.22353 | 1.00E-178 | 1 | hypothetical protein FLJ21952 (FLJ21952), mR |
| 151D2 | 1492 | 1694 | AL049951 | Hs.22370 | 4.00E-88 | 1 | cDNA DKFZp564O0122 (from clone DKFZp564O |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|---|
| 497E8 | 1581 | 4794 | D83781 | Hs.22559 | 0 | 3 | mRNA for KIAA0197 gene, partial cds /cds=(0,3945) /gb |
| 182D10 | 999 | 1830 | AL117513 | Hs.22583 | 0 | 5 | mRNA; cDNA DKFZp434K2235 (from clone DKFZp434K |
| 75B5 | 1775 | 2380 | AF006513 | Hs.22670 | 0 | 1 | CHD1 mRNA, complete cds /cds=(163,5292) /gb=A |
| 126H8 | 1776 | 2377 | NM_001270 | Hs.22670 | 0 | 1 | chromodomain helicase DNA binding protein 1 (|
| 73D5 | 1599 | 1696 | AK025485 | Hs.22678 | 2.00E-42 | 1 | FLJ21832 fis, clone HEP01571 /cds=(32,15 |
| 481D11 | 128 | 562 | BF968270 | Hs.22790 | 1.00E-172 | 1 | 602269653F1 cDNA, 5' end /clone=IMAGE:4357740 |
| 74E4 | 724 | 1195 | NM_012124 | Hs.22857 | 0 | 1 | chord domain-containing protein 1 (CHP1), mRN |
| 459C6 | 813 | 1472 | NM_012244 | Hs.22891 | 0 | 1 | solute carrier family 7 (cationic amino acid t |
| 462G7 | 2972 | 3144 | AB037784 | Hs.22941 | 2.00E-93 | 1 | mRNA for KIAA1363 protein, partial cds /cds=(0 |
| 70F12 | 37 | 846 | AB020623 | Hs.22960 | 0 | 3 | DAM1 mRNA, complete cds /cds=(48,725) /gb=AB0 |
| 585H10 | 91 | 748 | NM_005872 | Hs.22960 | 0 | 1 | breast carcinoma amplified sequence 2 (BCAS2) |
| 142C8 | 1359 | 1597 | AK024023 | Hs.23170 | 1.00E-103 | 1 | FLJ13961 fis, clone Y79AA1001236, highly |
| 164F2 | 1220 | 1474 | NM_012280 | Hs.23170 | 1.00E-135 | 1 | homolog of yeast SPB1 (JM23), mRNA /cds=(300,12 |
| 127F11 | 682 | 806 | AL046016 | Hs.23247 | 2.00E-58 | 1 | DKFZp434P246_r1 cDNA, 5' end /clone=DKFZp434P |
| 98G7 | 760 | 1368 | NM_022496 | Hs.23259 | 0 | 1 | hypothetical protein FLJ13433 (FLJ13433), mR |
| 470C9 | 2 | 538 | AL574514 | Hs.23294 | 0 | 2 | AL574514 cDNA /clone=CS0DI056YA07-(3-prime) |
| 458F12 | 4293 | 4917 | AB002365 | Hs.23311 | 0 | 1 | mRNA for KIAA0367 gene, partial cds /cds=(0,2150) /gb |
| 57D8 | 460 | 566 | BF439063 | Hs.23349 | 3.00E-54 | 1 | nab70e03.x1 cDNA /clone=IMAGE /gb=BF439063 / |
| 599G12 | 352 | 983 | NM_014814 | Hs.23488 | 0 | 2 | KIAA0107 gene product (KIAA0107), mRNA /cds=(|
| 112B3 | 2400 | 2715 | NM_014887 | Hs.23518 | 1.00E-172 | 1 | hypothetical protein from BCRA2 region (CG005 |
| 167C10 | 1771 | 2107 | NM_004380 | Hs.23598 | 1.00E-175 | 1 | CREB binding protein (Rubinstein-Taybi syndr |
| 196G9 | 114 | 307 | BF970427 | Hs.23703 | 1.00E-101 | 1 | 602272760F1 cDNA, 5' end /clone=IMAGE:4360767 |
| 184B3 | 2488 | 2882 | AK026983 | Hs.23803 | 0 | 1 | FLJ23330 fis, clone HEP12654 /cds=(69,13 |
| 480H4 | 4871 | 5467 | AB023227 | Hs.23860 | 0 | 1 | mRNA for KIAA1010 protein, partial cds /cds=(0 |
| 479C12 | 4 | 190 | NM_005556 | Hs.23881 | 4.00E-91 | 1 | keratin 7 (KRT7), mRNA /cds=(56,1465) /gb=NM_ |
| 36E7 | 742 | 1126 | AL360135 | Hs.23964 | 0 | 1 | full length insert cDNA clone EUROIMAGE 12 |
| 598B5 | 544 | 1271 | NM_005870 | Hs.23964 | 0 | 12 | sin3-associated polypeptide, 18kD (SAP18), m |
| 462D8 | 1205 | 1653 | NM_004790 | Hs.23965 | 0 | 1 | solute carrier family 22 (organic anion transp |
| 479A5 | 1817 | 2164 | NM_002967 | Hs.23978 | 0 | 1 | scaffold attachment factor B (SAFB), mRNA /cds |
| 188E2 | 1762 | 2160 | NM_014950 | Hs.24083 | 0 | 1 | KIAA0997 protein (KIAA0997), mRNA /cds=(262,2 |
| 67D2 | 1304 | 1856 | AK024240 | Hs.24115 | 0 | 2 | FLJ14178 fis, clone NT2RP2003339 /cds=UNK |
| 177D8 | 4674 | 5185 | AF251039 | Hs.24125 | 0 | 1 | putative zinc finger protein mRNA, complete cd |
| 190E1 | 5222 | 5394 | NM_016604 | Hs.24125 | 8.00E-73 | 1 | putative zinc finger protein (LOC51780), mRNA |
| 192A5 | 1517 | 1985 | NM_003387 | Hs.24143 | 1.00E-135 | 2 | Wiskott-Aldrich syndrome protein interacting |
| 170A4 | 1666 | 3280 | X86019 | Hs.24143 | 4.00E-23 | 1 | PRPL-2 protein /cds=(204,1688) /gb=X860 |
| 480B6 | 1517 | 1937 | NM_012155 | Hs.24178 | 1.00E-133 | 1 | microtubule-associated protein like echinode |
| 143H11 | 177 | 656 | BE877357 | Hs.24181 | 0 | 2 | 601485590F1 cDNA, 5' end /clone=IMAGE:3887951 |
| 473D10 | 146 | 491 | AW960486 | Hs.24252 | 0 | 1 | EST372557 cDNA /gb=AW960486 /gi=8150170 /ug= |
| 98H1 | 23 | 562 | NM_003945 | Hs.24322 | 0 | 1 | ATPase, H+ transporting, lysosomal (vacuolar |
| 169G2 | 391 | 638 | BE612847 | Hs.24349 | 4.00E-75 | 2 | 601452239F1 5' end /clone=IMAGE:3856304 |
| 479B12 | 1132 | 1599 | AY007126 | Hs.24435 | 0 | 1 | clone CDABP0028 mRNA sequence /cds=UNKNOWN /g |
| 480H9 | 4716 | 5012 | NM_006048 | Hs.24594 | 1.00E-145 | 1 | ubiquitination factor E4B (homologous to yeas |
| 110B10 | 520 | 1171 | AL163206 | Hs.24633 | 0 | 1 | chromosome 21 segment HS21C006 /cds=(82,1203) |
| 99A3 | 519 | 1000 | NM_022136 | Hs.24633 | 0 | 2 | SAM domain, SH3 domain and nuclear localisation |
| 109G7 | 2024 | 2350 | AB037797 | Hs.24684 | 1.00E-141 | 1 | for KIAA1376 protein, partial cds /cds=(1 |
| 61B7 | 485 | 1656 | AK024029 | Hs.24719 | 0 | 4 | FLJ13967 fis, clone Y79AA1001402, weakly |
| 166C11 | 1216 | 1509 | AF006516 | Hs.24752 | 1.00E-165 | 1 | eps8 binding protein e3B1 mRNA, complete cds / |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|---|--|
| 464D12 | 166 | 764 | NM_002882 | Hs.24763 | 0 | 1 | RAN binding protein 1 (RANBP1), mRNA /cds=(149 |
| 98C12 | 6523 | 8023 | AB051512 | Hs.25127 | 0 | 3 | mRNA for KIAA1725 protein, partial cds /cds=(0 |
| 63F7 | 2164 | 2802 | AL133611 | Hs.25362 | 0 | 1 | cDNA DKFZp434O1317 (from clone DKFZp434O |
| 41D11 | 45 | 463 | X53795 | Hs.25409 | 0 | 1 | R2 mRNA for an inducible membrane protein |
| | | | | | | | /cds=(156,95 |
| 62G6 | 1452 | 1827 | V01512 | Hs.25647 | 0 | 3 | cellular oncogene c-fos (complete sequence) /cds=(15 |
| 593D12 | 1135 | 2111 | NM_015832 | Hs.25674 | 0 | 8 | methyl-CpG binding domain protein 2 (MBD2), tr |
| 172G9 | 2014 | 2371 | NM_021211 | Hs.25726 | 0 | 1 | transposon-derived Buster1 transposase-like |
| 106D6 | 432 | 1878 | AF058696 | Hs.25812 | 0 | 2 | cell cycle regulatory protein p95 (NBS1) mRNA, |
| 98A4 | 533 | 3758 | NM_002485 | Hs.25812 | 0 | 2 | Nijmegen breakage syndrome 1 (nibrin) (NBS1), |
| 477H5 | 6320 | 6599 | NM_004638 | Hs.25911 | 1.00E-111 | 3 | HLA-B associated transcript-2 (D6S51E), mRNA |
| 71F11 | 2070 | 2931 | NM_019555 | Hs.25951 | 0 | 3 | Rho guanine nucleotide exchange factor (GEF) |
| 164B9 | 2163 | 2502 | AK023999 | Hs.26039 | 1.00E-159 | 1 | cDNA FLJ13937 fis, clone Y79AA1000805 /cds=UNK |
| 100A3 | 2043 | 2620 | M34668 | Hs.26045 | 0 | 1 | protein tyrosine phosphatase (PTPase-alpha) mRNA |
| | | | | | | | /c |
| 123A5 | 2046 | 2638 | NM_002836 | Hs.26045 | 0 | 1 | protein tyrosine phosphatase, receptor type, |
| 466E5 | 7817 | 8241 | NM_014112 | Hs.26102 | 0 | 2 | trichorhinophalangeal syndrome I gene (TRPS1) |
| 588A1 | 361 | 857 | AF070582 | Hs.26118 | 0 | 1 | clone 24766 mRNA sequence /cds=UNKNOWN |
| | | | | | | | /gb=AF |
| 526H12 | 176 | 1809 | NM_018384 | Hs.26194 | 0 | 5 | hypothetical protein FLJ11296 (FLJ11296), mR |
| 149G7 | 96 | 1123 | AK027016 | Hs.26198 | 0 | 3 | FLJ23363 fis, clone HEP15507 /cds=(206,1 |
| 122A4 | 1196 | 1332 | AL050166 | Hs.26295 | 3.00E-72 | 1 | mRNA; cDNA DKFZp586D1122 (from clone |
| | | | | | | | DKFZp586D |
| 122D5 | 1936 | 2435 | AB029006 | Hs.26334 | 0 | 1 | mRNA for KIAA1083 protein, complete cds /cds=(|
| 137G5 | 137 | 452 | AK025778 | Hs.26367 | 1.00E-145 | 1 | FLJ22125 fis, clone HEP19410 /cds=(119,5 |
| 595D2 | 1 | 372 | NM_022488 | Hs.26367 | 3.00E-89 | 3 | PC3-96 protein (PC3-96), mRNA /cds=(119,586) |
| 64D12 | 1024 | 1135 | NM_017746 | Hs.26369 | 2.00E-57 | 1 | hypothetical protein FLJ20287 (FLJ20287), mR |
| 39E4 | 2132 | 2750 | AK000367 | Hs.26434 | 0 | 1 | FLJ20360 fis, clone HEP16677 /cds=(79,230 |
| 473C10 | 4318 | 4623 | AF051782 | Hs.26584 | 1.00E-154 | 1 | diaphanous 1 (HDIA1) mRNA, complete cds /cds=(|
| 590C4 | 1740 | 2198 | AL050205 | Hs.26613 | 0 | 1 | mRNA; cDNA DKFZp586F1323 (from clone |
| | | | | | | | DKFZp586F |
| 523F3 | 454 | 792 | AC002073 | Hs.26670 | 1.00E-164 | 1 | PAC clone RP3-515N1 from 22q11.2-q22 /cds=(0,791) |
| | | | | | | | /g |
| 587E11 | 1226 | 1876 | NM_004779 | Hs.26703 | 0 | 2 | CCR4-NOT transcription complex, subunit 8 (C |
| 110G4 | 191 | 685 | BE868389 | Hs.26731 | 0 | 1 | 601444360F1 cDNA, 5' end /clone=IMAGE:3848487 |
| 110E11 | 1001 | 3955 | AL117448 | Hs.26797 | 0 | 2 | cDNA DKFZp586B1417 (from clone DKFZp586B |
| 152A8 | 12 | 112 | AI760224 | Hs.26873 | 2.00E-48 | 1 | wh62g06.x1 cDNA, 3' end /clone=IMAGE:2385370 |
| 467G11 | 528 | 858 | NM_016106 | Hs.27023 | 1.00E-174 | 1 | vesicle transport-related protein (KIAA0917) |
| 465E11 | 634 | 1065 | AL136656 | Hs.27181 | 3.00E-83 | 1 | mRNA; cDNA DKFZp564C1664 (from clone |
| | | | | | | | DKFZp564C |
| 58E11 | 1 | 551 | AJ238243 | Hs.27182 | 0 | 1 | mRNA for phospholipase A2 activating protein |
| 590H2 | 398 | 1016 | NM_014412 | Hs.27258 | 0 | 1 | calyculin binding protein (CACYBP), mRNA /cds |
| 179E9 | 1039 | 1905 | AK025586 | Hs.27268 | 0 | 4 | FLJ21933 fis, clone HEP04337 /cds=UNKNOW |
| 459D7 | 1293 | 1936 | AL050061 | Hs.27371 | 0 | 1 | mRNA; cDNA DKFZp566J123 (from clone |
| | | | | | | | DKFZp566J1 |
| 54A11 | 709 | 1542 | AK022811 | Hs.27475 | 0 | 1 | FLJ12749 fis, clone NT2RP2001149 /cds=UNK |
| 111A5 | 42 | 686 | NM_022485 | Hs.27556 | 0 | 1 | hypothetical protein FLJ22405 (FLJ22405), mR |
| 123D4 | 879 | 1005 | NM_016059 | Hs.27693 | 3.00E-49 | 1 | peptidylprolyl isomerase (cyclophilin)-like |
| 518E11 | 1245 | 2235 | AF332469 | Hs.27721 | 0 | 5 | putative protein WHSC1L1 (WHSC1L1) mRNA, comp |
| 103B11 | 631 | 1343 | NM_014805 | Hs.28020 | 0 | 1 | KIAA0766 gene product (KIAA0766), mRNA /cds=(|
| 479H3 | 4 | 100 | AB007928 | Hs.28169 | 7.00E-37 | 1 | mRNA for KIAA0459 protein, partial cds /cds=(0 |
| 526B3 | 1901 | 1995 | NM_007218 | Hs.28285 | 4.00E-47 | 1 | patched related protein translocated in renal |
| 480E4 | 4088 | 4596 | AB046766 | Hs.28338 | 0 | 1 | mRNA for KIAA1546 protein, partial cds /cds=(0 |
| 164D10 | 651 | 970 | NM_002970 | Hs.28491 | 1.00E-163 | 2 | spermidine/spermine N1-acetyltransferase (|
| 69E10 | 729 | 1588 | AB007888 | Hs.28578 | 0 | 2 | KIAA0428 mRNA, complete cds /cds=(1414,2526) |
| 49B1 | 632 | 4266 | NM_021038 | Hs.28578 | 0 | 4 | muscleblind (Drosophila)-like (MBNL), mRNA / |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|---|
| 173A10 | 2105 | 2391 | AL034548 | Hs.28608 | 1.00E-161 | 2 | DNA sequence from clone RP5-1103G7 on chromosome 20p1 |
| 156H8 | 467 | 585 | AV691642 | Hs.28739 | 8.00E-43 | 1 | AV691642 5' end /clone=GKCDJG11 /clone_ |
| 588D3 | 444 | 909 | NM_004800 | Hs.28757 | 1.00E-123 | 1 | transmembrane 9 superfamily member 2 (TM9SF2) |
| 493B12 | 500 | 930 | NM_003512 | Hs.28777 | 0 | 1 | H2A histone family, member L (H2AFL), mRNA /cd |
| 115C5 | 63 | 661 | BF341640 | Hs.28788 | 0 | 1 | 602016073F1 cDNA, 5' end /clone=IMAGE:4151706 |
| 524C10 | 37 | 412 | NM_007217 | Hs.28866 | 1.00E-179 | 1 | programmed cell death 10 (PDCD10), mRNA /cds=(|
| 39A8 | 1380 | 1873 | AK000196 | Hs.29052 | 0 | 1 | FLJ20189 fis, clone COLF0657 /cds=(122,84 |
| 477H7 | 690 | 1047 | NM_005859 | Hs.29117 | 1.00E-163 | 1 | purine-rich element binding protein A (PURA), |
| 134C8 | 2462 | 2789 | NM_002894 | Hs.29287 | 1.00E-173 | 1 | retinoblastoma-binding protein 8 (RBBP8), mR |
| 108A11 | 182 | 992 | M31165 | Hs.29352 | 0 | 9 | tumor necrosis factor-inducible (TSG-6) mRNA fragme |
| 99E8 | 179 | 992 | NM_007115 | Hs.29352 | 0 | 7 | tumor necrosis factor, alpha-induced protein |
| 169B3 | 2219 | 2683 | AF039942 | Hs.29417 | 0 | 1 | HCF-binding transcription factor Zhangfei (Z |
| 526A7 | 2219 | 2670 | NM_021212 | Hs.29417 | 0 | 1 | HCF-binding transcription factor Zhangfei (Z |
| 184H12 | 2380 | 4852 | AB033042 | Hs.29679 | 0 | 2 | KIAA1216 protein, partial cds /cds=(0 |
| 125G9 | 1169 | 1814 | AB037791 | Hs.29716 | 0 | 1 | mRNA for KIAA1370 protein, partial cds /cds=(4 |
| 68F3 | 1011 | 1892 | AK027197 | Hs.29797 | 0 | 5 | FLJ23544 fis, clone LNG08336 /cds=(125,5 |
| 72H12 | 2103 | 2564 | L27071 | Hs.29877 | 0 | 2 | tyrosine kinase (TXK) mRNA, complete cds /cds=(86,166 |
| 588D5 | 793 | 1321 | NM_003328 | Hs.29877 | 0 | 1 | TXK tyrosine kinase (TXK), mRNA /cds=(86,1669) |
| 127C3 | 1 | 1424 | AK024961 | Hs.29977 | 0 | 4 | cDNA: FLJ21308 fis, clone COL02131 /cds=(287,1 |
| 128H7 | 351 | 977 | NM_014188 | Hs.30026 | 0 | 1 | HSPC182 protein (HSPC182), mRNA /cds=(65,649) |
| 521G4 | 502 | 1260 | NM_004593 | Hs.30035 | 0 | 4 | splicing factor, arginine/serine-rich (trans |
| 47A2 | 503 | 1265 | U61267 | Hs.30035 | 0 | 4 | putative splice factor transformer2-beta mRN |
| 37G9 | 1287 | 1763 | M16967 | Hs.30054 | 0 | 2 | coagulation factor V mRNA, complete cds /cds=(90,6764 |
| 459E1 | 43 | 536 | NM_015919 | Hs.30303 | 0 | 1 | Kruppel-associated box protein (LOC51595), m |
| 465F6 | 256 | 573 | NM_005710 | Hs.30570 | 7.00E-75 | 1 | polyglutamine binding protein 1 (PQBP1), mRNA |
| 120H1 | 5305 | 5634 | NM_012296 | Hs.30687 | 1.00E-172 | 2 | GRB2-associated binding protein 2 (GAB2), mRN |
| 189G2 | 1 | 147 | BG260954 | Hs.30724 | 2.00E-68 | 1 | 602372562F1 cDNA, 5' end /clone=IMAGE:4480647 |
| 482E6 | 3086 | 3254 | AK023743 | Hs.30818 | 4.00E-91 | 1 | cDNA FLJ13681 fis, clone PLACE2000014, weakly |
| 179H5 | 20 | 1232 | AK001972 | Hs.30822 | 0 | 2 | FLJ11110 fis, clone PLACE1005921, weakly |
| 598B6 | 1 | 1169 | NM_018326 | Hs.30822 | 0 | 19 | hypothetical protein FLJ11110 (FLJ11110), mR |
| 126G10 | 1309 | 2463 | AK000689 | Hs.30882 | 0 | 18 | cDNA FLJ20682 fis, clone KAIA3543, highly simi |
| 126G7 | 5221 | 5904 | NM_019081 | Hs.30909 | 1.00E-163 | 2 | KIAA0430 gene product (KIAA0430), mRNA /cds=(|
| 483D1 | 1481 | 2098 | NM_003098 | Hs.31121 | 0 | 1 | syntrophin, alpha 1(dystrophin-associated p |
| 464C9 | 1188 | 1755 | NM_003273 | Hs.31130 | 0 | 1 | transmembrane 7 superfamily member 2 (TM7SF2), |
| 478A6 | 3024 | 3837 | NM_012238 | Hs.31176 | 1.00E-176 | 2 | sir2-like 1 (SIRT1), mRNA /cds=(53,2296) /gb= |
| 122E5 | 1060 | 1294 | NM_002893 | Hs.31314 | 1.00E-113 | 1 | retinoblastoma-binding protein 7 (RBBP7), mR |
| 117B1 | 2056 | 2489 | AF153419 | Hs.31323 | 0 | 1 | IkappaBkinase complex-associated protein (I |
| 462E10 | 337 | 569 | AV752358 | Hs.31409 | 1.00E-108 | 1 | AV752358 cDNA, 5' end /clone=NPDBHG03 /clone_ |
| 126E7 | 1962 | 2748 | AB014548 | Hs.31921 | 0 | 2 | mRNA for KIAA0648 protein, partial cds /cds=(0 |
| 186G11 | 729 | 954 | BC000152 | Hs.31989 | 1.00E-125 | 1 | Similar to DKFZP586G1722 protein, clone MGC: |
| 67H7 | 1705 | 2336 | AJ400877 | Hs.32017 | 0 | 2 | ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf1 |
| 102B11 | 175 | 874 | AK026455 | Hs.32148 | 0 | 1 | FLJ22802 fis, clone KAIA2682, highly sim |
| 458D4 | 46 | 449 | H14103 | Hs.32149 | 1.00E-167 | 1 | ym62a02.r1 cDNA, 5' end /clone=IMAGE:163466 / |
| 99A2 | 3991 | 4532 | AB007902 | Hs.32168 | 0 | 1 | KIAA0442 mRNA, partial cds /cds=(0,3519) /gb= |
| 458G5 | 27 | 540 | N30152 | Hs.32250 | 0 | 1 | yx81f03.s1 cDNA, 3' end /clone=IMAGE:268157 / |
| 112D11 | 4399 | 5040 | NM_005922 | Hs.32353 | 0 | 1 | mitogen-activated protein kinase kinase |
| 48C8 | 3278 | 3988 | AB002377 | Hs.32556 | 0 | 2 | mRNA for KIAA0379 protein, partial cds /cds=(0, |
| 515F9 | 761 | 989 | NM_003193 | Hs.32675 | 1.00E-116 | 1 | tubulin-specific chaperone e (TBCE), mRNA /c |
| 158C12 | 342 | 809 | NM_016063 | Hs.32826 | 0 | 1 | CGI-130 protein (LOC51020), /cds=(63,575 |
| 585E6 | 128 | 512 | NM_005694 | Hs.32916 | 0 | 3 | nascent-polypeptide-associated complex alp |
| 459B5 | 1271 | 1972 | NM_017632 | Hs.32922 | 0 | 1 | hypothetical protein FLJ20036 (FLJ20036), mR |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|-------|-------|-----------|----------|-----------|----|--|
| 469G12 | 2711 | 2978 | NM_001566 | Hs.32944 | 1.00E-136 | 1 | inositol polyphosphate-4-phosphatase, type |
| 71B7 | 483 | 1787 | NM_003037 | Hs.32970 | 0 | 29 | signaling lymphocytic activation molecule (S |
| 74G1 | 1 | 1780 | U33017 | Hs.32970 | 0 | 33 | signaling lymphocytic activation molecule (SLAM) mR |
| 473B11 | 2993 | 3361 | NM_006784 | Hs.33085 | 1.00E-111 | 1 | WD repeat domain 3 (WDR3), mRNA /cds=(47,2878) |
| 56B5 | 23 | 578 | AB019571 | Hs.33190 | 0 | 1 | expressed only in placental villi, clone |
| 469D12 | 187 | 394 | AL359654 | Hs.33756 | 1.00E-110 | 1 | mRNA full length insert cDNA clone EUROIMAGE 19 |
| 98H8 | 371 | 618 | AI114652 | Hs.33757 | 3.00E-98 | 1 | HA1247 cDNA /gb=AI114652 /gi=6359997 /ug=Hs. |
| 594E7 | 2134 | 2320 | NM_012123 | Hs.33979 | 5.00E-93 | 1 | CGI-02 protein (CGI-02), mRNA /cds=(268,2124) |
| 110D1 | 1158 | 1349 | NM_018579 | Hs.34401 | 1.00E-105 | 1 | hypothetical protein PRO1278 (PRO1278), mRNA |
| 596A6 | 1950 | 2144 | NM_022766 | Hs.34516 | 1.00E-102 | 2 | hypothetical protein FLJ23239 (FLJ23239), mR |
| 37B10 | 237 | 563 | AI123826 | Hs.34549 | 1.00E-145 | 1 | ow61c10.x1 cDNA, 3' end /clone=IMAGE:1651314 |
| 458H4 | 3656 | 4415 | AB040929 | Hs.35089 | 0 | 1 | mRNA for KIAA1496 protein, partial cds /cds=(0 |
| 100D1 | 3563 | 3777 | D25215 | Hs.35804 | 1.00E-105 | 1 | KIAA0032 gene, complete cds /cds=(166,3318) |
| 519A12 | 402 | 623 | AW960004 | Hs.36475 | 3.00E-48 | 1 | EST372075 cDNA /gb=AW960004 /gi=8149688 /ug= |
| 498H2 | 11143 | 11490 | NM_000081 | Hs.36508 | 0 | 1 | Chediak-Higashi syndrome 1 (CHS1), mRNA /cds=(|
| 521D6 | 304 | 791 | NM_002712 | Hs.36587 | 0 | 2 | protein phosphatase 1, regulatory subunit 7 (|
| 460E1 | 1200 | 1542 | AF319476 | Hs.36752 | 0 | 2 | GKAP42 (FKSG21) mRNA, complete cds /cds=(174,1 |
| 184G9 | 498 | 1191 | AF082569 | Hs.36794 | 0 | 2 | D-type cyclin-interacting protein 1 (DIP1) mR |
| 462D3 | 493 | 1517 | NM_012142 | Hs.36794 | 0 | 3 | D-type cyclin-interacting protein 1 (DIP1), m |
| 74E12 | 659 | 3054 | D86956 | Hs.36927 | 0 | 23 | KIAA0201 gene, complete cds /cds=(347,2923) |
| 58G5 | 1268 | 2888 | NM_006644 | Hs.36927 | 0 | 12 | heat shock 105kD (HSP105B), mRNA /cds=(313,275 |
| 52C10 | 1479 | 2588 | AK022546 | Hs.37747 | 0 | 2 | FLJ12484 fis, clone NT2RM1001102, weakly |
| 479F9 | 2066 | 2322 | AL136932 | Hs.37892 | 1.00E-119 | 1 | mRNA; cDNA DKFZp586H1322 (from clone DKFZp586H |
| 483C2 | 2222 | 2723 | NM_003173 | Hs.37936 | 0 | 1 | suppressor of variegation 3-9 (Drosophila) ho |
| 593G6 | 673 | 1213 | NM_004510 | Hs.38125 | 0 | 1 | interferon-induced protein 75, 52kD (IFI75), |
| 101G12 | 118 | 436 | N39230 | Hs.38218 | 1.00E-173 | 1 | yy50c03.s1 cDNA, 3' end /clone=IMAGE:276964 / |
| 107E5 | 238 | 525 | AW188135 | Hs.38664 | 1.00E-158 | 1 | xj92g04.x1 cDNA, 3' end /clone=IMAGE:2664726 |
| 596F2 | 9 | 504 | BF892532 | Hs.38664 | 0 | 9 | IL0-MT0152-061100-501-e04 cDNA /gb=BF892532 |
| 469D7 | 47 | 474 | NM_014343 | Hs.38738 | 0 | 1 | claudin 15 (CLDN15), mRNA /cds=(254,940) /gb= |
| 166H8 | 1 | 81 | BF103848 | Hs.39457 | 9.00E-34 | 1 | 601647352F1 cDNA, 5' end /clone=IMAGE:3931452 |
| 465F3 | 157 | 296 | NM_017859 | Hs.39850 | 2.00E-47 | 1 | hypothetical protein FLJ20517 (FLJ20517), mR |
| 195C12 | 2684 | 2944 | NM_000885 | Hs.40034 | 1.00E-146 | 1 | integrin, alpha 4 (antigen CD49D, alpha 4 subu |
| 151F11 | 1393 | 1661 | AL031427 | Hs.40094 | 6.00E-81 | 1 | DNA sequence from clone 167A19 on chromosome 1p32.1-33 |
| 134C12 | 4532 | 4802 | NM_004973 | Hs.40154 | 1.00E-114 | 1 | jumonji (mouse) homolog (JMJI), mRNA /cds=(244, |
| 115C9 | 5279 | 5614 | AB033085 | Hs.40193 | 1.00E-157 | 1 | mRNA for KIAA1259 protein, partial cds /cds=(1 |
| 119A8 | 862 | 2087 | NM_006152 | Hs.40202 | 0 | 3 | lymphoid-restricted membrane protein (LRMP), |
| 104D4 | 924 | 1398 | U10485 | Hs.40202 | 0 | 2 | lymphoid-restricted membrane protein (Jaw1) mRNA, c |
| 155G3 | 226 | 530 | AF047472 | Hs.40323 | 1.00E-114 | 1 | spleen mitotic checkpoint BUB3 (BUB3) mRNA, c |
| 521C2 | 233 | 710 | NM_004725 | Hs.40323 | 0 | 1 | BUB3 (budding uninhibited by benzimidazoles 3 |
| 107B8 | 187 | 545 | AI927454 | Hs.40328 | 0 | 1 | wo90a02.x1 cDNA, 3' end /clone=IMAGE:2462570 |
| 458F10 | 1 | 436 | BE782824 | Hs.40334 | 0 | 1 | 601472323F1 cDNA, 5' end /clone=IMAGE:3875501 |
| 463G6 | 16 | 496 | AI266255 | Hs.40411 | 0 | 1 | qx69f01.x1 cDNA, 3' end /clone=IMAGE:2006617 |
| 162F1 | 2711 | 2895 | D87468 | Hs.40888 | 4.00E-96 | 1 | KIAA0278 gene, partial cds /cds=(0,1383) /gb |
| 463E1 | 70 | 272 | AL137067 | Hs.40919 | 1.00E-109 | 1 | DNA sequence from clone RP11-13B9 on chromosome 9q22. |
| 458E7 | 107 | 774 | AK024474 | Hs.41045 | 0 | 1 | mRNA for FLJ00067 protein, partial cds /cds=(1 |
| 185G12 | 1051 | 2315 | AL050141 | Hs.41569 | 1.00E-140 | 11 | mRNA; cDNA DKFZp586O031 (from clone DKFZp586O0 |
| 593F5 | 2106 | 2490 | NM_006190 | Hs.41694 | 0 | 1 | origin recognition complex, subunit 2 (yeast h |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|--|
| 513H4 | 739 | 1249 | NM_002190 | Hs.41724 | 0 | 6 | interleukin 17 (cytotoxic T-lymphocyte-assoc |
| 155F4 | 739 | 1247 | U32659 | Hs.41724 | 0 | 1 | IL-17 mRNA, complete cds /cds=(53,520) /gb=U32659 /g |
| 108H12 | 892 | 1227 | L40377 | Hs.41726 | 1.00E-170 | 1 | cytoplasmic antiproteinase 2 (CAP2) mRNA, com |
| 477E7 | 249 | 404 | BG033294 | Hs.41989 | 6.00E-75 | 1 | 602298548F1 cDNA, 5' end /clone=IMAGE:4393186 |
| 143E2 | 5775 | 6018 | AB033112 | Hs.42179 | 1.00E-136 | 2 | for KIAA1286 protein, partial cds /cds=(1 |
| 586B10 | 720 | 1225 | NM_001952 | Hs.42287 | 0 | 1 | E2F transcription factor 6 (E2F6), mRNA /cds=(|
| 583A10 | 346 | 883 | NM_012097 | Hs.42500 | 0 | 1 | ADP-ribosylation factor-like 5 (ARL5), mRNA |
| 459A7 | 152 | 251 | BC003525 | Hs.42712 | 2.00E-50 | 1 | Similar to Max, clone MGC:10775, mRNA, comple |
| 37B7 | 43 | 2687 | AF006082 | Hs.42915 | 1.00E-130 | 2 | actin-related protein Arp2 (ARP2) mRNA, compl |
| 120E3 | 512 | 2426 | NM_005722 | Hs.42915 | 0 | 3 | ARP2 (actin-related protein 2, yeast) homolog |
| 99D1 | 3298 | 3761 | NM_014939 | Hs.42959 | 0 | 1 | KIAA1012 protein (KIAA1012), mRNA /cds=(57,43 |
| 473B2 | 3025 | 3425 | AK023647 | Hs.43047 | 1.00E-164 | 1 | cDNA FLJ13585 fis, clone PLACE1009150 /cds=UNK |
| 460E6 | 2988 | 3184 | AB033093 | Hs.43141 | 1.00E-105 | 1 | mRNA for KIAA1267 protein, partial cds /cds=(9 |
| 471F7 | 232 | 575 | AW993524 | Hs.43148 | 0 | 1 | RC3-BN0034-120200-011-h06 cDNA /gb=AW993524 |
| 460B10 | 402 | 706 | BE781009 | Hs.43273 | 1.00E-78 | 1 | 601469768F1 cDNA, 5' end /clone=IMAGE:3872704 |
| 36F6 | 2815 | 3403 | AK024439 | Hs.43616 | 0 | 1 | for FLJ00029 protein, partial cds /cds=(0 |
| 471G3 | 43 | 454 | NM_006021 | Hs.43628 | 1.00E-165 | 1 | deleted in lymphocytic leukemia, 2 (DLEU2), mR |
| 184H3 | 1819 | 2128 | D14043 | Hs.43910 | 1.00E-168 | 2 | MGC-24, complete cds /cds=(79,648) /gb=D1404 |
| 195F4 | 511 | 2370 | NM_006016 | Hs.43910 | 0 | 7 | CD164 antigen, sialomucin (CD164), mRNA /cds= |
| 188H9 | 1573 | 2277 | NM_006346 | Hs.43913 | 0 | 3 | PIBF1 gene product (PIBF1), mRNA /cds=(0,2276) |
| 177H6 | 1575 | 2272 | Y09631 | Hs.43913 | 0 | 2 | PIBF1 protein, complete /cds=(0,2276) / |
| 481E6 | 2529 | 2873 | AB032952 | Hs.44087 | 1.00E-159 | 1 | mRNA for KIAA1126 protein, partial cds /cds=(0 |
| 112F5 | 1105 | 1701 | AF197569 | Hs.44143 | 0 | 1 | BAF180 (BAF180) mRNA, complete cds /cds=(96,48 |
| 146F5 | 2620 | 3147 | AL117452 | Hs.44155 | 0 | 1 | DKFZp586G1517 (from clone DKFZp586G |
| 514C5 | 166 | 431 | NM_018838 | Hs.44163 | 1.00E-149 | 3 | 13kDa differentiation-associated protein (L |
| 71D9 | 1117 | 1800 | AF263613 | Hs.44198 | 0 | 2 | membrane-associated calcium-independent ph |
| 68E1 | 289 | 527 | AA576946 | Hs.44242 | 4.00E-83 | 1 | nm82b03.s1 cDNA, 3' end /clone=IMAGE:1074701 |
| 53H12 | 1925 | 2112 | X75042 | Hs.44313 | 4.00E-84 | 1 | rel proto-oncogene mRNA /cds=(177,2036) /gb=X75 |
| 595D4 | 21 | 402 | NM_017867 | Hs.44344 | 0 | 1 | hypothetical protein FLJ20534 (FLJ20534), mR |
| 165B10 | 250 | 658 | BC000758 | Hs.44468 | 0 | 1 | clone MGC:2698, mRNA, complete cds /cds=(168, |
| 592E9 | 37 | 2422 | NM_002687 | Hs.44499 | 0 | 5 | pinin, desmosome associated protein (PNN), mR |
| 69F10 | 14 | 1152 | Y09703 | Hs.44499 | 0 | 3 | MEMA protein /cds=(406,2166) /gb=Y09703 |
| 458H6 | 1 | 352 | NM_015697 | Hs.44563 | 0 | 1 | hypothetical protein (CL640), mRNA /cds=(0,39 |
| 182C11 | 690 | 1324 | AB046861 | Hs.44566 | 0 | 4 | mRNA for KIAA1641 protein, partial cds /cds=(6 |
| 115G3 | 318 | 731 | BG288837 | Hs.44577 | 0 | 1 | 602388170F1 cDNA, 5' end /clone=IMAGE:4517129 |
| 70B11 | 1879 | 4363 | U58334 | Hs.44585 | 0 | 3 | Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mRNA |
| 165F10 | 265 | 496 | AV726117 | Hs.44656 | 6.00E-66 | 1 | AV726117 cDNA, 5' end /clone=HTCAXB05 /clone_ |
| 36F1 | 444 | 1176 | AK001332 | Hs.44672 | 0 | 1 | FLJ10470 fis, clone NT2RP2000032, weakly |
| 596H1 | 1073 | 2711 | AF288571 | Hs.44865 | 0 | 14 | lymphoid enhancer factor-1 (LEF1) mRNA, compl |
| 41C4 | 2876 | 3407 | X60708 | Hs.44926 | 0 | 1 | pCHDP7 mRNA for liver dipeptidyl peptidase IV /cds=(75 |
| 588A7 | 7564 | 7849 | AL031667 | Hs.45207 | 1.00E-158 | 1 | DNA sequence from clone RP4-620E11 on chromosome 20q1 |
| 183G6 | 3967 | 4942 | AB020630 | Hs.45719 | 0 | 5 | mRNA for KIAA0823 protein, partial cds /cds=(0 |
| 465C9 | 700 | 1325 | BC002796 | Hs.46446 | 0 | 1 | lymphoblastic leukemia derived sequence 1, |
| 464B1 | 1519 | 1997 | NM_006019 | Hs.46465 | 0 | 1 | T-cell, immune regulator 1 (TCIRG1), mRNA /cds |
| 466F10 | 455 | 518 | AW974756 | Hs.46476 | 6.00E-26 | 1 | EST386846 cDNA /gb=AW974756 /gi=8165944 /ug= |
| 110E7 | 620 | 1153 | AF223469 | Hs.46847 | 0 | 1 | AD022 protein (AD022) mRNA, complete cds /cds= |
| 112D5 | 618 | 1197 | NM_016614 | Hs.46847 | 0 | 4 | TRAF and TNF receptor-associated protein (AD0 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|--|
| 172G6 | 4157 | 4527 | NM_003954 | Hs.47007 | 0 | 1 | mitogen-activated protein kinase kinase kina |
| 177C8 | 4217 | 4469 | Y10256 | Hs.47007 | 1.00E-96 | 1 | serine/threonine protein kinase, NIK /c |
| 458H9 | 18 | 457 | AW291458 | Hs.47325 | 0 | 1 | UI-H-BI2-agh-c-02-0-UI.s1 cDNA, 3' end /clon |
| 62B6 | 562 | 697 | BE872760 | Hs.47334 | 7.00E-54 | 1 | 601450902F1 cDNA, 5' end /clone=IMAGE:3854544 |
| 178F12 | 169 | 2413 | AF307339 | Hs.47783 | 0 | 2 | B aggressive lymphoma short isoform (BAL) mRNA |
| 460G4 | 598 | 1081 | NM_005985 | Hs.48029 | 0 | 1 | snail 1 (drosophila homolog), zinc finger prot |
| 70D12 | 1 | 2038 | AK027070 | Hs.48320 | 0 | 13 | FLJ23417 fis, clone HEP20868 /cds=(59,12 |
| 41G5 | 6587 | 7128 | NM_014345 | Hs.48433 | 0 | 1 | endocrine regulator (HRIHFB2436), mRNA /cds= |
| 516H2 | 1 | 212 | NM_017948 | Hs.48712 | 2.00E-90 | 2 | hypothetical protein FLJ20736 (FLJ20736), mR |
| 517G9 | 665 | 1649 | NM_004462 | Hs.48876 | 0 | 2 | farnesyl-diphosphate farnesyltransferase 1 |
| 146A2 | 88 | 440 | X76770 | Hs.49007 | 0 | 1 | PAP /cds=UNKNOWN /gb=X76770 /gi=556782 /ug |
| 174H4 | 2612 | 3200 | AF189011 | Hs.49163 | 0 | 1 | ribonuclease III (RN3) mRNA, complete cds /cds |
| 121G3 | 463 | 829 | NM_017917 | Hs.49376 | 0 | 1 | hypothetical protein FLJ20644 (FLJ20644), mR |
| 170B9 | 2260 | 2948 | AK023825 | Hs.49391 | 0 | 1 | FLJ13763 fis, clone PLACE4000089 /cds=(56 |
| 65E2 | 629 | 1798 | AF062075 | Hs.49587 | 0 | 4 | leupaxin mRNA, complete cds /cds=(93,1253) /g |
| 518B2 | 26 | 1798 | NM_004811 | Hs.49587 | 0 | 12 | leupaxin (LPXN), mRNA /cds=(93,1253) /gb=NM_0 |
| 472E8 | 1182 | 1516 | AL390132 | Hs.49822 | 0 | 1 | mRNA; cDNA DKFZp547E107 (from clone DKFZp547E1 |
| 41B12 | 57 | 576 | AB000887 | Hs.50002 | 0 | 1 | for EBI1-ligand chemokine, complete cds |
| 41D1 | 1 | 310 | U86358 | Hs.50404 | 1.00E-135 | 1 | chemokine (TECK) mRNA, complete cds /cds=(0,452) /gb |
| 107C9 | 2861 | 3541 | M64174 | Hs.50651 | 0 | 3 | protein-tyrosine kinase (JAK1) mRNA, complete cds /c |
| 599H12 | 202 | 3541 | NM_002227 | Hs.50651 | 0 | 11 | Janus kinase 1 (a protein tyrosine kinase) (JAK |
| 105E3 | 621 | 1101 | AF047442 | Hs.50785 | 0 | 1 | vesicle trafficking protein sec22b mRNA, comp |
| 129B5 | 2489 | 2919 | X16354 | Hs.50964 | 0 | 2 | transmembrane carcinoembryonic antigen BGPa |
| 587H2 | 748 | 1673 | NM_000521 | Hs.51043 | 0 | 2 | hexosaminidase B (beta polypeptide) (HEXB), m |
| 458H12 | 4043 | 4561 | NM_000887 | Hs.51077 | 0 | 1 | integrin, alpha X (antigen CD11C (p150), alpha |
| 129C9 | 4055 | 4567 | Y00093 | Hs.51077 | 0 | 1 | leukocyte adhesion glycoprotein p150,95 |
| 125D8 | 2502 | 3966 | AF016266 | Hs.51233 | 0 | 3 | TRAIL receptor 2 mRNA, complete cds /cds=(117,1 |
| 179E1 | 17 | 343 | M22538 | Hs.51299 | 1.00E-179 | 1 | nuclear-encoded mitochondrial NADH-ubiquinone redu |
| 165D7 | 35 | 754 | NM_021074 | Hs.51299 | 0 | 4 | NADH dehydrogenase (ubiquinone) flavoprotein |
| 107F10 | 2632 | 2993 | Y11251 | Hs.51957 | 0 | 2 | novel member of serine-arginine domain p |
| 195B12 | 1344 | 1590 | NM_017903 | Hs.52184 | 3.00E-96 | 1 | hypothetical protein FLJ20618 (FLJ20618), mR |
| 69D7 | 3046 | 3568 | AB014569 | Hs.52526 | 0 | 4 | for KIAA0669 protein, complete cds /cds=(|
| 55D1 | 2607 | 2847 | NM_014779 | Hs.52526 | 1.00E-130 | 1 | KIAA0669 gene product (KIAA0669), mRNA /cds=(|
| 480B8 | 1943 | 2062 | AL080213 | Hs.52792 | 8.00E-44 | 1 | mRNA; cDNA DKFZp586I1823 (from clone DKFZp586I |
| 72G7 | 1236 | 1348 | NM_018607 | Hs.52891 | 2.00E-55 | 1 | hypothetical protein PRO1853 (PRO1853), mRNA |
| 526D1 | 1 | 256 | NM_004597 | Hs.53125 | 1.00E-114 | 1 | small nuclear ribonucleoprotein D2 polypeptid |
| 458E8 | 1182 | 1701 | NM_002621 | Hs.53155 | 0 | 1 | properdin P factor, complement (PFC), mRNA /cd |
| 458G2 | 2171 | 2836 | NM_001204 | Hs.53250 | 0 | 1 | bone morphogenetic protein receptor, type II |
| 458F7 | 30 | 650 | NM_002200 | Hs.54434 | 0 | 1 | interferon regulatory factor 5 (IRF5), mRNA / |
| 459F12 | 2023 | 3325 | NM_006060 | Hs.54452 | 0 | 2 | zinc finger protein, subfamily 1A, 1 (Ikaro) (|
| 41A6 | 498 | 755 | U46573 | Hs.54460 | 1.00E-140 | 1 | eotaxin precursor mRNA, complete cds /cds=(53,346) / |
| 590A10 | 243 | 659 | NM_004688 | Hs.54483 | 0 | 2 | N-myc (and STAT) interactor (NMI), mRNA /cds=(|
| 461C11 | 872 | 1415 | NM_014291 | Hs.54609 | 0 | 1 | glycine C-acetyltransferase (2-amino-3-keto |
| 170H5 | 412 | 1630 | AJ243721 | Hs.54642 | 0 | 3 | for dTDP-4-keto-6-deoxy-D-glucose 4-re |
| 521F5 | 270 | 1491 | NM_013283 | Hs.54642 | 0 | 8 | methionine adenosyltransferase II, beta (MAT |
| 189H5 | 737 | 1049 | X76302 | Hs.54649 | 1.00E-131 | 2 | H.sapiens RY-1 mRNA for putative nucleic acid binding protei |
| 599D10 | 2614 | 3035 | AB029015 | Hs.54886 | 0 | 5 | mRNA for KIAA1092 protein, partial cds /cds=(0 |
| 458D5 | 1026 | 1676 | AK027243 | Hs.54890 | 0 | 1 | cDNA: FLJ23590 fis, clone LNG14491 /cds=(709,1 |
| 37A10 | 1633 | 2040 | AK026024 | Hs.55024 | 0 | 1 | FLJ22371 fis, clone HRC06680 /cds=(77,12 |
| 121A8 | 799 | 1217 | NM_018053 | Hs.55024 | 1.00E-160 | 1 | hypothetical protein FLJ10307 (FLJ10307), mR |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|-------|-------|-----------|----------|-----------|----|---|
| 460B1 | 11195 | 11326 | AF231023 | Hs.55173 | 1.00E-45 | 1 | protocadherin Flamingo 1 (FMI1) mRNA, complete |
| 57F1 | 1450 | 2070 | NM_003447 | Hs.55481 | 0 | 2 | zinc finger protein 165 (ZNF165), mRNA /cds=(5 |
| 68D10 | 979 | 2070 | U78722 | Hs.55481 | 0 | 4 | zinc finger protein 165 (Zpf165) mRNA, complete |
| 584G7 | 268 | 1674 | NM_003753 | Hs.55682 | 0 | 4 | eukaryotic translation initiation factor 3, |
| 161C8 | 63 | 394 | NM_017897 | Hs.55781 | 1.00E-177 | 1 | hypothetical protein FLJ20604 (FLJ20604), mR |
| 588F6 | 1 | 387 | NM_016497 | Hs.55847 | 0 | 1 | hypothetical protein (LOC51258), mRNA /cds=(|
| 597E10 | 334 | 2073 | NM_004446 | Hs.55921 | 0 | 5 | glutamyl-prolyl-tRNA synthetase (EPRS), mRN |
| 138H10 | 3603 | 4112 | X54326 | Hs.55921 | 0 | 1 | glutamyl-tRNA synthetase /cds=(58,43 |
| 121D5 | 3959 | 4192 | AB018348 | Hs.55947 | 1.00E-130 | 1 | mRNA for KIAA0805 protein, partial cds /cds=(0 |
| 473D12 | 1428 | 1866 | AJ245539 | Hs.55968 | 0 | 2 | partial mRNA for GalNAc-T5 (GALNT5 gene) /cds= |
| 71E3 | 843 | 1724 | NM_005542 | Hs.56205 | 0 | 30 | insulin induced gene 1 (INSIG1), mRNA /cds=(414 |
| 73F4 | 843 | 2495 | U96876 | Hs.56205 | 0 | 32 | insulin induced protein 1 (INSIG1) gene, compl |
| 75C8 | 180 | 2439 | AJ277832 | Hs.56247 | 0 | 13 | for inducible T-cell co-stimulator (ICOS |
| 187A6 | 2073 | 2255 | AF195530 | Hs.56542 | 2.00E-99 | 1 | soluble aminopeptidase P (XPNPEP1) mRNA, comp |
| 584H5 | 1496 | 1889 | NM_001494 | Hs.56845 | 1.00E-151 | 1 | GDP dissociation inhibitor 2 (GDI2), mRNA /cds |
| 460C5 | 2395 | 2860 | AK022936 | Hs.56847 | 0 | 1 | cDNA FLJ12874 fis, clone NT2RP2003769 /cds=UNK |
| 460B5 | 164 | 741 | BC003581 | Hs.56851 | 0 | 1 | Similar to RIKEN cDNA 2900073H19 gene, clone |
| 54G4 | 1359 | 1761 | AK027232 | Hs.57209 | 0 | 2 | FLJ23579 fis, clone LNG13017 /cds=UNKNOWN |
| 192D8 | 1576 | 2872 | AL136703 | Hs.57209 | 0 | 3 | mRNA; cDNA DKFZp566J091 (from clone |
| 66F9 | 618 | 1056 | U41654 | Hs.57304 | 0 | 1 | DKFZp566J0 |
| 183A1 | 2093 | 2334 | NM_003751 | Hs.57783 | 1.00E-132 | 1 | adenovirus protein E3-14.7k interacting protein 1 (|
| 117B3 | 6933 | 7225 | NM_022898 | Hs.57987 | 1.00E-154 | 3 | eukaryotic translation initiation factor 3, |
| 74C11 | 273 | 359 | BE739287 | Hs.58066 | 7.00E-21 | 1 | B-cell lymphoma/leukaemia 11B (BCL11B), mRNA |
| 174H2 | 5591 | 5977 | AJ131693 | Hs.58103 | 0 | 1 | 601556492F1 cDNA, 5' end /clone=IMAGE:3826247 |
| 599H8 | 26 | 993 | NM_003756 | Hs.58189 | 0 | 3 | mRNA for AKAP450 protein /cds=(222,11948) /gb |
| 168F12 | 295 | 593 | U54559 | Hs.58189 | 1.00E-166 | 1 | eukaryotic translation initiation factor 3, |
| 68B11 | 1 | 297 | BE867841 | Hs.58297 | 1.00E-146 | 1 | translation initiation factor eIF3 p40 subuni |
| 104A6 | 376 | 2578 | AF001862 | Hs.58435 | 0 | 3 | 601443614F1 cDNA, 5' end /clone=IMAGE:3847827 |
| 192E3 | 230 | 648 | NM_001465 | Hs.58435 | 0 | 4 | FYN binding protein mRNA, complete cds /cds=(67 |
| 73B4 | 1287 | 1763 | AK022834 | Hs.58488 | 0 | 1 | FYN-binding protein (FYN-120/130) (FYN), mRN |
| 100G3 | 1568 | 1786 | NM_004850 | Hs.58617 | 1.00E-108 | 1 | FLJ12772 fis, clone NT2RP2001634, highly |
| 116G9 | 1997 | 2464 | NM_013352 | Hs.58636 | 0 | 1 | Rho-associated, coiled-coil containing prot |
| 178C6 | 5 | 710 | AV760147 | Hs.58643 | 1.00E-111 | 5 | squamous cell carcinoma antigen recognized by |
| 519B1 | 2203 | 2320 | NM_014207 | Hs.58685 | 1.00E-56 | 1 | AV760147 cDNA, 5' end /clone=MDSEP12 /clone_ |
| 40B6 | 1655 | 2283 | X04391 | Hs.58685 | 0 | 1 | CD5 antigen (p56-62) (CD5), mRNA /cds=(72,1559 |
| 466B9 | 262 | 534 | AI684437 | Hs.58774 | 1.00E-107 | 1 | lymphocyte glycoprotein T1/Leu-1 /cds=(72,1 |
| 480H7 | 86 | 234 | NM_006568 | Hs.59106 | 1.00E-54 | 1 | wa82a04.x1 cDNA, 3' end /clone=IMAGE:2302638 |
| 44A7 | 2229 | 2703 | X17094 | Hs.59242 | 0 | 1 | cell growth regulatory with ring finger domain |
| 106D12 | 21 | 380 | M96982 | Hs.59271 | 0 | 2 | fur mRNA for furin /cds=(216,2600) /gb=X17094 |
| 39C5 | 1821 | 2653 | AB011098 | Hs.59403 | 0 | 1 | /gi=314 |
| 185H7 | 1826 | 2352 | NM_004863 | Hs.59403 | 0 | 1 | U2 snRNP auxiliary factor small subunit, compl |
| 459C5 | 126 | 443 | AA889552 | Hs.59459 | 1.00E-158 | 1 | for KIAA0526 protein, complete cds /cds=(|
| 108B8 | 2760 | 3079 | AJ132592 | Hs.59757 | 1.00E-138 | 1 | serine palmitoyltransferase, long chain base |
| 194F7 | 2074 | 2461 | NM_018227 | Hs.59838 | 0 | 1 | ak20d12.s1 cDNA, 3' end /clone=IMAGE:1406519 |
| 465D4 | 2 | 132 | AI440512 | Hs.59844 | 7.00E-67 | 1 | for zinc finger protein, 3115 /cds=(107,27 |
| 161H10 | 1 | 381 | AA004799 | Hs.60088 | 1.00E-169 | 1 | hypothetical protein FLJ10808 (FLJ10808), mR |
| 465B6 | 228 | 383 | NM_018986 | Hs.61053 | 1.00E-66 | 1 | tc83f09.x1 cDNA, 3' end /clone=IMAGE:2072777 |
| 102G9 | 359 | 725 | D11094 | Hs.61153 | 0 | 1 | zh96b05.s1 cDNA, 3' end /clone=IMAGE:429105 / |
| 193C6 | 359 | 725 | NM_002803 | Hs.61153 | 1.00E-174 | 2 | hypothetical protein (FLJ20356), mRNA /cds=(|
| 99E7 | 1768 | 2339 | AL023653 | Hs.61469 | 0 | 10 | MSS1, complete cds /cds=(66,1367) /gb=D11094 |
| 462B9 | 5 | 411 | BE779284 | Hs.61472 | 1.00E-152 | 1 | proteasome (prosome, macropain) 26S subunit, |
| 594F11 | 220 | 569 | NM_003905 | Hs.61828 | 1.00E-159 | 2 | DNA sequence from clone 753P9 on chromosome |
| | | | | | | | Xq25-26.1. |
| | | | | | | | 601464557F1 cDNA, 5' end /clone=IMAGE:3867566 |
| | | | | | | | amyloid beta precursor protein-binding prote |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|---|
| 102E7 | 1216 | 1921 | AF046001 | Hs.62112 | 0 | 3 | zinc finger transcription factor (ZNF207) mRNA |
| 192B4 | 754 | 934 | NM_003457 | Hs.62112 | 2.00E-98 | 2 | zinc finger protein 207 (ZNF207), mRNA /cds=(2 |
| 41G9 | 1664 | 2096 | J02931 | Hs.62192 | 0 | 1 | placental tissue factor (two forms) mRNA, complete cd |
| 482E12 | 1857 | 2149 | NM_001993 | Hs.62192 | 5.00E-87 | 1 | coagulation factor III (thromboplastin, tiss |
| 459C10 | 1548 | 1845 | AB011114 | Hs.62209 | 1.00E-166 | 1 | mRNA for KIAA0542 protein, partial cds /cds=(39 |
| 114D6 | 2251 | 2712 | NM_002053 | Hs.62661 | 0 | 1 | guanylate binding protein 1, interferon-induc |
| 590C9 | 83 | 760 | NM_002032 | Hs.62954 | 0 | 43 | ferritin, heavy polypeptide 1 (FTH1), mRNA /c |
| 458C5 | 1798 | 2407 | AB033118 | Hs.63128 | 0 | 1 | mRNA for KIAA1292 protein, partial cds /cds=(0 |
| 109E5 | 4661 | 5114 | AB002369 | Hs.63302 | 0 | 1 | KIAA0371 gene, complete cds /cds=(247,3843) |
| 589G9 | 250 | 5650 | NM_021090 | Hs.63302 | 0 | 6 | myotubularin related protein 3 (MTMR3), mRNA |
| 182E4 | 1751 | 2144 | NM_002831 | Hs.63489 | 0 | 1 | protein tyrosine phosphatase, non-receptor t |
| 589C8 | 1787 | 2222 | AK023529 | Hs.63525 | 0 | 2 | cDNA FLJ13467 fis, clone PLACE1003519, highly |
| 458D7 | 1595 | 1912 | NM_022727 | Hs.63609 | 1.00E-180 | 1 | HpaII tiny fragments locus 9C (HTF9C), mRNA /c |
| 193A2 | 144 | 2588 | NM_003264 | Hs.63668 | 0 | 5 | toll-like receptor 2 (TLR2), mRNA /cds=(129,24 |
| 117C3 | 1504 | 2366 | AF131762 | Hs.64001 | 0 | 3 | clone 25218 mRNA sequence /cds=UNKNOWN /gb=AF |
| 109F1 | 568 | 2157 | AL031602 | Hs.64239 | 0 | 3 | DNA sequence from clone RP5-1174N9 on chromosome 1p34 |
| 40D5 | 698 | 1192 | U32324 | Hs.64310 | 0 | 1 | interleukin-11 receptor alpha chain mRNA, complete c |
| 522F4 | 12 | 504 | NM_006356 | Hs.64593 | 0 | 1 | ATP synthase, H ⁺ transporting, mitochondrial |
| 462E9 | 215 | 891 | NM_015423 | Hs.64595 | 0 | 1 | aminoadipate-semialdehyde dehydrogenase-ph |
| 164G10 | 37 | 889 | NM_006851 | Hs.64639 | 0 | 2 | glioma pathogenesis-related protein (RTVP1), |
| 155G10 | 1 | 601 | U16307 | Hs.64639 | 0 | 1 | glioma pathogenesis-related protein (GliPR) mRNA, c |
| 110D11 | 341 | 712 | S60099 | Hs.64797 | 0 | 1 | APPH=amyloid precursor protein homolog [human, placenta, |
| 513E8 | 3411 | 3986 | AF148537 | Hs.65450 | 0 | 7 | reticulin 4a mRNA, complete cds /cds=(141,3719 |
| 460F4 | 1415 | 1749 | NM_018174 | Hs.66048 | 1.00E-163 | 1 | hypothetical protein FLJ10669 (FLJ10669), mR |
| 478H8 | 486 | 1037 | NM_001775 | Hs.66052 | 0 | 1 | CD38 antigen (p45) (CD38), mRNA /cds=(69,971) |
| 461A6 | 2977 | 3516 | AB051540 | Hs.66053 | 0 | 1 | mRNA for KIAA1753 protein, partial cds /cds=(0 |
| 191E7 | 1 | 494 | AL157438 | Hs.66151 | 0 | 6 | mRNA; cDNA DKFZp434A115 (from clone DKFZp434A1 |
| 464B6 | 76 | 623 | NM_002528 | Hs.66196 | 0 | 1 | nth (E.coli endonuclease III)-like 1 (NTHL1), |
| 473C6 | 149 | 517 | BE673759 | Hs.66357 | 0 | 1 | 7d69d02.x1 cDNA, 3' end /clone=IMAGE:3278211 |
| 171G11 | 1001 | 1385 | Z98884 | Hs.66708 | 0 | 1 | DNA sequence from clone RP3-467L1 on chromosome 1p36. |
| 169H3 | 15 | 1800 | X82200 | Hs.68054 | 0 | 4 | Staf50 /cds=(122,1450) /gb=X82200 /gi=8992 |
| 167G9 | 747 | 1104 | NM_005932 | Hs.68583 | 1.00E-101 | 1 | mitochondrial intermediate peptidase (MIPEP) |
| 170H3 | 747 | 1104 | U80034 | Hs.68583 | 6.00E-99 | 1 | mitochondrial intermediate peptidase precurs |
| 69F9 | 321 | 1348 | U78027 | Hs.69089 | 0 | 5 | Bruton's tyrosine kinase (BTK), alpha-D-galac |
| 586D6 | 16 | 676 | NM_006360 | Hs.69469 | 1.00E-173 | 2 | dendritic cell protein (GA17), mRNA /cds=(51,1 |
| 591E3 | 74 | 189 | NM_002385 | Hs.69547 | 2.00E-59 | 1 | myelin basic protein (MBP), mRNA /cds=(10,570) |
| 597H2 | 482 | 2702 | NM_007158 | Hs.69855 | 0 | 8 | NRAS-related gene (D1S155E), mRNA /cds=(420,2 |
| 515C5 | 3257 | 3421 | NM_003169 | Hs.70186 | 8.00E-45 | 1 | suppressor of Ty (S.cerevisiae) 5 homolog (SUP |
| 461B9 | 44 | 425 | H06786 | Hs.70258 | 0 | 1 | yl83g05.r1 cDNA, 5' end /clone=IMAGE:44737 /c |
| 525H4 | 2834 | 2978 | NM_014933 | Hs.70266 | 4.00E-77 | 1 | yeast Sec31p homolog (KIAA0905), mRNA /cds=(53 |
| 521C3 | 1 | 1165 | NM_016628 | Hs.70333 | 1.00E-176 | 2 | hypothetical protein (LOC51322), mRNA /cds=(|
| 460E5 | 414 | 994 | AF138903 | Hs.70337 | 0 | 1 | immunoglobulin superfamily protein beta-like |
| 190C7 | 1406 | 1788 | D50926 | Hs.70359 | 0 | 1 | mRNA for KIAA0136 gene, partial cds /cds=(0,2854) /gb |
| 497F10 | 653 | 1096 | NM_014210 | Hs.70499 | 0 | 3 | ecotropic viral integration site 2A (EVI2A), m |
| 37C11 | 820 | 1523 | AB002368 | Hs.70500 | 0 | 4 | KIAA0370 gene, partial cds /cds=(0,2406) /gb |
| 464B2 | 496 | 721 | BG283002 | Hs.71243 | 3.00E-99 | 1 | 602406192F1 cDNA, 5' end /clone=IMAGE:4518214 |
| 69G4 | 1292 | 2708 | AL161991 | Hs.71252 | 0 | 4 | cDNA DKFZp761C169 (from clone DKFZp761C1 |
| 485E4 | 176 | 485 | AA131524 | Hs.71433 | 1.00E-151 | 1 | zl31h02.s1 cDNA, 3' end /clone=IMAGE:503571 / |
| 161G2 | 1338 | 1877 | NM_003129 | Hs.71465 | 0 | 1 | squalene epoxidase (SQLE), mRNA /cds=(214,193 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|---------------|----|---|
| 188D6 | 328 | 597 | NM_016630 | Hs.71475 | 1.00E-129 | 1 | hypothetical protein (LOC51324), mRNA /cds=(|
| 483B5 | 12 | 384 | NM_021128 | Hs.71618 | 0 | 1 | polymerase (RNA) II (DNA directed) polypeptide |
| 161F6 | 675 | 1114 | U79277 | Hs.71848 | 0 | 1 | clone 23548 mRNA sequence /cds=UNKNOWN |
| | | | | | /gb=U79277 /g | | |
| 473F8 | 377 | 729 | BE889075 | Hs.71941 | 1.00E-146 | 1 | 601513514F1 cDNA, 5' end /clone=IMAGE:3915003 |
| 102A6 | 1129 | 1560 | AK023183 | Hs.72782 | 0 | 1 | FLJ13121 fis, clone NT2RP3002687 /cds=(39 |
| 41E2 | 56 | 539 | M57506 | Hs.72918 | 0 | 1 | secreted protein (I-309) gene, complete cds /cds=(72, |
| 476E12 | 1790 | 2311 | S76638 | Hs.73090 | 0 | 2 | p50-NF-kappa B homolog [human, peripheral blood T |
| | | | | | | | cells, mR |
| 41G7 | 3116 | 3469 | U64198 | Hs.73165 | 1.00E-173 | 1 | IL-12 receptor beta2 mRNA, complete cds |
| | | | | | | | /cds=(640,322 |
| 51C9 | 1721 | 2339 | NM_005263 | Hs.73172 | 0 | 4 | growth factor independent 1 (GFI1), mRNA /cds= |
| 67H6 | 1723 | 2342 | U67369 | Hs.73172 | 0 | 1 | growth factor independence-1 (Gfi-1) mRNA, complete |
| 179E7 | 211 | 610 | M92444 | Hs.73722 | 0 | 1 | apurinic/aprimidinic endonuclease (HAP1) g |
| 585G3 | 174 | 589 | NM_001641 | Hs.73722 | 0 | 8 | APEX nuclease (multifunctional DNA repair enz |
| 138A11 | 1360 | 1717 | M72709 | Hs.73737 | 1.00E-151 | 1 | alternative splicing factor mRNA, complete cds /cds= |
| 49C8 | 1628 | 2276 | AK001313 | Hs.73742 | 0 | 4 | cDNA FLJ10451 fis, clone NT2RP1000959, highly |
| 41D7 | 2760 | 3563 | J03565 | Hs.73792 | 0 | 1 | Epstein-Barr virus complement receptor type II(cr2) |
| 121F8 | 2470 | 2815 | AL136131 | Hs.73793 | 1.00E-123 | 1 | DNA sequence from clone RP1-261G23 on |
| | | | | | | | chromosome 6p12 |
| 482C7 | 2864 | 3199 | NM_003005 | Hs.73800 | 1.00E-165 | 3 | selectin P (granule membrane protein 140kD, an |
| 153E12 | 160 | 778 | D90144 | Hs.73817 | 0 | 22 | gene for LD78 alpha precursor, complete cds /c |
| 489E12 | 161 | 776 | NM_002983 | Hs.73817 | 0 | 6 | small inducible cytokine A3 (homologous to mo |
| 177D7 | 112 | 388 | BF673951 | Hs.73818 | 1.00E-143 | 1 | 602137331F1 cDNA, 5' end /clone=IMAGE:4274094 |
| 587E10 | 5 | 387 | NM_006004 | Hs.73818 | 1.00E-155 | 6 | ubiquinol-cytochrome c reductase hinge prote |
| 142H11 | 119 | 436 | AL110183 | Hs.73851 | 1.00E-148 | 1 | cDNA DKFZp566A221 (from clone DKFZp566A2 |
| 190G11 | 1 | 375 | NM_001685 | Hs.73851 | 0 | 6 | ATP synthase, H+ transporting, mitochondrial |
| 119D10 | 675 | 1700 | BC001267 | Hs.73957 | 0 | 4 | RAB5A, member RAS oncogene family, clone MGC: |
| 135H12 | 1244 | 1772 | NM_003016 | Hs.73965 | 0 | 2 | splicing factor, arginine/serine-rich 2 (SFR |
| 160E6 | 1811 | 2196 | X75755 | Hs.73965 | 0 | 5 | PR264 gene /cds=(98,763) /gb=X75755 /gi=455418 |
| 175F9 | 791 | 1446 | L29218 | Hs.73986 | 0 | 2 | clk2 mRNA, complete cds /cds=(129,1628) /gb=L2 |
| 516D9 | 782 | 1144 | NM_003992 | Hs.73987 | 0 | 1 | CDC-like kinase 3 (CLK3), transcript variant p |
| 469F3 | 1778 | 1956 | NM_002286 | Hs.74011 | 4.00E-78 | 1 | lymphocyte-activation gene 3 (LAG3), mRNA /cd |
| 481D6 | 1323 | 1805 | Z22970 | Hs.74076 | 1.00E-173 | 1 | H.sapiens mRNA for M130 antigen cytoplasmic variant |
| | | | | | | | 2 /cds=(|
| 193H9 | 813 | 1569 | NM_007360 | Hs.74085 | 1.00E-127 | 3 | DNA segment on chromosome 12 (unique) 2489 expr |
| 39D9 | 810 | 994 | X54870 | Hs.74085 | 1.00E-100 | 1 | NKG2-D gene /cds=(338,988) /gb=X54870 /gi=3 |
| 71F3 | 3014 | 3858 | NM_004430 | Hs.74088 | 1.00E-114 | 4 | early growth response 3 (EGR3), mRNA /cds=(357, |
| 74B12 | 3651 | 4214 | S40832 | Hs.74088 | 1.00E-114 | 7 | EGR3=EGR3 protein mRNA, |
| 105E11 | 2 | 142 | AL050391 | Hs.74122 | 6.00E-72 | 2 | cDNA DKFZp586A181 (from clone DKFZp586A1 |
| 174A12 | 141 | 1072 | NM_001225 | Hs.74122 | 0 | 9 | caspase 4, apoptosis-related cysteine protea |
| 599E9 | 351 | 1864 | AF279903 | Hs.74267 | 0 | 6 | 60S ribosomal protein L15 (EC45) mRNA, complet |
| 74F7 | 126 | 1867 | AF283772 | Hs.74267 | 0 | 8 | clone TCBAPO781 mRNA sequence /cds=(40,654) / |
| 156G12 | 554 | 831 | AF034607 | Hs.74276 | 1.00E-156 | 1 | chloride channel ABP mRNA, complete cds /cds=(|
| 118F4 | 1 | 148 | BG112085 | Hs.74313 | 7.00E-65 | 2 | 602283260F1 cDNA, 5' end /clone=IMAGE:4370727 |
| 70G10 | 1 | 2177 | M16660 | Hs.74335 | 0 | 26 | 90-kDa heat-shock protein gene, cDNA, complete cds |
| | | | | | | | /c |
| 64D1 | 330 | 2219 | NM_007355 | Hs.74335 | 0 | 26 | heat shock 90kD protein 1, beta (HSPCB), mRNA / |
| 121E12 | 700 | 1033 | NM_006826 | Hs.74405 | 0 | 1 | tyrosine 3-monooxygenase/tryptophan 5-monoo |
| 177D3 | 480 | 1645 | X57347 | Hs.74405 | 0 | 2 | HS1 protein /cds=(100,837) /gb=X57347 / |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|---|
| 155A5 | 680 | 1176 | U86602 | Hs.74407 | 0 | 1 | nucleolar protein p40 mRNA, complete cds /cds=(142,10 |
| 181G10 | 1802 | 2302 | NM_012381 | Hs.74420 | 0 | 2 | origin recognition complex, subunit 3 (yeast h |
| 66D8 | 927 | 1490 | X86691 | Hs.74441 | 0 | 1 | 218kD Mi-2 protein /cds=(89,5827) /gb=X |
| 189D10 | 383 | 1102 | NM_001749 | Hs.74451 | 0 | 7 | calpain 4, small subunit (30K) (CAPN4), mRNA / |
| 171A3 | 721 | 1092 | X04106 | Hs.74451 | 1.00E-174 | 1 | calcium dependent protease (small subunit) / |
| 173F3 | 1069 | 1468 | NM_004559 | Hs.74497 | 0 | 1 | nuclease sensitive element binding protein 1 |
| 176B7 | 1592 | 1990 | NM_001178 | Hs.74515 | 0 | 1 | aryl hydrocarbon receptor nuclear translocato |
| 481A11 | 2012 | 2210 | NM_000947 | Hs.74519 | 2.00E-61 | 1 | primase, polypeptide 2A (58kD) (PRIM2A), mRNA |
| 116G8 | 689 | 1417 | NM_002537 | Hs.74563 | 0 | 4 | ornithine decarboxylase antizyme 2 (OAZ2), mR |
| 526F6 | 185 | 1088 | NM_003145 | Hs.74564 | 0 | 3 | signal sequence receptor, beta (translocon-as |
| 104D3 | 713 | 1127 | X79353 | Hs.74576 | 0 | 1 | XAP-4 mRNA for GDP-dissociation inhibitor /cds=(|
| 518G1 | 2725 | 2993 | NM_001357 | Hs.74578 | 1.00E-134 | 1 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide |
| 459H1 | 3093 | 3268 | NM_014767 | Hs.74583 | 3.00E-67 | 1 | KIAA0275 gene product (KIAA0275), mRNA /cds=(|
| 69C5 | 2304 | 2781 | M97287 | Hs.74592 | 0 | 3 | MAR/SAR DNA binding protein (SATB1) mRNA |
| 587F12 | 930 | 2777 | NM_002971 | Hs.74592 | 0 | 6 | special AT-rich sequence binding protein 1 (b |
| 124H10 | 1240 | 1812 | NM_002808 | Hs.74619 | 0 | 2 | proteasome (prosome, macropain) 26S subunit, |
| 57F10 | 700 | 2310 | NM_000311 | Hs.74621 | 0 | 60 | prion protein (p27-30) (Creutzfeld-Jakob dis |
| 74A10 | 870 | 2252 | U29185 | Hs.74621 | 0 | 34 | prion protein (PrP) gene, complete cds /cds=(24 |
| 176H10 | 465 | 923 | NM_000108 | Hs.74635 | 0 | 1 | dihydrolipoamide dehydrogenase (E3 component |
| 98F4 | 870 | 2566 | NM_003217 | Hs.74637 | 0 | 7 | testis enhanced gene transcript (TEGT), mRNA |
| 179H8 | 1 | 1210 | X75861 | Hs.74637 | 0 | 3 | TEGT gene /cds=(40,753) /gb=X75861 /gi=456258 / |
| 125C4 | 417 | 1425 | NM_014280 | Hs.74711 | 0 | 2 | splicing factor similar to dnaJ (SPF31), mRNA |
| 74C5 | 21 | 177 | BE549137 | Hs.74861 | 4.00E-65 | 1 | 601076443F1 cDNA, 5' end /clone=IMAGE:3462154 |
| 497B12 | 124 | 384 | NM_006713 | Hs.74861 | 1.00E-123 | 2 | activated RNA polymerase II transcription cof |
| 191E10 | 497 | 859 | NM_022451 | Hs.74899 | 0 | 1 | hypothetical protein FLJ12820 (FLJ12820), mR |
| 114A3 | 1032 | 1446 | AY007131 | Hs.75061 | 0 | 1 | clone CDABP0045 mRNA sequence |
| 117G3 | 279 | 799 | NM_004622 | Hs.75066 | 0 | 1 | translin (TSN), mRNA /cds=(81,767) /gb=Nm_004 |
| 483G2 | 3293 | 3639 | NM_006148 | Hs.75080 | 1.00E-180 | 1 | LIM and SH3 protein 1 (LASP1), /cds=(75,860) /g |
| 181E11 | 8314 | 8804 | NM_000038 | Hs.75081 | 0 | 1 | adenomatous polyposis coli (APC), mRNA /cds= |
| 597G6 | 374 | 2361 | NM_003406 | Hs.75103 | 0 | 6 | tyrosine 3-monooxygenase/tryptophan 5-monoo |
| 596F11 | 684 | 1088 | NM_002097 | Hs.75113 | 0 | 1 | general transcription factor IIIA (GTF3A), mR |
| 69C9 | 995 | 1564 | AF113702 | Hs.75117 | 0 | 4 | clone FLC1353 PRO3063 mRNA, complete cds /cds= |
| 46E7 | 128 | 1519 | NM_004515 | Hs.75117 | 1.00E-164 | 2 | interleukin enhancer binding factor 2, 45kD (|
| 481B10 | 66 | 515 | NM_003201 | Hs.75133 | 0 | 1 | transcription factor 6-like 1 (mitochondrial |
| 469C5 | 368 | 969 | NM_006708 | Hs.75207 | 0 | 1 | glyoxalase I (GLO1), mRNA /cds=(87,641) /gb=N |
| 71B4 | 939 | 2049 | NM_002539 | Hs.75212 | 0 | 24 | ornithine decarboxylase 1 (ODC1) mRNA /cds=(33 |
| 75E10 | 173 | 1991 | X16277 | Hs.75212 | 0 | 51 | ornithine decarboxylase ODC (EC 4.1.1.17) /c |
| 166G9 | 2077 | 2632 | L36870 | Hs.75217 | 0 | 1 | MAP kinase kinase 4 (MKK4) mRNA, complete cds / |
| 167A12 | 2074 | 2619 | NM_003010 | Hs.75217 | 0 | 1 | mitogen-activated protein kinase kinase 4 (M |
| 105B12 | 3030 | 5207 | D67029 | Hs.75232 | 0 | 3 | SEC14L mRNA, complete cds |
| 125D1 | 4782 | 5209 | NM_003003 | Hs.75232 | 0 | 1 | SEC14 (S. cerevisiae)-like 1 (SEC14L1), mRNA |
| 184E4 | 2075 | 3174 | D42040 | Hs.75243 | 0 | 5 | KIAA9001 gene, complete cds /cds=(1701,4106) |
| 191E5 | 2071 | 3174 | NM_005104 | Hs.75243 | 0 | 2 | bromodomain-containing 2 (BRD2), mRNA /cds=(1 |
| 186C12 | 4159 | 4866 | NM_001068 | Hs.75248 | 0 | 6 | topoisomerase (DNA) II beta (180kD) (TOP2B), m |
| 177C9 | 4473 | 4866 | X68060 | Hs.75248 | 0 | 1 | topIIb mRNA for topoisomerase IIb /cds=(0,4865) |
| 39D8 | 743 | 1980 | D31885 | Hs.75249 | 0 | 6 | KIAA0069 gene, partial cds /cds=(0,680) /gb= |
| 127G2 | 1363 | 1769 | NM_016166 | Hs.75251 | 0 | 1 | DEAD/H (Asp-Glu-Ala-Asp/His) box binding pro |
| 64E5 | 4 | 1214 | NM_002922 | Hs.75256 | 0 | 6 | regulator of G-protein signalling 1 (RGS1), mR |
| 69G5 | 276 | 914 | S59049 | Hs.75256 | 0 | 6 | BL34=B cell activation gene [human, mRNA, 1398 nt] |
| 101F6 | 315 | 758 | AF054174 | Hs.75258 | 0 | 1 | histone macroH2A1.2 mRNA, complete cds /cds=(|
| 596E10 | 320 | 1667 | NM_004893 | Hs.75258 | 0 | 5 | H2A histone family, member Y (H2AFY), mRNA /cds |
| 587G10 | 639 | 953 | NM_001628 | Hs.75313 | 1.00E-147 | 1 | aldo-keto reductase family 1, member B1 (aldo |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|---|
| 128F7 | 181 | 933 | X06956 | Hs.75318 | 0 | 4 | HALPHA44 gene for alpha-tubulin, exons 1-3 |
| 74A1 | 321 | 3290 | D21262 | Hs.75337 | 0 | 10 | KIAA0035 gene, partial cds /cds=(0,2125) /gb |
| 50D8 | 2 | 667 | BF303895 | Hs.75344 | 0 | 4 | 601886515F2 cDNA, 5' end /clone=IMAGE:4120514 |
| 179F7 | 379 | 720 | L07633 | Hs.75348 | 1.00E-179 | 4 | (clone 1950.2) interferon-gamma IEF SSP 5111 m |
| 191F3 | 158 | 872 | NM_006263 | Hs.75348 | 0 | 18 | proteasome (prosome, macropain) activator su |
| 463G4 | 1849 | 2394 | NM_001873 | Hs.75360 | 0 | 1 | carboxypeptidase E (CPE), mRNA /cds=(290,1720 |
| 117D6 | 224 | 671 | AB023200 | Hs.75361 | 0 | 1 | mRNA for KIAA0983 protein, complete cds /cds=(|
| 73E8 | 1 | 2339 | D89077 | Hs.75367 | 0 | 8 | for Src-like adapter protein, complete cd |
| 49H5 | 1 | 2388 | NM_006748 | Hs.75367 | 0 | 4 | Src-like-adapter (SLA), mRNA /cds=(41,871) / |
| 134A3 | 550 | 1126 | NM_005917 | Hs.75375 | 0 | 1 | malate dehydrogenase 1, NAD (soluble) (MDH1), |
| 462F2 | 73 | 361 | NM_004172 | Hs.75379 | 1.00E-158 | 1 | solute carrier family 1 (glial high affinity gl |
| 477G6 | 769 | 2043 | NM_004300 | Hs.75393 | 0 | 3 | acid phosphatase 1, soluble (ACP1), transcript |
| 62A10 | 1028 | 2528 | X87949 | Hs.75410 | 0 | 7 | BiP protein /cds=(222,2183) /gb=X87949 |
| 125H4 | 510 | 807 | NM_006010 | Hs.75412 | 1.00E-130 | 2 | Arginine-rich protein (ARP), mRNA /cds=(132,8 |
| 70H1 | 29 | 2349 | AK026463 | Hs.75415 | 0 | 30 | FLJ22810 fis, clone KAIA2933, highly sim |
| 60D3 | 160 | 1666 | D31767 | Hs.75416 | 0 | 6 | KIAA0058 gene, complete cds /cds=(69,575) /g |
| 98D5 | 103 | 1233 | NM_014764 | Hs.75416 | 0 | 10 | DAZ associated protein 2 (DAZAP2), mRNA /cds=(|
| 55H1 | 1183 | 1390 | NM_016525 | Hs.75425 | 2.00E-81 | 1 | ubiquitin associated protein (UBAP), mRNA /cd |
| 44B12 | 51 | 480 | BF131654 | Hs.75428 | 0 | 3 | 601820480F1 cDNA, 5' end /clone=IMAGE:4052586 |
| 64E11 | 1 | 177 | NM_000454 | Hs.75428 | 7.00E-94 | 1 | superoxide dismutase 1, soluble (amyotrophic |
| 65D3 | 387 | 969 | L33842 | Hs.75432 | 0 | 4 | (clone FFE-7) type II inosine monophosphate de |
| 58F9 | 379 | 672 | NM_000884 | Hs.75432 | 1.00E-149 | 1 | IMP (inosine monophosphate) dehydrogenase 2 |
| 73B1 | 87 | 291 | BE790474 | Hs.75458 | 5.00E-71 | 2 | 601476059F1 cDNA, 5' end /clone=IMAGE:3878799 |
| 585G5 | 1 | 302 | NM_000979 | Hs.75458 | 1.00E-170 | 8 | ribosomal protein L18 (RPL18), mRNA /cds=(15,5 |
| 173A1 | 1893 | 2653 | NM_006763 | Hs.75462 | 0 | 2 | BTG family, member 2 (BTG2), mRNA /cds=(71,547) |
| 166A10 | 601 | 1147 | AB000115 | Hs.75470 | 0 | 1 | mRNA expressed in osteoblast, complete cds /cd |
| 180D10 | 601 | 1045 | NM_006820 | Hs.75470 | 0 | 1 | hypothetical protein, expressed in osteoblast |
| 122D9 | 3322 | 5191 | AB023173 | Hs.75478 | 0 | 2 | mRNA for KIAA0956 protein, partial cds /cds=(0 |
| 461E5 | 2484 | 2804 | AL133074 | Hs.75497 | 1.00E-144 | 1 | mRNA; cDNA DKFZp434M1317 (from clone DKFZp434M |
| 512D6 | 69 | 799 | NM_004591 | Hs.75498 | 0 | 12 | small inducible cytokine subfamily A (Cys-Cys |
| 146B12 | 54 | 783 | U64197 | Hs.75498 | 0 | 4 | chemokine exodus-1 mRNA, complete cds /cds=(4 |
| 596H5 | 685 | 1952 | NM_001157 | Hs.75510 | 0 | 5 | annexin A11 (ANXA11), mRNA /cds=(178,1695) /g |
| 179D6 | 215 | 603 | D23662 | Hs.75512 | 1.00E-168 | 2 | ubiquitin-like protein, complete cds |
| 522G12 | 52 | 603 | NM_006156 | Hs.75512 | 0 | 2 | neural precursor cell expressed, developmenta |
| 46B6 | 1108 | 1418 | NM_000270 | Hs.75514 | 1.00E-166 | 1 | nucleoside phosphorylase (NP), mRNA /cds=(109 |
| 73H11 | 83 | 1418 | X00737 | Hs.75514 | 1.00E-104 | 3 | purine nucleoside phosphorylase (PNP; EC 2. |
| 154F7 | 1279 | 2056 | L05425 | Hs.75528 | 0 | 3 | nucleolar GTPase mRNA, complete cds /cds=(79,2 |
| 164C10 | 1268 | 1910 | NM_013285 | Hs.75528 | 0 | 2 | nucleolar GTPase (HUMAUAANTIG), mRNA /cds=(79, |
| 106C8 | 76 | 322 | Z25749 | Hs.75538 | 1.00E-130 | 3 | gene for ribosomal protein S7 /cds=(81,665) /gb= |
| 98E5 | 474 | 1188 | NM_003405 | Hs.75544 | 0 | 1 | tyrosine 3-monooxygenase/tryptophan 5-monoo |
| 459G10 | 2160 | 2717 | NM_000418 | Hs.75545 | 0 | 1 | interleukin 4 receptor (IL4R), mRNA /cds=(175, |
| 44B2 | 71 | 692 | U03851 | Hs.75546 | 0 | 1 | capping protein alpha mRNA, partial cds /cds=(16,870) |
| 483F2 | 1207 | 1392 | NM_004357 | Hs.75564 | 1.00E-80 | 1 | CD151 antigen (CD151), mRNA /cds=(84,845) /gb |
| 596D6 | 1968 | 2392 | NM_021975 | Hs.75569 | 0 | 1 | v-rel avian reticuloendotheliosis viral onco |
| 466G10 | 679 | 896 | NM_014763 | Hs.75574 | 1.00E-120 | 2 | mitochondrial ribosomal protein L19 (MRPL19), |
| 524B3 | 6194 | 6477 | NM_001759 | Hs.75586 | 1.00E-147 | 1 | cyclin D2 (CCND2), mRNA /cds=(269,1138) /gb=N |
| 481B4 | 3423 | 3804 | NM_000878 | Hs.75596 | 1.00E-160 | 2 | interleukin 2 receptor, beta (IL2RB), mRNA /cd |
| 162B5 | 753 | 1694 | M29064 | Hs.75598 | 0 | 6 | hnRNP B1 protein mRNA /cds=(149,1210) /gb=M29064 /gi |
| 176F5 | 730 | 922 | NM_002137 | Hs.75598 | 1.00E-106 | 1 | heterogeneous nuclear ribonucleoprotein A2/ |
| 106C2 | 1654 | 2589 | D10522 | Hs.75607 | 0 | 8 | for 80K-L protein, complete cds /cds=(369, |
| 98C5 | 1538 | 2589 | NM_002356 | Hs.75607 | 0 | 20 | myristoylated alanine-rich protein kinase C |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|-----|--|
| 192E5 | 1007 | 1416 | NM_006819 | Hs.75612 | 0 | 1 | stress-induced-phosphoprotein 1 (Hsp70/Hsp9 |
| 40E12 | 836 | 1765 | M98399 | Hs.75613 | 0 | 2 | antigen CD36 (clone 21) mRNA, complete cds /cds=(254,1 |
| 107C6 | 1491 | 1595 | AF113676 | Hs.75621 | 3.00E-51 | 1 | clone FLB2803 PRO0684 mRNA, complete cds /cds= |
| 117E9 | 149 | 1033 | NM_001779 | Hs.75626 | 0 | 2 | CD58 antigen, (lymphocyte function-associate |
| 482H10 | 740 | 1367 | NM_000591 | Hs.75627 | 0 | 1 | CD14 antigen (CD14), mRNA /cds=(119,1246) /gb |
| 482D4 | 1342 | 1659 | NM_006163 | Hs.75643 | 3.00E-82 | 1 | nuclear factor (erythroid-derived 2), 45kD (N |
| 73F8 | 2864 | 3657 | L49169 | Hs.75678 | 0 | 20 | G0S3 mRNA, complete cds /cds=(593,1609) /gb=L49169 / |
| 58G3 | 3222 | 3657 | NM_006732 | Hs.75678 | 0 | 6 | FBJ murine osteosarcoma viral oncogene homolo |
| 53A7 | 30 | 836 | J04130 | Hs.75703 | 0 | 138 | activation (Act-2) mRNA, complete cds /cds=(108,386) |
| 500E11 | 41 | 688 | NM_002984 | Hs.75703 | 0 | 128 | small inducible cytokine A4 (homologous to mo |
| 170E9 | 415 | 2376 | M16985 | Hs.75709 | 0 | 6 | cation-dependent mannose 6-phosphate-specific rece |
| 591E8 | 1759 | 2401 | NM_002355 | Hs.75709 | 0 | 3 | mannose-6-phosphate receptor (cation depende |
| 191A11 | 20 | 1900 | NM_002575 | Hs.75716 | 0 | 13 | serine (or cysteine) proteinase inhibitor, cl |
| 184F5 | 18 | 1900 | Y00630 | Hs.75716 | 0 | 8 | Arg-Serpin (plasminogen activator-inhibito |
| 593G8 | 238 | 747 | NM_005022 | Hs.75721 | 1.00E-110 | 2 | profilin 1 (PFN1), mRNA /cds=(127,549) /gb=NM |
| 178G9 | 504 | 2101 | NM_002951 | Hs.75722 | 0 | 2 | ribophorin II (RPN2), mRNA /cds=(288,2183) /g |
| 138F12 | 2341 | 2488 | Y00282 | Hs.75722 | 4.00E-60 | 1 | ribophorin II /cds=(288,2183) /gb=Y00282 /g |
| 37F7 | 1328 | 1863 | AK023290 | Hs.75748 | 0 | 3 | FLJ13228 fis, clone OVARC1000085, highly |
| 119C7 | 3736 | 4103 | NM_003137 | Hs.75761 | 1.00E-172 | 1 | SFRS protein kinase 1 (SRPK1), mRNA /cds=(108,2 |
| 52E8 | 574 | 1106 | M36820 | Hs.75765 | 0 | 2 | cytokine (GRO-beta) mRNA, complete cds /cds=(74,397) |
| 74C8 | 2055 | 3026 | M10901 | Hs.75772 | 0 | 4 | glucocorticoid receptor alpha mRNA, complete cds /cd |
| 196C5 | 2600 | 4591 | NM_000176 | Hs.75772 | 0 | 5 | nuclear receptor subfamily 3, group C, member |
| 68E7 | 2194 | 2597 | D87953 | Hs.75789 | 0 | 1 | RTP, complete cds /cds=(122,1306) /gb=D87953 |
| 116E3 | 289 | 621 | NM_016470 | Hs.75798 | 0 | 1 | hypothetical protein (HSPC207), mRNA /cds=(0 |
| 107C10 | 650 | 1165 | AK025732 | Hs.75811 | 0 | 1 | FLJ22079 fis, clone HEP13180, highly sim |
| 123C12 | 459 | 969 | NM_004315 | Hs.75811 | 0 | 1 | N-acylsphingosine amidohydrolase (acid cera |
| 99E11 | 1007 | 2346 | NM_014761 | Hs.75824 | 0 | 2 | KIAA0174 gene product (KIAA0174), mRNA /cds=(|
| 128C11 | 377 | 906 | NM_006817 | Hs.75841 | 0 | 2 | endoplasmic reticulum luminal protein (ERP28 |
| 175F5 | 455 | 843 | X94910 | Hs.75841 | 1.00E-173 | 1 | ERp28 protein /cds=(11,796) /gb=X9491 |
| 182F12 | 4263 | 4842 | D86550 | Hs.75842 | 0 | 1 | mRNA for serine/threonine protein kinase, complete c |
| 175E3 | 3255 | 3787 | AL110132 | Hs.75875 | 0 | 1 | mRNA; cDNA DKFZp564H192 (from clone DKFZp564H1 |
| 195G3 | 1435 | 2132 | NM_003349 | Hs.75875 | 0 | 2 | ubiquitin-conjugating enzyme E2 variant 1 (U |
| 184B12 | 17 | 282 | BF698920 | Hs.75879 | 1.00E-138 | 8 | 602126495F1 cDNA, 5' end /clone=IMAGE:4283350 |
| 67G6 | 1218 | 1605 | AK000639 | Hs.75884 | 1.00E-173 | 1 | FLJ20632 fis, clone KAT03756, highly simi |
| 516A11 | 721 | 1109 | NM_015416 | Hs.75884 | 0 | 2 | DKFZP586A011 protein (DKFZP586A011), mRNA /c |
| 44B1 | 1066 | 4914 | NM_004371 | Hs.75887 | 0 | 4 | coatome protein complex, subunit alpha (COPA |
| 594D3 | 3971 | 4158 | NM_003791 | Hs.75890 | 1.00E-73 | 1 | site-1 protease (subtilisin-like, sterol-reg |
| 459H8 | 5291 | 5688 | D87446 | Hs.75912 | 1.00E-160 | 1 | mRNA for KIAA0257 gene, partial cds /cds=(0,5418) /gb |
| 113F6 | 2281 | 2807 | NM_006842 | Hs.75916 | 0 | 1 | splicing factor 3b, subunit 2, 145kD (SF3B2), m |
| 104F9 | 2334 | 2804 | U41371 | Hs.75916 | 0 | 1 | spliceosome associated protein (SAP 145) mRNA, compl |
| 100F12 | 656 | 825 | AK024890 | Hs.75932 | 6.00E-83 | 1 | FLJ21237 fis, clone COL01114 /cds=UNKNOW |
| 39E1 | 40 | 526 | BF217687 | Hs.75968 | 1.00E-124 | 2 | 601882510F1 cDNA, 5' end /clone=IMAGE:4094907 |
| 111G8 | 41 | 547 | NM_021109 | Hs.75968 | 1.00E-166 | 19 | thymosin, beta 4, X chromosome (TMSB4X), mRNA |
| 478A7 | 1335 | 1653 | NM_006813 | Hs.75969 | 1.00E-119 | 1 | proline-rich protein with nuclear targeting s |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|-------|-------|-----------|----------|-----------|----|---|
| 70E9 | 652 | 1065 | U03105 | Hs.75969 | 0 | 1 | B4-2 protein mRNA, complete cds /cds=(113,1096) /gb=U |
| 596B9 | 508 | 1461 | NM_003133 | Hs.75975 | 0 | 2 | signal recognition particle 9kD (SRP9), mRNA |
| 513F12 | 1359 | 2169 | NM_005151 | Hs.75981 | 0 | 3 | ubiquitin specific protease 14 (tRNA-guanine |
| 74B3 | 1361 | 2166 | U30888 | Hs.75981 | 0 | 2 | tRNA-guanine transglycosylase mRNA, complete cds /c |
| 67B6 | 81 | 1457 | X17025 | Hs.76038 | 0 | 4 | homolog of yeast IPP isomerase /cds=(50,736) /gb=X170 |
| 586F2 | 1471 | 2197 | NM_004396 | Hs.76053 | 0 | 13 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide |
| 70B3 | 762 | 2211 | X52104 | Hs.76053 | 0 | 12 | p68 protein /cds=(175,2019) /gb=X52104 /gi=3 |
| 73B2 | 32 | 494 | BF214146 | Hs.76064 | 0 | 1 | 601847762F1 cDNA, 5' end /clone=IMAGE:4078622 |
| 523E6 | 10 | 441 | NM_000990 | Hs.76064 | 0 | 2 | ribosomal protein L27a (RPL27A), mRNA /cds=(1 |
| 38F7 | 6 | 372 | Z23090 | Hs.76067 | 0 | 2 | 28 kDa heat shock protein /cds=(491,1108) |
| 59B6 | 916 | 1274 | AF071596 | Hs.76095 | 1.00E-174 | 1 | apoptosis inhibitor (IEX-1L) gene, complete c |
| 493B3 | 540 | 1206 | NM_003897 | Hs.76095 | 0 | 3 | immediate early response 3 (IER3), mRNA /cds=(|
| 483D7 | 1399 | 2063 | NM_005626 | Hs.76122 | 0 | 1 | splicing factor, arginine/serine-rich 4 (SFR |
| 591C12 | 13412 | 13873 | NM_003922 | Hs.76127 | 0 | 3 | hect (homologous to the E6-AP (UBE3A) carboxyl |
| 65H7 | 12209 | 12580 | U50078 | Hs.76127 | 0 | 1 | guanine nucleotide exchange factor p532 mRNA, complet |
| 160B6 | 79 | 535 | X77584 | Hs.76136 | 1.00E-140 | 1 | ATL-derived factor/thioredoxin /cds=(80 |
| 596A9 | 1 | 124 | NM_001009 | Hs.76194 | 3.00E-62 | 1 | ribosomal protein S5 (RPS5), mRNA /cds=(37,651 |
| 51H5 | 2834 | 3174 | AK025353 | Hs.76230 | 1.00E-180 | 1 | cDNA: FLJ21700 fis, clone COL09849, highly sim |
| 115C8 | 1589 | 2005 | NM_001748 | Hs.76288 | 0 | 1 | calpain 2, (mII) large subunit (CAPN2), mRNA |
| 588C5 | 4 | 336 | NM_004492 | Hs.76362 | 0 | 2 | general transcription factor IIA, 2 (12kD subu |
| 111D9 | 732 | 1077 | NM_004930 | Hs.76368 | 1.00E-161 | 2 | capping protein (actin filament) muscle Z-lin |
| 192A11 | 1589 | 1995 | NM_002462 | Hs.76391 | 0 | 3 | myxovirus (Influenza) resistance 1, homolog o |
| 39F5 | 8481 | 8730 | Y00285 | Hs.76473 | 1.00E-111 | 1 | insuline-like growth factor II receptor /cds |
| 98C4 | 487 | 3719 | NM_002298 | Hs.76506 | 0 | 38 | lymphocyte cytosolic protein 1 (L-plastin) (L |
| 124H12 | 611 | 1747 | NM_004862 | Hs.76507 | 0 | 5 | LPS-induced TNF-alpha factor (PIG7), mRNA /cd |
| 37A6 | 920 | 1524 | U77396 | Hs.76507 | 1.00E-162 | 2 | LPS-Induced TNF-Alpha Factor (LITAF) mRNA, co |
| 71E9 | 759 | 3362 | D00099 | Hs.76549 | 0 | 4 | mRNA for Na,K-ATPase alpha-subunit, complete |
| 73F5 | 951 | 1277 | AK001361 | Hs.76556 | 1.00E-168 | 1 | FLJ10499 fis, clone NT2RP2000346, weakly |
| 48H6 | 1097 | 1603 | NM_014330 | Hs.76556 | 0 | 2 | growth arrest and DNA-damage-inducible 34 (G |
| 160C8 | 74 | 181 | BE730376 | Hs.76572 | 2.00E-40 | 1 | 601563816F1 5' end /clone=IMAGE:3833690 |
| 589D11 | 86 | 455 | NM_001697 | Hs.76572 | 0 | 2 | ATP synthase, H+ transporting, mitochondrial |
| 38B1 | 227 | 886 | NM_014059 | Hs.76640 | 0 | 9 | RGC32 protein (RGC32), mRNA /cds=(146,499) /g |
| 174B12 | 3024 | 4628 | D80005 | Hs.76666 | 1.00E-136 | 4 | mRNA for KIAA0183 gene, partial cds /cds=(0,3190) /gb |
| 37A11 | 1788 | 3255 | AF070673 | Hs.76691 | 0 | 5 | stannin mRNA, complete cds /cds=(175,441) /gb |
| 58H11 | 1706 | 2088 | AL136807 | Hs.76698 | 0 | 2 | mRNA; cDNA DKFZp434L1621 (from clone DKFZp434L |
| 477F9 | 6930 | 7298 | AB002299 | Hs.76730 | 0 | 2 | mRNA for KIAA0301 gene, partial cds /cds=(0,6144) /gb |
| 40G7 | 293 | 819 | NM_000118 | Hs.76753 | 0 | 1 | endoglin (Osler-Rendu-Weber syndrome 1) (EN |
| 75C11 | 10 | 1113 | J00194 | Hs.76807 | 0 | 5 | human hla-dr antigen alpha-chain mrna & ivs fragments /cds= |
| 99F4 | 10 | 969 | NM_019111 | Hs.76807 | 0 | 6 | major histocompatibility complex, class II, |
| 61G12 | 1870 | 2511 | AL133096 | Hs.76853 | 0 | 1 | cDNA DKFZp434N1728 (from clone DKFZp434N |
| 599C2 | 41 | 346 | NM_002790 | Hs.76913 | 1.00E-124 | 1 | proteasome (prosome, macropain) subunit, alp |
| 155C2 | 508 | 870 | X61970 | Hs.76913 | 0 | 1 | for macropain subunit zeta /cds=(21,746) /g |
| 70C5 | 3398 | 3754 | AF002020 | Hs.76918 | 0 | 1 | Niemann-Pick C disease protein (NPC1) mRNA, co |
| 57A11 | 2173 | 2764 | NM_000271 | Hs.76918 | 0 | 1 | Niemann-Pick disease, type C1 (NPC1), mRNA /cd |
| 158C9 | 314 | 1233 | NM_001679 | Hs.76941 | 0 | 3 | ATPase, Na+/K+ transporting, beta 3 polypeptid |
| 520E1 | 4175 | 4502 | NM_014757 | Hs.76986 | 1.00E-158 | 1 | mastermind (Drosophila), homolog of (MAML1), |
| 587D8 | 22 | 869 | NM_001006 | Hs.77039 | 0 | 5 | ribosomal protein S3A (RPS3A), mRNA /cds=(36,8 |
| 481F2 | 440 | 1488 | NM_001731 | Hs.77054 | 0 | 3 | B-cell translocation gene 1, anti-proliferati |
| 53G11 | 340 | 1490 | X61123 | Hs.77054 | 0 | 3 | BTG1 mRNA /cds=(308,823) /gb=X61123 /gi=29508 /ug=Hs |
| 521A6 | 147 | 1325 | D55716 | Hs.77152 | 0 | 2 | mRNA for P1cdc47, complete cds /cds=(116,2275) /gb=D |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|--|
| 37H9 | 2109 | 2530 | X07109 | Hs.77202 | 0 | 1 | protein kinase C (PKC) type /cds=(136,2157) / |
| 167H5 | 3915 | 4508 | NM_006437 | Hs.77225 | 0 | 1 | ADP-ribosyltransferase (NAD+; poly (ADP-ribo |
| 139G5 | 2183 | 2389 | U61145 | Hs.77256 | 1.00E-111 | 1 | enhancer of zeste homolog 2 (EZH2) mRNA, complete cds |
| 109H2 | 2502 | 2893 | D38549 | Hs.77257 | 0 | 1 | KIAA0068 gene, partial cds /cds=(0,3816) /gb |
| 184B7 | 619 | 1111 | L25080 | Hs.77273 | 0 | 1 | GTP-binding protein (rhoA) mRNA, complete cds |
| 587H1 | 614 | 1371 | NM_001664 | Hs.77273 | 0 | 9 | ras homolog gene family, member A (ARHA), mRNA |
| 99G10 | 1387 | 2219 | NM_002658 | Hs.77274 | 0 | 1 | plasminogen activator, urokinase (PLAU), mRNA |
| 143C12 | 2403 | 2905 | AL049332 | Hs.77311 | 0 | 2 | cDNA DKFZp564L176 (from clone DKFZp564L1 |
| 519B11 | 5248 | 5555 | NM_000430 | Hs.77318 | 1.00E-160 | 1 | platelet-activating factor acetylhydrolase, |
| 52F10 | 3249 | 3459 | AF095901 | Hs.77324 | 1.00E-114 | 2 | eRF1 gene, complete cds /cds=(136,1449) /gb=A |
| 494G1 | 3255 | 3453 | NM_004730 | Hs.77324 | 1.00E-109 | 2 | eukaryotic translation termination factor 1 |
| 517E4 | 305 | 973 | NM_014754 | Hs.77329 | 0 | 2 | phosphatidylserine synthase 1 (PTDSS1), mRNA |
| 72F9 | 1934 | 4605 | AF187320 | Hs.77356 | 0 | 10 | transferrin receptor (TFRC) gene, complete cd |
| 46D6 | 241 | 4902 | NM_003234 | Hs.77356 | 0 | 2 | transferrin receptor (p90, CD71) (TFRC), mRNA |
| 113A12 | 1028 | 1290 | NM_024033 | Hs.77365 | 1.00E-145 | 1 | hypothetical protein MGC5242 (MGC5242), mRNA |
| 173A7 | 1142 | 1649 | AK026164 | Hs.77385 | 0 | 2 | cDNA: FLJ22511 fis, clone HRC11837, highly sim |
| 189E7 | 466 | 798 | NM_002004 | Hs.77393 | 0 | 1 | farnesyl diphosphate synthase (farnesyl pyro |
| 479B1 | 306 | 482 | NM_000566 | Hs.77424 | 8.00E-55 | 1 | Fc fragment of IgG, high affinity Ia, receptor |
| 41E12 | 351 | 898 | X14356 | Hs.77424 | 0 | 1 | high affinity Fc receptor (FcRI) /cds=(36,116 |
| 122D3 | 562 | 855 | NM_002664 | Hs.77436 | 1.00E-145 | 1 | pleckstrin (PLEK), mRNA /cds=(60,1112) /gb=N |
| 59C11 | 1 | 2745 | X07743 | Hs.77436 | 0 | 5 | pleckstrin (P47) /cds=(60,1112) /gb=X07743 |
| 590B1 | 5185 | 5274 | NM_001379 | Hs.77462 | 1.00E-44 | 1 | DNA (cytosine-5-)-methyltransferase 1 (DNMT1 |
| 522D1 | 572 | 956 | NM_001929 | Hs.77494 | 0 | 1 | deoxyguanosine kinase (DGUOK), mRNA /cds=(11, |
| 109E12 | 723 | 2474 | D87684 | Hs.77495 | 1.00E-163 | 5 | for KIAA0242 protein, partial cds /cds=(0, |
| 148E2 | 61 | 271 | BE737246 | Hs.77496 | 1.00E-81 | 1 | 601305556F1 5' end /clone=IMAGE:3640165 |
| 586D4 | 1887 | 2362 | NM_003363 | Hs.77500 | 0 | 1 | ubiquitin specific protease 4 (proto-oncogene |
| 57E8 | 29 | 2808 | BC001854 | Hs.77502 | 0 | 30 | methionine adenosyltransferase II, alpha, c |
| 70H9 | 87 | 1283 | X68836 | Hs.77502 | 0 | 14 | S-adenosylmethionine synthetase /cds=(|
| 69B2 | 778 | 3033 | M20867 | Hs.77508 | 0 | 2 | glutamate dehydrogenase (GDH) mRNA, complete cds /cd |
| 513F9 | 2694 | 2929 | NM_005271 | Hs.77508 | 1.00E-105 | 1 | glutamate dehydrogenase 1 (GLUD1), mRNA /cds= |
| 75A3 | 190 | 701 | X62744 | Hs.77522 | 0 | 1 | RING6 mRNA for HLA class II alpha product /cds=(45,830 |
| 105E10 | 72 | 597 | BE673364 | Hs.77542 | 0 | 3 | 7d34a03.x1 cDNA, 3' end /clone=IMAGE:3249100 |
| 124B2 | 85 | 683 | BF508702 | Hs.77542 | 0 | 8 | UI-H-BI4-aop-g-05-0-UI.s1 cDNA, 3' end /clon |
| 524C9 | 829 | 1233 | AK021563 | Hs.77558 | 0 | 3 | cDNA FLJ11501 fis, clone HEMBA1002100 /cds=UNK |
| 523B12 | 7580 | 8153 | NM_004652 | Hs.77578 | 0 | 2 | ubiquitin specific protease 9, X chromosome (D |
| 166F3 | 169 | 340 | AL021546 | Hs.77608 | 7.00E-63 | 1 | DNA sequence from BAC 15E1 on chromosome 12. Contains |
| 195A11 | 164 | 451 | NM_003769 | Hs.77608 | 1.00E-162 | 1 | splicing factor, arginine/serine-rich 9 (SF |
| 595E1 | 618 | 1461 | AF056322 | Hs.77617 | 0 | 7 | SP100-HMG nuclear autoantigen (SP100) mRNA, c |
| 115A6 | 2954 | 3541 | AL137938 | Hs.77646 | 0 | 2 | mRNA; cDNA DKFZp761M0223 (from clone DKFZp761M |
| 592H6 | 261 | 951 | NM_014752 | Hs.77665 | 0 | 3 | KIAA0102 gene product (KIAA0102), mRNA /cds=(|
| 461F3 | 4657 | 4980 | NM_014749 | Hs.77724 | 1.00E-174 | 1 | KIAA0586 gene product (KIAA0586), mRNA /cds=(|
| 98C8 | 27 | 1961 | NM_002543 | Hs.77729 | 0 | 4 | oxidised low density lipoprotein (lectin-like |
| 598A12 | 101 | 1396 | NM_006759 | Hs.77837 | 0 | 4 | UDP-glucose pyrophosphorylase 2 (UGP2), mRNA |
| 594H8 | 1 | 872 | NM_006802 | Hs.77897 | 1.00E-144 | 2 | splicing factor 3a, subunit 3, 60kD (SF3A3), mR |
| 171E4 | 1140 | 1394 | X81789 | Hs.77897 | 1.00E-110 | 1 | for splicing factor SF3a60 /cds=(565,2070) |
| 500F1 | 2185 | 2496 | AK025736 | Hs.77910 | 1.00E-160 | 1 | cDNA: FLJ22083 fis, clone HEP14459, highly sim |
| 525B10 | 1696 | 2060 | NM_000122 | Hs.77929 | 0 | 1 | excision repair cross-complementing rodent r |
| 53E1 | 877 | 1539 | AK026595 | Hs.77961 | 0 | 7 | FLJ22942 fis, clone KAT08170, highly sim |
| 521C6 | 631 | 1089 | NM_005514 | Hs.77961 | 1.00E-115 | 4 | major histocompatibility complex, class I, B |
| 588C3 | 300 | 653 | NM_004792 | Hs.77965 | 0 | 1 | Clk-associating RS-cyclophilin (CYP), mRNA |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|--|
| 523C6 | 277 | 582 | NM_001912 | Hs.78056 | 1.00E-143 | 1 | cathepsin L (CTSL), mRNA /cds=(288,1289) /gb= |
| 140D10 | 292 | 1549 | X12451 | Hs.78056 | 0 | 3 | pro-cathepsin L (major excreted protein MEP) |
| 463E5 | 129 | 552 | NM_005969 | Hs.78103 | 0 | 1 | nucleosome assembly protein 1-like 4 (NAP1L4) |
| 166H3 | 540 | 895 | U77456 | Hs.78103 | 0 | 1 | nucleosome assembly protein 2 mRNA, complete cds /cd |
| 40B10 | 2433 | 2543 | M28526 | Hs.78146 | 5.00E-29 | 1 | platelet endothelial cell adhesion molecule (PECAM-1 |
| 114E5 | 1671 | 2029 | NM_000442 | Hs.78146 | 1.00E-162 | 1 | platelet/endothelial cell adhesion molecule |
| 513D11 | 28 | 1399 | NM_000700 | Hs.78225 | 0 | 5 | annexin A1 (ANXA1), mRNA /cds=(74,1114) /gb=N |
| 331B3 | 219 | 1370 | X05908 | Hs.78225 | 0 | 3 | lipocortin /cds=(74,1114) /gb=X05908 /gi=34 |
| 56A12 | 1383 | 2379 | X94232 | Hs.78335 | 0 | 4 | novel T-cell activation protein /cds=(14 |
| 465H1 | 386 | 904 | NM_002812 | Hs.78466 | 0 | 2 | proteasome (prosome, macropain) 26S subunit, |
| 108H7 | 2067 | 2486 | L42572 | Hs.78504 | 0 | 1 | p87/89 gene, complete cds /cds=(92,2368) /gb= |
| 187E9 | 729 | 1494 | NM_006839 | Hs.78504 | 0 | 2 | inner membrane protein, mitochondrial (mitofi |
| 102F2 | 672 | 2947 | L14561 | Hs.78546 | 0 | 2 | plasma membrane calcium ATPase isoform 1 (ATP |
| 591H12 | 42 | 1949 | NM_004034 | Hs.78637 | 0 | 3 | annexin A7 (ANXA7), transcript variant 2, mRN |
| 595H3 | 2775 | 3030 | NM_003470 | Hs.78683 | 3.00E-96 | 1 | ubiquitin specific protease 7 (herpes virus-as |
| 62F5 | 2775 | 3838 | Z72499 | Hs.78683 | 0 | 2 | herpesvirus associated ubiquitin-speci |
| 46G4 | 2632 | 3238 | NM_003580 | Hs.78687 | 0 | 1 | neutral sphingomyelinase (N-SMase) activatio |
| 513A11 | 342 | 1258 | NM_002635 | Hs.78713 | 0 | 10 | solute carrier family 25 (mitochondrial carri |
| 472A4 | 3018 | 3286 | NM_024298 | Hs.78768 | 1.00E-132 | 1 | malignant cell expression-enhanced gene/tumo |
| 177A3 | 377 | 1186 | AL049589 | Hs.78771 | 0 | 3 | DNA sequence from clone 570L12 on chromosome Xq13.1-2 |
| 71E6 | 303 | 1767 | NM_000291 | Hs.78771 | 0 | 12 | phosphoglycerate kinase 1 (PGK1), mRNA /cds=(|
| 181D8 | 2104 | 3677 | NM_018834 | Hs.78825 | 0 | 4 | matrin 3 (MATR3), mRNA /cds=(254,2800) /gb=NM |
| 126G6 | 2498 | 2959 | AL162049 | Hs.78829 | 0 | 1 | mRNA; cDNA DKFZp762E1712 (from clone DKFZp762E |
| 41C3 | 1743 | 2340 | M31932 | Hs.78864 | 0 | 2 | IgG low affinity Fc fragment receptor (FcRIIa) mRNA, c |
| 166D11 | 1696 | 2156 | M81601 | Hs.78869 | 0 | 1 | transcription elongation factor (SII) mRNA, complete |
| 517B3 | 565 | 1392 | D42039 | Hs.78871 | 0 | 3 | mRNA for KIAA0081 gene, partial cds /cds=(0,702) /gb= |
| 180G11 | 59 | 517 | NM_020548 | Hs.78888 | 0 | 1 | diazepam binding inhibitor (GABA receptor mod |
| 99B7 | 2356 | 3329 | U07802 | Hs.78909 | 0 | 45 | Tis11d gene, complete cds /cds=(291,1739) /gb=U07802 |
| 54C4 | 557 | 1101 | U13045 | Hs.78915 | 0 | 1 | nuclear respiratory factor-2 subunit beta 1 mRNA, com |
| 44A5 | 634 | 1128 | U29607 | Hs.78935 | 0 | 2 | methionine aminopeptidase mRNA, complete cds /cds=(2 |
| 63A2 | 964 | 1050 | X92106 | Hs.78943 | 7.00E-31 | 1 | bleomycin hydrolase /cds=(78,1445) /gb |
| 163G9 | 228 | 877 | L13463 | Hs.78944 | 0 | 3 | helix-loop-helix basic phosphoprotein (G0S8) mRNA, |
| 119H6 | 472 | 877 | NM_002923 | Hs.78944 | 0 | 1 | regulator of G-protein signalling 2, 24kD (RG |
| 166E2 | 5629 | 5764 | U51903 | Hs.78993 | 2.00E-69 | 1 | RasGAP-related protein (IQGAP2) mRNA, complete cds |
| 40F9 | 66 | 603 | M15796 | Hs.78996 | 0 | 1 | cyclin protein gene, complete cds /cds=(118,903) /gb |
| 593E5 | 156 | 854 | NM_012245 | Hs.79008 | 0 | 5 | SKI-INTERACTING PROTEIN (SNW1), mRNA /cds=(2 |
| 485B7 | 276 | 599 | AF063591 | Hs.79015 | 1.00E-136 | 1 | brain my033 protein mRNA, complete cds /cds=(5 |
| 61B4 | 125 | 732 | X05323 | Hs.79015 | 0 | 2 | MRC OX-2 gene signal sequence /cds=(0,824) /gb=X05323 |
| 71C8 | 330 | 1958 | NM_005261 | Hs.79022 | 0 | 24 | GTP-binding protein overexpressed in skeletal |
| 75G8 | 330 | 1957 | U10550 | Hs.79022 | 0 | 63 | Gem GTPase (gem) mRNA, complete cds /cds=(213,1103) / |
| 584G1 | 4424 | 5153 | AF226044 | Hs.79025 | 0 | 2 | HSNFRK (HSNFRK) mRNA, complete cds /cds=(641,2 |
| 117C5 | 358 | 933 | NM_012413 | Hs.79033 | 0 | 1 | glutaminyl-peptide cyclotransferase (glutam |
| 72B2 | 910 | 2015 | AJ250915 | Hs.79037 | 0 | 9 | p10 gene for chaperonin 10 (Hsp10 protein) and |
| 71G11 | 880 | 1981 | NM_002156 | Hs.79037 | 0 | 5 | heat shock 60kD protein 1 (chaperonin) (HSPD1) |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|---|
| 193H12 | 1859 | 2474 | NM_003243 | Hs.79059 | 0 | 5 | transforming growth factor, beta receptor III |
| 460B4 | 846 | 1325 | NM_001930 | Hs.79064 | 0 | 1 | deoxyhypusine synthase (DHPS), transcript va |
| 75C4 | 1166 | 2087 | K02276 | Hs.79070 | 0 | 85 | (Daudi) translocated t(8;14) c-myc oncogene mRNA, co |
| 71G10 | 1274 | 2121 | NM_002467 | Hs.79070 | 0 | 12 | v-myc avian myelocytomatosis viral oncogene h |
| 183D8 | 385 | 741 | NM_002710 | Hs.79081 | 0 | 1 | protein phosphatase 1, catalytic subunit, gam |
| 170A12 | 741 | 1203 | X74008 | Hs.79081 | 0 | 1 | protein phosphatase 1 gamma /cds=(154,11 |
| 121D9 | 2920 | 3385 | NM_006378 | Hs.79089 | 0 | 1 | sema domain, immunoglobulin domain (Ig), tran |
| 40C12 | 2933 | 4108 | U60800 | Hs.79089 | 0 | 4 | semaphorin (CD100) mRNA, complete cds /cds=(87,2675) |
| 104E1 | 1708 | 1932 | L35263 | Hs.79107 | 1.00E-101 | 1 | CSAids binding protein (CSBP1) mRNA, complete cds /cd |
| 70B2 | 913 | 2497 | AK000221 | Hs.79110 | 0 | 9 | FLJ20214 fis, clone COLF2014, highly simi |
| 123B12 | 1929 | 2644 | D42043 | Hs.79123 | 0 | 3 | mRNA for KIAA0084 gene, partial cds /cds=(0,1946) /gb |
| 193G7 | 802 | 1425 | NM_004379 | Hs.79194 | 0 | 2 | cAMP responsive element binding protein 1 (CR |
| 75D5 | 158 | 2139 | NM_004233 | Hs.79197 | 0 | 16 | CD83 antigen (activated B lymphocytes, immuno |
| 74H2 | 98 | 1357 | NM_001154 | Hs.79274 | 0 | 2 | annexin A5 (ANXA5), mRNA /cds=(192,1154) /gb= |
| 519G7 | 5358 | 5496 | D86985 | Hs.79276 | 2.00E-69 | 1 | mRNA for KIAA0232 protein, partial cds /cds=(0, |
| 462C2 | 1477 | 2031 | NM_003006 | Hs.79283 | 0 | 1 | selectin P ligand (SELPLG), mRNA /cds=(59,1267 |
| 65C6 | 23 | 1609 | M15353 | Hs.79306 | 0 | 6 | cap-binding protein mRNA, complete cds /cds=(1 |
| 64H8 | 326 | 1610 | NM_001968 | Hs.79306 | 0 | 3 | eukaryotic translation initiation factor 4E |
| 52C3 | 1333 | 1904 | X64318 | Hs.79334 | 0 | 1 | E4BP4 gene /cds=(213,1601) /gb=X64318 /gi=30955 |
| 39F7 | 1179 | 1740 | AF109733 | Hs.79335 | 0 | 1 | SWI/SNF-related, matrix-associated, actin-d |
| 194A7 | 1512 | 1803 | NM_003076 | Hs.79335 | 1.00E-118 | 1 | SWI/SNF related, matrix associated, actin dep |
| 463E12 | 4326 | 4831 | NM_015148 | Hs.79337 | 0 | 1 | KIAA0135 protein (KIAA0135), mRNA /cds=(1803, |
| 526B5 | 1420 | 1867 | NM_002958 | Hs.79350 | 0 | 2 | RYK receptor-like tyrosine kinase (RYK), mRNA |
| 460F3 | 1755 | 2242 | NM_006285 | Hs.79358 | 0 | 2 | testis-specific kinase 1 (TESK1), mRNA /cds=(|
| 98B11 | 2076 | 4834 | X76061 | Hs.79362 | 0 | 11 | H.sapiens p130 mRNA for 130K protein /cds=(69,3488) /gb=X76 |
| 45F3 | 2286 | 2666 | NM_001423 | Hs.79368 | 0 | 1 | epithelial membrane protein 1 (EMP1), mRNA /cd |
| 50C10 | 2016 | 2666 | Y07909 | Hs.79368 | 0 | 2 | Progression Associated Protein /cds=(21 |
| 118E3 | 549 | 1078 | NM_012198 | Hs.79381 | 0 | 1 | grancalcin (GCL), mRNA /cds=(119,772) /gb=NM_ |
| 181F4 | 657 | 1271 | NM_002805 | Hs.79387 | 0 | 2 | proteasome (prosome, macropain) 26S subunit, |
| 105H3 | 1114 | 1538 | D83018 | Hs.79389 | 0 | 1 | for nel-related protein 2, complete cds / |
| 173B2 | 429 | 3009 | NM_006159 | Hs.79389 | 0 | 5 | nel (chicken)-like 2 (NELL2), mRNA /cds=(96,25 |
| 177B3 | 662 | 991 | AC004382 | Hs.79402 | 0 | 1 | Chromosome 16 BAC clone CIT987SK-A-152E5 /cds |
| 590H3 | 663 | 1002 | NM_002694 | Hs.79402 | 0 | 1 | polymerase (RNA) II (DNA directed) polypeptide |
| 523B7 | 223 | 582 | NM_002946 | Hs.79411 | 0 | 1 | replication protein A2 (32kD) (RPA2), mRNA /c |
| 182B10 | 472 | 1024 | U02019 | Hs.79625 | 1.00E-121 | 2 | AU-rich element RNA-binding protein AUF1 mRNA, comple |
| 479F3 | 100 | 301 | NM_001783 | Hs.79630 | 2.00E-86 | 1 | CD79A antigen (immunoglobulin-associated al |
| 40H9 | 582 | 1107 | U05259 | Hs.79630 | 0 | 1 | MB-1 gene, complete cds /cds=(36,716) /gb=U05259 /gi |
| 116A2 | 1003 | 1368 | NM_006224 | Hs.79709 | 1.00E-176 | 1 | phosphatidylinositol transfer protein (PITPN |
| 74G8 | 252 | 1297 | D21853 | Hs.79768 | 0 | 5 | KIAA0111 gene, complete cds /cds=(214,1449) |
| 525G2 | 830 | 1297 | NM_014740 | Hs.79768 | 0 | 2 | KIAA0111 gene product (KIAA0111), mRNA /cds=(|
| 125G3 | 2757 | 3339 | AF072928 | Hs.79877 | 0 | 1 | myotubularin related protein 6 mRNA, partial c |
| 184A2 | 532 | 1102 | AF135162 | Hs.79933 | 0 | 1 | cyclin I (CYC1) mRNA, complete cds /cds=(199,13 |
| 514C6 | 329 | 1256 | NM_006835 | Hs.79933 | 0 | 6 | cyclin I (CCNI), mRNA /cds=(0,1133) /gb=NM_006 |
| 116G5 | 824 | 1058 | NM_006875 | Hs.80205 | 1.00E-121 | 1 | pim-2 oncogene (PIM2), mRNA /cds=(185,1189) / |
| 106C11 | 1700 | 1995 | U77735 | Hs.80205 | 1.00E-125 | 1 | pim-2 protooncogene homolog pim-2h mRNA, complete cd |
| 110E3 | 276 | 653 | AL136139 | Hs.80261 | 0 | 1 | DNA sequence from clone RP4-76112 on chromosome 6 Con |
| 478D1 | 1067 | 2761 | NM_006403 | Hs.80261 | 2.00E-70 | 2 | enhancer of filamentation 1 (cas-like docking; |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|--|
| 178C8 | 880 | 1226 | AL050192 | Hs.80285 | 0 | 1 | mRNA; cDNA DKFZp586C1723 (from clone DKFZp586C |
| 494F11 | 477 | 5535 | NM_014739 | Hs.80338 | 0 | 8 | KIAA0164 gene product (KIAA0164), mRNA /cds=(|
| 190A1 | 1165 | 1540 | NM_004156 | Hs.80350 | 1.00E-166 | 2 | protein phosphatase 2 (formerly 2A), catalytic |
| 461A1 | 4639 | 4913 | NM_004653 | Hs.80358 | 1.00E-140 | 1 | SMC (mouse) homolog, Y chromosome (SMCY), mRNA |
| 158A8 | 2656 | 3229 | L24498 | Hs.80409 | 0 | 1 | gadd45 gene, complete cds /cds=(2327,2824) /gb=L2449 |
| 41E6 | 2385 | 2992 | U84487 | Hs.80420 | 0 | 2 | CX3C chemokine precursor, mRNA, alternatively splice |
| 40H4 | 2830 | 3605 | NM_000129 | Hs.80424 | 0 | 1 | coagulation factor XIII, A1 polypeptide (F13A |
| 464D3 | 214 | 835 | NM_004899 | Hs.80426 | 0 | 2 | brain and reproductive organ-expressed (TNFR |
| 75H8 | 1180 | 4930 | U12767 | Hs.80561 | 0 | 60 | mitogen induced nuclear orphan receptor (MINOR) mRNA |
| 593E10 | 1 | 510 | NM_004552 | Hs.80595 | 1.00E-158 | 5 | NADH dehydrogenase (ubiquinone) Fe-S protein |
| 113C5 | 1182 | 1583 | NM_003336 | Hs.80612 | 0 | 1 | ubiquitin-conjugating enzyme E2A (RAD6 homol |
| 515B7 | 268 | 538 | NM_001020 | Hs.80617 | 2.00E-91 | 3 | ribosomal protein S16 (RPS16), mRNA /cds=(37,4 |
| 477F12 | 460 | 606 | NM_018996 | Hs.80618 | 1.00E-47 | 1 | hypothetical protein (FLJ20015), mRNA /cds=(|
| 41A8 | 1331 | 1788 | L78440 | Hs.80642 | 0 | 1 | STAT4 mRNA, complete cds /cds=(81,2327) /gb=L |
| 594C1 | 1594 | 2586 | NM_003151 | Hs.80642 | 0 | 4 | signal transducer and activator of transcripti |
| 112C8 | 1802 | 1932 | NM_002198 | Hs.80645 | 2.00E-35 | 1 | interferon regulatory factor 1 (IRF1), mRNA / |
| 522H8 | 1130 | 1533 | NM_003355 | Hs.80658 | 1.00E-135 | 4 | uncoupling protein 2 (mitochondrial, proton c |
| 123E4 | 259 | 757 | NM_002129 | Hs.80684 | 0 | 4 | high-mobility group (nonhistone chromosomal) |
| 109H1 | 263 | 754 | X62534 | Hs.80684 | 0 | 1 | HMG-2 mRNA /cds=(214,843) /gb=X62534 /gi=32332 |
| 149G9 | 1020 | 1607 | J05032 | Hs.80758 | 0 | 2 | aspartyl-tRNA synthetase alpha-2 subunit mRNA, compl |
| 461F12 | 1702 | 2246 | AL031600 | Hs.80768 | 0 | 1 | DNA sequence from clone 390E6 on chromosome 16. Contai |
| 102B2 | 1486 | 2008 | M16038 | Hs.80887 | 0 | 1 | lyn mRNA encoding a tyrosine kinase /cds=(297,1835) / |
| 125B11 | 1260 | 2013 | NM_002350 | Hs.80887 | 0 | 5 | v-yes-1 Yamaguchi sarcoma viral related oncog |
| 37C9 | 2901 | 5260 | D79990 | Hs.80905 | 0 | 8 | KIAA0168 gene, complete cds /cds=(196,1176) |
| 196D6 | 2949 | 5261 | NM_014737 | Hs.80905 | 0 | 9 | Ras association (RalGDS/AF-6) domain family 2 |
| 584H1 | 4072 | 4296 | NM_002693 | Hs.80961 | 3.00E-91 | 1 | polymerase (DNA directed), gamma (POLG), nucl |
| 584F9 | 31 | 568 | AF174605 | Hs.81001 | 0 | 5 | F-box protein Fbx25 (FBX25) mRNA, partial cds |
| 102D11 | 1037 | 1632 | J03459 | Hs.81118 | 0 | 1 | leukotriene A-4 hydrolase mRNA, complete cds /cds=(68 |
| 193F8 | 1037 | 1643 | NM_000895 | Hs.81118 | 0 | 2 | leukotriene A4 hydrolase (LTA4H), mRNA /cds=(|
| 118H7 | 354 | 1148 | U65590 | Hs.81134 | 0 | 5 | IL-1 receptor antagonist IL-1Ra (IL-1RN) gene |
| 41H1 | 2549 | 2936 | X60992 | Hs.81226 | 0 | 1 | CD6 mRNA for T cell glycoprotein CD6 /cds=(120,152 |
| 171B9 | 2070 | 2479 | AF248648 | Hs.81248 | 0 | 1 | RNA-binding protein BRUNOL2 (BRUNOL2) mRNA, c |
| 590A6 | 291 | 512 | NM_002961 | Hs.81256 | 3.00E-66 | 1 | S100 calcium-binding protein A4 (calcium prot |
| 73H2 | 389 | 1481 | M69043 | Hs.81328 | 0 | 14 | MAD-3 mRNA encoding Ikb-like activity, complet |
| 513G1 | 637 | 1481 | NM_020529 | Hs.81328 | 0 | 13 | nuclear factor of kappa light polypeptide gene |
| 488F2 | 1065 | 1417 | NM_004499 | Hs.81361 | 1.00E-180 | 4 | heterogeneous nuclear ribonucleoprotein A/B |
| 151C8 | 1260 | 1423 | U76713 | Hs.81361 | 1.00E-61 | 1 | apobec-1 binding protein 1 mRNA, complete cds /cds=(15 |
| 593B9 | 41 | 954 | NM_001688 | Hs.81634 | 0 | 3 | ATP synthase, H+ transporting, mitochondrial |
| 104H12 | 352 | 912 | X60221 | Hs.81634 | 0 | 1 | H+-ATP synthase subunit b /cds=(32,802) |
| 141G8 | 1132 | 1642 | AK001883 | Hs.81648 | 0 | 1 | FLJ11021 fis, clone PLACE1003704, weakly |
| 41A1 | 4214 | 4395 | X06182 | Hs.81665 | 5.00E-67 | 1 | c-kit proto-oncogene mRNA /cds=(21,2951) /gb=X06182 |
| 102F5 | 3037 | 3646 | D38551 | Hs.81848 | 0 | 1 | KIAA0078 gene, complete cds /cds=(184,2079) |
| 111E11 | 1375 | 1752 | NM_006265 | Hs.81848 | 0 | 1 | RAD21 (S. pombe) homolog (RAD21), mRNA /cds=(1 |
| 592F8 | 38 | 720 | NM_014736 | Hs.81892 | 0 | 1 | KIAA0101 gene product (KIAA0101), mRNA /cds=(|

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|---|
| 194F1 | 6886 | 7115 | AF241785 | Hs.81897 | 1.00E-117 | 1 | NPD012 (NPD012) mRNA, complete cds /cds=(552,2 |
| 525C6 | 1 | 615 | NM_005563 | Hs.81915 | 0 | 4 | leukemia-associated phosphoprotein p18 (sta |
| 101D12 | 3249 | 3508 | D38555 | Hs.81964 | 1.00E-143 | 1 | KIAA0079 gene, complete cds /cds=(114,3491) |
| 176D11 | 2996 | 3168 | NM_004922 | Hs.81964 | 9.00E-94 | 2 | SEC24 (S. cerevisiae) related gene family, mem |
| 129B7 | 5068 | 5759 | D50683 | Hs.82028 | 0 | 4 | for TGF-betaIIIR alpha, complete cds /cds= |
| 195H6 | 946 | 1208 | NM_006023 | Hs.82043 | 6.00E-74 | 1 | D123 gene product (D123), mRNA /cds=(280,1290) |
| 481D9 | 2709 | 3085 | NM_002184 | Hs.82065 | 1.00E-134 | 1 | interleukin 6 signal transducer (gp130, oncos |
| 129A5 | 1338 | 1802 | M14083 | Hs.82085 | 0 | 1 | beta-migrating plasminogen activator inhibitor I mR |
| 57G9 | 500 | 1561 | AF220656 | Hs.82101 | 1.00E-145 | 3 | apoptosis-associated nuclear protein PHLDA1 |
| 40C11 | 3748 | 4497 | M27492 | Hs.82112 | 0 | 1 | interleukin 1 receptor mRNA, complete cds /cds=(82,17 |
| 481B6 | 3164 | 3609 | NM_000877 | Hs.82112 | 0 | 1 | interleukin 1 receptor, type I (IL1R1), mRNA / |
| 40H6 | 161 | 557 | AB049113 | Hs.82113 | 0 | 1 | DUT mRNA for dUTP pyrophosphatase, complete cd |
| 592B7 | 184 | 568 | NM_001948 | Hs.82113 | 1.00E-111 | 2 | dUTP pyrophosphatase (DUT), mRNA /cds=(29,523 |
| 114F1 | 465 | 720 | U70451 | Hs.82116 | 1.00E-135 | 1 | myeloid differentiation primary response protein My |
| 71H5 | 194 | 3415 | NM_006186 | Hs.82120 | 0 | 36 | nuclear receptor subfamily 4, group A, member |
| 75C1 | 1264 | 3422 | X75918 | Hs.82120 | 0 | 84 | NOT /cds=(317,2113) /gb=X75918 /gi=4158 |
| 40D1 | 1621 | 2080 | M90391 | Hs.82127 | 0 | 1 | putative IL-16 protein precursor, mRNA, comple |
| 71C4 | 678 | 5065 | NM_002460 | Hs.82132 | 0 | 88 | interferon regulatory factor 4 (IRF4), mRNA / |
| 75G12 | 3219 | 5316 | U52682 | Hs.82132 | 0 | 27 | lymphocyte specific interferon regulatory factor/in |
| 193G6 | 1118 | 2682 | NM_006874 | Hs.82143 | 1.00E-178 | 3 | E74-like factor 2 (ets domain transcription fa |
| 147F6 | 1484 | 1951 | AK025643 | Hs.82148 | 0 | 1 | FLJ21990 fls, clone HEP06386 /cds=(22,49 |
| 155E4 | 853 | 1264 | M64992 | Hs.82159 | 0 | 1 | prosome protein P30-33K (pros-30) mRNA, complete cd |
| 595F1 | 30 | 614 | NM_002786 | Hs.82159 | 0 | 3 | proteasome (prosome, macropain) subunit, alp |
| 58A4 | 473 | 1715 | NM_005655 | Hs.82173 | 0 | 3 | TGFB inducible early growth response (TIEG), m |
| 67E6 | 784 | 2109 | S81439 | Hs.82173 | 0 | 7 | EGR alpha=early growth response gene alpha [human, prostate |
| 593H2 | 132 | 722 | NM_000985 | Hs.82202 | 0 | 2 | ribosomal protein L17 (RPL17), mRNA /cds=(138, |
| 40H5 | 283 | 1442 | M37033 | Hs.82212 | 0 | 12 | CD53 glycoprotein mRNA, complete cds /cds=(93,752) / |
| 592C4 | 1 | 1442 | NM_000560 | Hs.82212 | 0 | 11 | CD53 antigen (CD53), mRNA /cds=(93,752) /gb=N |
| 460D4 | 1519 | 1845 | NM_002510 | Hs.82226 | 1.00E-160 | 1 | glycoprotein (transmembrane) nmb (GPNMB), mR |
| 61A8 | 507 | 736 | AF045229 | Hs.82280 | 1.00E-116 | 1 | regulator of G protein signaling 10 mRNA, compl |
| 45F7 | 418 | 651 | NM_002925 | Hs.82280 | 1.00E-119 | 1 | regulator of G-protein signalling 10 (RGS10), |
| 49C2 | 416 | 1323 | NM_006417 | Hs.82316 | 0 | 7 | interferon-induced, hepatitis C-associated |
| 41C11 | 847 | 1716 | X63717 | Hs.82359 | 0 | 2 | APO-1 cell surface antigen /cds=(220,122 |
| 71H4 | 15 | 1627 | NM_001781 | Hs.82401 | 0 | 21 | CD69 antigen (p60, early T-cell activation ant |
| 75B10 | 9 | 1627 | Z22576 | Hs.82401 | 0 | 33 | CD69 gene /cds=(81,680) /gb=Z22576 /gi=397938 / |
| 117B7 | 1441 | 1515 | NM_022059 | Hs.82407 | 7.00E-28 | 1 | CXC chemokine ligand 16 (CXCL16), mRNA /cds=(4 |
| 110D6 | 1219 | 1721 | AF006088 | Hs.82425 | 0 | 1 | Arp2/3 protein complex subunit p16-Arc (ARC16) |
| 598F10 | 39 | 1497 | NM_005717 | Hs.82425 | 0 | 5 | actin related protein 2/3 complex, subunit 5 (|
| 99A9 | 621 | 1214 | D26018 | Hs.82502 | 0 | 1 | mRNA for KIAA0039 gene, partial cds /cds=(0,1475) /gb |
| 183F6 | 222 | 2235 | NM_001637 | Hs.82542 | 0 | 2 | acyloxyacyl hydrolase (neutrophil) (AOAH), m |
| 459G4 | 5196 | 5801 | NM_003682 | Hs.82548 | 0 | 1 | MAP-kinase activating death domain (MADD), mR |
| 75A6 | 301 | 2231 | D85429 | Hs.82646 | 0 | 44 | heat shock protein 40, complete cds /c |
| 64A5 | 300 | 2008 | NM_006145 | Hs.82646 | 0 | 17 | heat shock 40kD protein 1 (HSPF1), mRNA /cds=(4 |
| 50E5 | 628 | 2399 | AK025459 | Hs.82689 | 0 | 2 | FLJ21806 fls, clone HEP00829, highly sim |
| 115C6 | 23 | 589 | NM_005087 | Hs.82712 | 0 | 1 | fragile X mental retardation, autosomal homol |
| 105H10 | 1017 | 1429 | M61199 | Hs.82767 | 0 | 1 | cleavage signal 1 protein mRNA, complete cds /cds=(97, |
| 461A11 | 204 | 748 | NM_006296 | Hs.82771 | 0 | 1 | vaccinia related kinase 2 (VRK2), mRNA /cds=(1 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|--|
| 39B4 | 1049 | 1203 | M25393 | Hs.82829 | 8.00E-83 | 1 | protein tyrosine phosphatase (PTPase) mRNA, complete |
| 590F5 | 123 | 436 | NM_002828 | Hs.82829 | 1.00E-178 | 1 | protein tyrosine phosphatase, non-receptor t |
| 517F10 | 1038 | 2618 | AK025583 | Hs.82845 | 0 | 9 | cDNA: FLJ21930 fis, clone HEP04301, highly sim |
| 40B7 | 972 | 1933 | M25280 | Hs.82848 | 0 | 6 | lymph node homing receptor mRNA, complete cds /cds=(11 |
| 515B1 | 1 | 2322 | NM_000655 | Hs.82848 | 0 | 12 | selectin L (lymphocyte adhesion molecule 1) (|
| 587A10 | 190 | 685 | NM_001344 | Hs.82890 | 0 | 1 | defender against cell death 1 (DAD1), mRNA /cd |
| 113G9 | 1 | 2812 | AF208850 | Hs.82911 | 0 | 7 | BM-008 mRNA, complete cds /cds=(341,844) /gb= |
| 127H6 | 1828 | 2501 | NM_003591 | Hs.82919 | 0 | 2 | cullin 2 (CUL2), mRNA /cds=(146,2383) /gb=NM_0 |
| 477E3 | 931 | 1777 | NM_006416 | Hs.82921 | 0 | 2 | solute carrier family 35 (CMP-sialic acid tran |
| 184D2 | 1355 | 1773 | AL049795 | Hs.83004 | 1.00E-164 | 1 | DNA sequence from clone RP4-622L5 on chromosome 1p34. |
| 41F10 | 507 | 774 | D49950 | Hs.83077 | 1.00E-150 | 1 | for interferon-gamma inducing factor(IGI |
| 482E7 | 499 | 774 | NM_001562 | Hs.83077 | 5.00E-97 | 1 | interleukin 18 (interferon-gamma-inducing f |
| 515C6 | 111 | 1162 | L38935 | Hs.83086 | 1.00E-107 | 2 | GT212 mRNA /cds=UNKNOWN /gb=L38935 /gi=100884 |
| 479D3 | 1775 | 2028 | NM_001760 | Hs.83173 | 1.00E-122 | 1 | cyclin D3 (CCND3), mRNA /cds=(165,1043) /gb=N |
| 583H12 | 945 | 1655 | NM_012151 | Hs.83363 | 0 | 9 | coagulation factor VIII-associated (intronic |
| 47B3 | 2140 | 3625 | M58603 | Hs.83428 | 0 | 13 | nuclear factor kappa-B DNA binding subunit (NF-kappa- |
| 58G1 | 2538 | 3625 | NM_003998 | Hs.83428 | 0 | 4 | nuclear factor of kappa light polypeptide gene |
| 477C6 | 1628 | 2131 | Z49995 | Hs.83465 | 0 | 1 | H.sapiens mRNA (non-coding; clone h2A) /cds=UNKNOWN /gb=Z4 |
| 587D10 | 1576 | 1900 | AF064839 | Hs.83530 | 0 | 2 | map 3p21; 3.15 cR from WI-9324 region, complete |
| 516B9 | 1662 | 3296 | X59405 | Hs.83532 | 0 | 4 | H.sapiens, gene for Membrane cofactor protein /cds=UNKNOWN |
| 459A5 | 120 | 298 | NM_017459 | Hs.83551 | 7.00E-42 | 1 | microfibrillar-associated protein 2 (MFAP2), |
| 591A12 | 321 | 1116 | NM_005731 | Hs.83583 | 0 | 17 | actin related protein 2/3 complex, subunit 2 (|
| 102C1 | 554 | 1127 | AK025198 | Hs.83623 | 0 | 1 | FLJ21545 fis, clone COL06195 /cds=UNKNOWN |
| 458C8 | 1022 | 1831 | NM_001619 | Hs.83636 | 0 | 1 | adrenergic, beta, receptor kinase 1 (ADRBK1), |
| 107G1 | 303 | 1008 | L20688 | Hs.83656 | 0 | 4 | GDP-dissociation inhibitor protein (Ly-GDI) mRNA, c |
| 597F8 | 293 | 1180 | NM_001175 | Hs.83656 | 0 | 55 | Rho GDP dissociation inhibitor (GDI) beta (AR |
| 591G5 | 1 | 216 | NM_003142 | Hs.83715 | 1.00E-108 | 3 | Sjogren syndrome antigen B (autoantigen La) (|
| 184H9 | 240 | 392 | X69804 | Hs.83715 | 4.00E-77 | 2 | for La/SS-B protein /cds=UNKNOWN /gb=X69804 |
| 193C10 | 1 | 1605 | BC000957 | Hs.83724 | 1.00E-154 | 4 | Similar to hypothetical protein MNCb-2146, c |
| 40A2 | 1101 | 1294 | U90904 | Hs.83724 | 1.00E-72 | 1 | clone 23773 mRNA sequence /cds=UNKNOWN /gb=U90904 /g |
| 57H2 | 191 | 422 | NM_001827 | Hs.83758 | 1.00E-126 | 1 | CDC28 protein kinase 2 (CKS2), mRNA /cds=(95,33 |
| 60E10 | 191 | 422 | X54942 | Hs.83758 | 1.00E-129 | 1 | ckshs2 mRNA for Cks1 protein homologue /cds=(95,3 |
| 164F5 | 1896 | 2293 | NM_016325 | Hs.83761 | 0 | 1 | zinc finger protein 274 (ZNF274), mRNA /cds=(4 |
| 463E6 | 555 | 1128 | NM_000791 | Hs.83765 | 0 | 1 | dihydrofolate reductase (DHFR), mRNA /cds=(47 |
| 194F8 | 1806 | 2223 | NM_002199 | Hs.83795 | 1.00E-161 | 1 | interferon regulatory factor 2 (IRF2), mRNA / |
| 520D11 | 180 | 1229 | NM_000365 | Hs.83848 | 0 | 5 | triosephosphate isomerase 1 (TPI1), mRNA /cds |
| 168B6 | 530 | 891 | U47924 | Hs.83848 | 0 | 1 | chromosome 12p13 sequence /cds=(373,1122) /gb=U4792 |
| 331E11 | 2591 | 3485 | NM_000480 | Hs.83918 | 0 | 8 | adenosine monophosphate deaminase (isoform E |
| 458A11 | 125 | 409 | NM_000396 | Hs.83942 | 1.00E-108 | 1 | cathepsin K (pseudosclerosis) (CTSK), mRNA / |
| 185H2 | 2501 | 2690 | NM_000195 | Hs.83951 | 3.00E-85 | 1 | Hermansky-Pudlak syndrome (HPS), mRNA /cds=(2 |
| 99D2 | 977 | 1191 | NM_019006 | Hs.83954 | 1.00E-97 | 1 | protein associated with PRK1 (AWP1), mRNA /cds |
| 167D5 | 2275 | 2755 | NM_000211 | Hs.83968 | 0 | 4 | integrin, beta 2 (antigen CD18 (p95), lymphocyt |
| 524B2 | 262 | 575 | BF028896 | Hs.83992 | 1.00E-155 | 1 | 601765270F1 cDNA, 5' end /clone=IMAGE:3997576 |
| 523B2 | 688 | 1065 | NM_015937 | Hs.84038 | 0 | 1 | CGI-06 protein (LOC51604), mRNA /cds=(6,1730) |
| 102F1 | 951 | 1416 | M63180 | Hs.84131 | 0 | 1 | threonyl-tRNA synthetase mRNA, complete cds /cds=(13 |
| 589D5 | 863 | 1700 | NM_006400 | Hs.84153 | 0 | 3 | dynactin 2 (p50) (DCTN2), mRNA /cds=(136,1356) |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|---|
| 108F6 | 448 | 704 | U70439 | Hs.84264 | 1.00E-117 | 1 | silver-stainable protein SSP29 mRNA, complete cds / |
| 146D6 | 1022 | 1253 | K01144 | Hs.84298 | 6.00E-95 | 2 | major histocompatibility class II antigen gamma chain |
| 188B10 | 823 | 1302 | NM_004355 | Hs.84298 | 0 | 1 | CD74 antigen (invariant polypeptide of major |
| 175D2 | 1060 | 1479 | M63488 | Hs.84318 | 1.00E-158 | 1 | replication protein A 70kDa subunit mRNA complete cds |
| 115F4 | 2305 | 2393 | NM_002945 | Hs.84318 | 2.00E-43 | 1 | replication protein A1 (70kD) (RPA1), mRNA /cd |
| 595H4 | 5400 | 5649 | NM_004239 | Hs.85092 | 1.00E-131 | 1 | thyroid hormone receptor interactor 11 (TRIP1 |
| 106F1 | 493 | 1371 | NM_017491 | Hs.85100 | 0 | 3 | WD repeat domain 1 (WDR1), transcript variant 1 |
| 40C10 | 438 | 880 | X57025 | Hs.85112 | 0 | 1 | IGF-I mRNA for insulin-like growth factor I /cds=(166, |
| 44C5 | 2247 | 2430 | AF017257 | Hs.85146 | 5.00E-89 | 1 | chromosome 21 derived BAC containing erythrobl |
| 45D4 | 1962 | 3324 | X79067 | Hs.85155 | 0 | 6 | H.sapiens ERF-1 mRNA 3' end /cds=UNKNOWN /gb=X79067 /gi=483 |
| 591B9 | 2378 | 2603 | NM_002880 | Hs.85181 | 1.00E-109 | 1 | v-raf-1 murine leukemia viral oncogene homolo |
| 39E2 | 67 | 2493 | X76488 | Hs.85226 | 0 | 3 | lysosomal acid lipase /cds=(145,1344) / |
| 62H12 | 1249 | 1975 | M12824 | Hs.85258 | 0 | 3 | T-cell differentiation antigen Leu-2/T8 mRNA, partia |
| 40C8 | 4505 | 4856 | X53587 | Hs.85266 | 0 | 1 | integrin beta 4 /cds=UNKNOWN /gb=X53587 /gi= |
| 40E11 | 1983 | 2633 | S53911 | Hs.85289 | 0 | 1 | CD34=glycoprotein expressed in lymphohematopoietic proge |
| 135A2 | 121 | 695 | BC001646 | Hs.85301 | 0 | 2 | clone MGC:2392, mRNA, complete cds /cds=(964, |
| 459H4 | 33 | 244 | AK027067 | Hs.85567 | 2.00E-90 | 1 | cDNA: FLJ23414 fis, clone HEP20704 /cds=(37,10 |
| 479A4 | 5556 | 5974 | AB040974 | Hs.85752 | 1.00E-171 | 1 | mRNA for KIAA1541 protein, partial cds /cds=(9 |
| 146C3 | 1610 | 2062 | AL049796 | Hs.85769 | 0 | 1 | DNA sequence from clone RP4-561L24 on chromosome 1p22 |
| 463H11 | 871 | 1153 | NM_006546 | Hs.86088 | 5.00E-83 | 1 | IGF-II mRNA-binding protein 1 (IMP-1), mRNA / |
| 480A12 | 2 | 165 | NM_004876 | Hs.86371 | 7.00E-84 | 1 | zinc finger protein 254 (ZNF254), mRNA /cds=(1 |
| 192F7 | 2854 | 3462 | AF198614 | Hs.86386 | 0 | 3 | Mcl-1 (MCL-1) and Mcl-1 delta S/TM (MCL-1) gene |
| 459G3 | 12 | 577 | AL049340 | Hs.86405 | 0 | 1 | mRNA; cDNA DKFZp564P056 (from clone DKFZp564P0 |
| 460E4 | 2361 | 2787 | NM_000161 | Hs.86724 | 0 | 2 | GTP cyclohydrolase 1 (dopa-responsive dystoni |
| 62F9 | 834 | 1282 | M60724 | Hs.86858 | 0 | 1 | p70 ribosomal S6 kinase alpha-I mRNA, complete cds /cd |
| 187E7 | 84 | 766 | NM_001695 | Hs.86905 | 0 | 1 | ATPase, H+ transporting, lysosomal (vacuolar |
| 159D4 | 315 | 559 | J03798 | Hs.86948 | 1.00E-113 | 1 | autoantigen small nuclear ribonucleoprotein Sm-D mR |
| 459F9 | 1557 | 1619 | NM_006938 | Hs.86948 | 2.00E-25 | 1 | small nuclear ribonucleoprotein D1 polypeptid |
| 480G11 | 87 | 603 | BG168139 | Hs.87113 | 0 | 1 | 602341526F1 cDNA, 5' end /clone=IMAGE:4449343 |
| 41D6 | 2208 | 2320 | M35999 | Hs.87149 | 4.00E-39 | 1 | platelet glycoprotein IIIa (GPIIIa) mRNA, complete c |
| 462H11 | 387 | 648 | NM_003806 | Hs.87247 | 1.00E-133 | 1 | harakiri, BCL2-interacting protein (contains |
| 99D7 | 614 | 5517 | NM_003246 | Hs.87409 | 0 | 62 | thrombospondin 1 (THBS1), mRNA /cds=(111,3623 |
| 39B8 | 2130 | 5517 | X14787 | Hs.87409 | 0 | 33 | thrombospondin /cds=(111,3623) /gb=X14787 |
| 525A2 | 329 | 560 | NM_007047 | Hs.87497 | 1.00E-129 | 2 | butyrophilin, subfamily 3, member A2 (BTN3A2) |
| 583F2 | 3303 | 3622 | D63876 | Hs.87726 | 1.00E-155 | 1 | mRNA for KIAA0154 gene, partial cds /cds=(0,2080) /gb |
| 184D7 | 2211 | 2556 | M34181 | Hs.87773 | 1.00E-165 | 1 | testis-specific cAMP-dependent protein kinase catal |
| 460A4 | 499 | 1074 | AL117637 | Hs.87794 | 0 | 1 | mRNA; cDNA DKFZp434I225 (from clone DKFZp434I2 |
| 459G2 | 258 | 452 | AW967701 | Hs.87912 | 8.00E-88 | 1 | EST379776 cDNA /gb=AW967701 /gi=8157540 /ug= |
| 74H7 | 1660 | 2397 | AK026960 | Hs.88044 | 0 | 9 | FLJ23307 fis, clone HEP11549, highly sim |
| 463D12 | 351 | 568 | AI184553 | Hs.88130 | 1.00E-118 | 1 | qd60a05.x1 cDNA, 3' end /clone=IMAGE:1733840 |
| 595B1 | 309 | 986 | NM_003454 | Hs.88219 | 0 | 1 | zinc finger protein 200 (ZNF200), mRNA /cds=(2 |
| 458D3 | 1018 | 1285 | NM_000487 | Hs.88251 | 6.00E-74 | 1 | arylsulfatase A (ARSA), mRNA /cds=(375,1898) |
| 462F4 | 4272 | 4846 | AJ271878 | Hs.88414 | 0 | 1 | mRNA for putative transcription factor (BACH2 |
| 460B12 | 1267 | 2022 | NM_006800 | Hs.88764 | 0 | 3 | male-specific lethal-3 (Drosophila)-like 1 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|-----|--|
| 461A4 | 2039 | 2421 | AL161659 | Hs.88820 | 0 | 1 | DNA sequence from clone RP11-526K24 on chromosome 20 |
| 460F9 | 3413 | 3654 | NM_000397 | Hs.88974 | 1.00E-133 | 1 | cytochrome b-245, beta polypeptide (chronic g |
| 459G9 | 790 | 1160 | NM_006228 | Hs.89040 | 1.00E-145 | 1 | prepronociceptin (PNOC), mRNA /cds=(211,741) |
| 70H12 | 1 | 661 | AV716500 | Hs.89104 | 0 | 274 | AV716500 cDNA, 5' end /clone=DCBAKA08 /clone_ |
| 469H5 | 1620 | 2142 | AB040961 | Hs.89135 | 0 | 1 | mRNA for KIAA1528 protein, partial cds /cds=(4 |
| 175G6 | 2069 | 2501 | D83243 | Hs.89385 | 0 | 1 | NPAT mRNA, complete cds /cds=(66,4349) /gb=D83243 /g |
| 592B10 | 3703 | 3936 | NM_002519 | Hs.89385 | 1.00E-130 | 1 | nuclear protein, ataxia-telangiectasia locu |
| 120B7 | 337 | 630 | NM_005176 | Hs.89399 | 1.00E-114 | 1 | ATP synthase, H+ transporting, mitochondrial |
| 39D2 | 370 | 1892 | AF147204 | Hs.89414 | 0 | 68 | chemokine receptor CXCR4-Lo (CXCR4) mRNA, alt |
| 99H4 | 7 | 1625 | NM_003467 | Hs.89414 | 0 | 137 | chemokine (C-X-C motif), receptor 4 (fusin) (C |
| 106D2 | 2 | 266 | U03644 | Hs.89421 | 1.00E-143 | 1 | receptin mRNA, complete cds /cds=(32,1387) /gb=U03644 |
| 41F5 | 1203 | 1522 | M16336 | Hs.89476 | 1.00E-170 | 1 | T-cell surface antigen CD2 (T11) mRNA, complete cds, c |
| 463A3 | 876 | 1025 | NM_000698 | Hs.89499 | 1.00E-79 | 1 | arachidonate 5-lipoxygenase (ALOX5), mRNA /c |
| 47D12 | 1198 | 4887 | AB028969 | Hs.89519 | 0 | 2 | for KIAA1046 protein, complete cds /cds=(|
| 498G2 | 4420 | 5265 | NM_014928 | Hs.89519 | 0 | 2 | KIAA1046 protein (KIAA1046), mRNA /cds=(577,1 |
| 589G3 | 598 | 689 | NM_002796 | Hs.89545 | 4.00E-45 | 2 | proteasome (prosome, macropain) subunit, bet |
| 331B1 | 699 | 788 | S71381 | Hs.89545 | 1.00E-41 | 1 | prosome beta-subunit=multicatalytic proteinase complex |
| 110A2 | 1403 | 1739 | AK026432 | Hs.89555 | 1.00E-177 | 1 | FLJ22779 fis, clone KAIA1741 /cds=(234,1 |
| 118E4 | 780 | 1672 | NM_002110 | Hs.89555 | 0 | 5 | hemopoietic cell kinase (HCK), mRNA /cds=(168, |
| 41B8 | 570 | 1166 | M89957 | Hs.89575 | 0 | 1 | immunoglobulin superfamily member B cell receptor co |
| 44A11 | 2567 | 2808 | L20814 | Hs.89582 | 1.00E-115 | 1 | glutamate receptor 2 (HBGR2) mRNA, complete cds /cds=(|
| 191G11 | 309 | 596 | NM_006284 | Hs.89657 | 1.00E-162 | 11 | TATA box binding protein (TBP)-associated fac |
| 72G5 | 1172 | 1575 | AX023367 | Hs.89679 | 0 | 38 | Sequence 38 from Patent WO0006605 |
| 71B12 | 40 | 559 | NM_000586 | Hs.89679 | 0 | 13 | interleukin 2 (IL2), mRNA /cds=(47,517) /gb=N |
| 179G12 | 158 | 737 | M36821 | Hs.89690 | 0 | 1 | cytokine (GRO-gamma) mRNA, complete cds |
| 193B5 | 680 | 1146 | NM_002994 | Hs.89714 | 0 | 17 | small inducible cytokine subfamily B (Cys-X-Cy |
| 182G10 | 681 | 1146 | X78686 | Hs.89714 | 0 | 7 | ENA-78 mRNA /cds=(106,450) /gb=X78686 /gi=47124 |
| 191C6 | 617 | 1597 | NM_021950 | Hs.89751 | 0 | 2 | membrane-spanning 4-domains, subfamily A, m |
| 40H3 | 1347 | 1597 | X07203 | Hs.89751 | 3.00E-71 | 1 | CD20 receptor (S7) /cds=(90,983) /gb=X07203 |
| 458H2 | 3524 | 4331 | NM_002024 | Hs.89764 | 0 | 2 | fragile X mental retardation 1 (FMR1), mRNA /c |
| 40F6 | 1665 | 2210 | D38081 | Hs.89887 | 0 | 1 | thromboxane A2 receptor, complete cds /cds=(9 |
| 473E1 | 578 | 956 | AL515381 | Hs.89986 | 1.00E-172 | 1 | AL515381 cDNA /clone=CL0BB017ZH06-(3-prime) |
| 126A12 | 770 | 982 | AL558028 | Hs.90035 | 1.00E-102 | 1 | AL558028 cDNA /clone=CS0DJ002YF02-(5-prime) |
| 183E12 | 2203 | 2814 | NM_001316 | Hs.90073 | 0 | 1 | chromosome segregation 1 (yeast homolog)-like |
| 145H12 | 1602 | 1811 | AK026766 | Hs.90077 | 1.00E-113 | 2 | FLJ23113 fis, clone LNG07875, highly sim |
| 62C2 | 1472 | 2610 | AB023420 | Hs.90093 | 0 | 2 | for heat shock protein apg-2, complete cds |
| 46H6 | 3172 | 3411 | D26488 | Hs.90315 | 6.00E-86 | 1 | mRNA for KIAA0007 gene, partial cds /cds=(0,2062) /gb |
| 116E2 | 1637 | 2016 | AK025800 | Hs.90421 | 1.00E-118 | 1 | cDNA: FLJ22147 fis, clone HEP22163, highly sim |
| 525H3 | 6 | 1231 | NM_004261 | Hs.90606 | 0 | 2 | 15 kDa selenoprotein (SEP15), mRNA /cds=(4,492 |
| 184D8 | 287 | 387 | BE888304 | Hs.90654 | 1.00E-46 | 2 | 601514033F1 cDNA, 5' end /clone=IMAGE:3915177 |
| 99D4 | 1948 | 4309 | D50918 | Hs.90998 | 0 | 5 | mRNA for KIAA0128 gene, partial cds /cds=(0,1276) /gb |
| 72B9 | 571 | 1312 | AK026954 | Hs.91065 | 0 | 1 | FLJ23301 fis, clone HEP11120 /cds=(2,188 |
| 586H8 | 189 | 478 | NM_000987 | Hs.91379 | 2.00E-83 | 1 | ribosomal protein L26 (RPL26), mRNA /cds=(6,44 |
| 160A12 | 1 | 132 | X69392 | Hs.91379 | 4.00E-69 | 5 | ribosomal protein L26 /cds=(6,443) /gb= |
| 331H4 | 1632 | 2166 | AK027210 | Hs.91448 | 0 | 1 | FLJ23557 fis, clone LNG09686, highly sim |
| 473E6 | 915 | 1390 | NM_004556 | Hs.91640 | 0 | 2 | nuclear factor of kappa light polypeptide gene |
| 69E4 | 673 | 1328 | AB007956 | Hs.92381 | 1.00E-122 | 2 | mRNA, chromosome 1 specific transcript KIAA04 |
| 182F10 | 117 | 781 | AF070523 | Hs.92384 | 0 | 1 | JWA protein mRNA, complete cds /cds=(115,681) |
| 585F10 | 77 | 1890 | NM_006407 | Hs.92384 | 0 | 13 | vitamin A responsive; cytoskeleton related (J |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----------|-----------|----|--|
| 469G3 | 2061 | 2293 | AK025683 | Hs.92414 | 1.00E-110 | 1 | cDNA: FLJ22030 fis, clone HEP08669 /cds=UNKNOWN |
| 472H4 | 247 | 671 | AW978555 | Hs.92448 | 0 | 1 | EST390664 cDNA /gb=AW978555 /gi=8169822 /ug= |
| 193F11 | 2051 | 4721 | NM_003103 | Hs.92909 | 0 | 3 | SON DNA binding protein (SON), mRNA /cds=(414,4 |
| 37E7 | 1287 | 1805 | AK002059 | Hs.92918 | 0 | 1 | FLJ11197 fis, clone PLACE1007690 /cds=(37 |
| 111D7 | 244 | 596 | NM_016623 | Hs.92918 | 1.00E-166 | 1 | hypothetical protein (BM-009), mRNA /cds=(385 |
| 41B10 | 1216 | 1530 | U24577 | Hs.93304 | 1.00E-173 | 1 | LDL-phospholipase A2 mRNA, complete cds /cds=(216,15 |
| 48B4 | 76 | 723 | NM_001417 | Hs.93379 | 0 | 5 | eukaryotic translation initiation factor 4B |
| 39F8 | 76 | 876 | X55733 | Hs.93379 | 0 | 1 | initiation factor 4B cDNA /cds=(0,1835) /gb=X557 |
| 471B10 | 660 | 886 | NM_007020 | Hs.93502 | 1.00E-125 | 1 | U1-snRNP binding protein homolog (70kD) (U1SN |
| 467A3 | 1189 | 1284 | X91348 | Hs.93522 | 3.00E-36 | 1 | H.sapiens predicted non coding cDNA (DGCR5) /cds=UNKNOWN / |
| 461B5 | 652 | 874 | NM_003367 | Hs.93649 | 1.00E-104 | 1 | upstream transcription factor 2, c-fos intera |
| 62B8 | 1386 | 1739 | J05016 | Hs.93659 | 1.00E-170 | 1 | (clone pA3) protein disulfide isomerase related prote |
| 461E7 | 1931 | 2086 | NM_004911 | Hs.93659 | 1.00E-65 | 1 | protein disulfide isomerase related protein (|
| 458G11 | 2423 | 3161 | AB040959 | Hs.93836 | 0 | 1 | mRNA for KIAA1526 protein, partial cds /cds=(0 |
| 104E3 | 516 | 981 | AK000967 | Hs.93872 | 0 | 1 | FLJ10105 fis, clone HEMBA1002542 /cds=UN |
| 41B6 | 87 | 846 | X04430 | Hs.93913 | 0 | 2 | IFN-beta 2a mRNA for interferon-beta-2 /cds=(86,724) |
| 179H7 | 1610 | 1682 | AF009746 | Hs.94395 | 9.00E-34 | 1 | peroxisomal membrane protein 69 (PMP69) mRNA, |
| 470G3 | 74 | 493 | NM_007221 | Hs.94446 | 0 | 1 | polyamine-modulated factor 1 (PMF1), mRNA /c |
| 472A5 | 2325 | 2429 | AK022267 | Hs.94576 | 2.00E-48 | 1 | cDNA FLJ12205 fis, clone MAMMA1000931 /cds=UNK |
| 459C9 | 5356 | 6120 | NM_006421 | Hs.94631 | 0 | 3 | brefeldin A-inhibited guanine nucleotide-exc |
| 465F8 | 3580 | 4049 | NM_015125 | Hs.94970 | 0 | 1 | KIAA0306 protein (KIAA0306), mRNA /cds=(0,436 |
| 57B9 | 4145 | 4379 | NM_005109 | Hs.95220 | 1.00E-126 | 1 | oxidative-stress responsive 1 (OSR1), mRNA /c |
| 160D6 | 30 | 480 | X01451 | Hs.95327 | 0 | 2 | gene for 20K T3 glycoprotein (T3-delta-chain) of T-c |
| 512G1 | 1 | 415 | BF107010 | Hs.95388 | 1.00E-175 | 2 | 601824367F1 cDNA, 5' end /clone=IMAGE:4043920 |
| 593E11 | 24 | 273 | BG291649 | Hs.95835 | 1.00E-79 | 10 | 602385778F1 cDNA, 5' end /clone=IMAGE:4514827 |
| 41H2 | 1011 | 1306 | M28170 | Hs.96023 | 1.00E-114 | 1 | cell surface protein CD19 (CD19) gene, complete cds /c |
| 149G8 | 213 | 435 | BF222826 | Hs.96487 | 1.00E-119 | 2 | 7q23f06.x1 /clone=IMAGE /gb=BF222826 /g |
| 101G7 | 2266 | 3173 | AL133227 | Hs.96560 | 0 | 2 | DNA sequence from clone RP11-394O2 on chromosome 20 C |
| 103E6 | 2840 | 3451 | BC000143 | Hs.96560 | 0 | 1 | Similar to hypothetical protein FLJ11656, cl |
| 107G5 | 226 | 2349 | BF673956 | Hs.96566 | 7.00E-24 | 1 | 602137338F1 cDNA, 5' end /clone=IMAGE:4274048 |
| 461A12 | 3602 | 4135 | AB014555 | Hs.96731 | 0 | 2 | mRNA for KIAA0655 protein, partial cds /cds=(0 |
| 595A8 | 82 | 1571 | NM_000734 | Hs.97087 | 1.00E-147 | 10 | CD3Z antigen, zeta polypeptide (TIT3 complex) |
| 479H8 | 883 | 1378 | NM_014373 | Hs.97101 | 0 | 3 | putative G protein-coupled receptor (GPCR150) |
| 466D12 | 2001 | 5732 | NM_012072 | Hs.97199 | 0 | 2 | complement component C1q receptor (C1QR), mRN |
| 194B3 | 1835 | 2898 | NM_002990 | Hs.97203 | 0 | 2 | small inducible cytokine subfamily A (Cys-Cys) |
| 109E9 | 2880 | 3536 | AF083322 | Hs.97437 | 0 | 1 | centriole associated protein CEP110 mRNA, com |
| 459H5 | 9 | 230 | BF438062 | Hs.97896 | 1.00E-116 | 1 | 7q66e08.x1 cDNA /clone=IMAGE /gb=BF438062 /g |
| 473A4 | 871 | 1327 | NM_007015 | Hs.97932 | 0 | 1 | chondromodulin I precursor (CHM-I), mRNA /cds |
| 466E9 | 1408 | 1808 | AL442083 | Hs.98026 | 1.00E-172 | 2 | mRNA; cDNA DKFZp547D144 (from clone DKFZp547D1 |
| 460E3 | 1290 | 1687 | AF038564 | Hs.98074 | 0 | 1 | atrophin-1 interacting protein 4 (AIP4) mRNA, |
| 462E6 | 103 | 642 | NM_016440 | Hs.98289 | 0 | 1 | VRK3 for vaccinia related kinase 3 (LOC51231), |
| 460B8 | 114 | 546 | AA418743 | Hs.98306 | 1.00E-178 | 1 | zv98f06.s1 cDNA, 3' end /clone=IMAGE:767843 / |
| 124A8 | 1 | 157 | NM_019044 | Hs.98324 | 2.00E-69 | 1 | hypothetical protein (FLJ10996), mRNA /cds=(|
| 71B10 | 79 | 520 | AI761058 | Hs.98531 | 1.00E-112 | 34 | wi69b03.x1 cDNA, 3' end /clone=IMAGE:2398541 |
| 49F1 | 36 | 435 | AA913840 | Hs.98903 | 0 | 1 | ol39d11.s1 cDNA, 3' end /clone=IMAGE:1525845 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|--|
| 462F6 | 61 | 201 | AC006276 | Hs.99093 | 2.00E-74 | 1 | chromosome 19, cosmid R28379 /cds=(0,633) /gb |
| 473A2 | 47 | 475 | BE326857 | Hs.99237 | 0 | 1 | hr65h06.x1 cDNA, 3' end /clone=IMAGE:3133403 |
| 599D8 | 1468 | 1748 | NM_005825 | Hs.99491 | 1.00E-132 | 1 | RAS guanyl releasing protein 2 (calcium and DA |
| 459F8 | 300 | 541 | AW444899 | Hs.99665 | 1.00E-123 | 1 | UI-H-B13-ajz-d-07-0-UI.s1 cDNA, 3' end /clon |
| 163H9 | 8 | 141 | AL049319 | Hs.99821 | 2.00E-58 | 1 | cDNA DKFZp564C046 (from clone DKFZp564C0 |
| 165H8 | 1176 | 1930 | NM_015400 | Hs.99843 | 0 | 2 | DKFZP586N0721 protein (DKFZP586N0721), mRNA |
| 188C9 | 543 | 998 | NM_001436 | Hs.99853 | 0 | 2 | fibrillarin (FBL), mRNA /cds=(59,1024) /gb=N |
| 37H2 | 759 | 2017 | AC018755 | Hs.99855 | 0 | 4 | chromosome 19, BAC BC330783 (CIT-HSPC_470E3), |
| 127H3 | 758 | 2183 | NM_001462 | Hs.99855 | 0 | 5 | formyl peptide receptor-like 1 (FPRL1), mRNA |
| 62F2 | 1 | 642 | BF315159 | Hs.99858 | 0 | 6 | 601899519F1 cDNA, 5' end /clone=IMAGE:4128749 |
| 599A7 | 26 | 838 | NM_000972 | Hs.99858 | 0 | 11 | ribosomal protein L7a (RPL7A), mRNA /cds=(31,8 |
| 167B3 | 1994 | 2101 | AB032251 | Hs.99872 | 2.00E-37 | 1 | BPTF mRNA for bromodomain PHD finger transcript |
| 41G8 | 461 | 751 | L08096 | Hs.99899 | 1.00E-161 | 1 | CD27 ligand mRNA, complete cds /cds=(150,731) /gb=L08 |
| 479C10 | 327 | 738 | NM_001252 | Hs.99899 | 0 | 1 | tumor necrosis factor (ligand) superfamily, m |
| 36D8 | 1180 | 2315 | AL162047 | Hs.99908 | 0 | 7 | cDNA DKFZp762E1112 (from clone DKFZp762E |
| 593E2 | 62 | 435 | NM_000983 | Hs.99914 | 1.00E-145 | 1 | ribosomal protein L22 (RPL22), mRNA /cds=(51,4 |
| 478C8 | 48 | 311 | NM_000023 | Hs.99931 | 1.00E-112 | 1 | sarcoglycan, alpha (50kD dystrophin-associat |
| 61A1 | 827 | 1053 | S62140 | Hs.99969 | 1.00E-126 | 1 | TLS=translocated in liposarcoma [human, mRNA, 1824 nt] /cd |
| 40C7 | 971 | 1724 | X69819 | Hs.99995 | 0 | 1 | ICAM-3 mRNA /cds=(8,1651) /gb=X69819 /gi=32627 |
| 116F8 | 109 | 376 | NM_002964 | Hs.100000 | 1.00E-123 | 5 | S100 calcium-binding protein A8 (calgranulin |
| 121F4 | 30 | 540 | NM_001629 | Hs.100194 | 1.00E-118 | 7 | arachidonate 5-lipoxygenase-activating pro |
| 46G10 | 5175 | 5624 | NM_003605 | Hs.100293 | 0 | 2 | O-linked N-acetylglucosamine (GlcNAc) transf |
| 49E4 | 1279 | 2585 | NM_006773 | Hs.100555 | 0 | 4 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide |
| 61E1 | 1279 | 1767 | X98743 | Hs.100555 | 0 | 2 | RNA helicase (Myc-regulated dead box pro |
| 460A10 | 824 | 1321 | NM_018099 | Hs.100895 | 0 | 1 | hypothetical protein FLJ10462 (FLJ10462), mR |
| 458F1 | 1 | 303 | R18757 | Hs.100896 | 1.00E-157 | 1 | yg17e04.r1 cDNA, 5' end /clone=IMAGE:32522 /c |
| 64B8 | 2062 | 2711 | AB007859 | Hs.100955 | 0 | 1 | mRNA for KIAA0399 protein, partial cds /cds=(0, |
| 515H6 | 131 | 201 | NM_001207 | Hs.101025 | 6.00E-33 | 1 | basic transcription factor 3 (BTF3), mRNA /cd |
| 472H12 | 10 | 358 | AW968686 | Hs.101340 | 0 | 1 | EST380762 cDNA /gb=AW968686 /gi=8158527 /ug= |
| 99G6 | 2427 | 4860 | AB002384 | Hs.101359 | 0 | 9 | mRNA for KIAA0386 gene, complete cds /cds=(177,3383) |
| 62E12 | 193 | 573 | AI936516 | Hs.101370 | 1.00E-100 | 6 | wd28h07.x1 cDNA, 3' end /clone=IMAGE:2329501 |
| 493B9 | 3 | 638 | AL583391 | Hs.101370 | 0 | 8 | AL583391 cDNA /clone=CS0DL012YA12-(3-prime) |
| 117D4 | 2812 | 2966 | NM_006291 | Hs.101382 | 7.00E-79 | 1 | tumor necrosis factor, alpha-induced protein |
| 462A9 | 382 | 620 | BC000764 | Hs.101514 | 1.00E-133 | 1 | hypothetical protein FLJ10342, clone MGC:27 |
| 193G3 | 3368 | 3659 | AL139349 | Hs.102178 | 3.00E-88 | 1 | DNA sequence from clone RP11-261P9 on chromosome 20. |
| 62H6 | 3035 | 4257 | AF193339 | Hs.102506 | 0 | 5 | eukaryotic translation initiation factor 2 a |
| 46E2 | 3223 | 4023 | NM_004836 | Hs.102506 | 0 | 2 | eukaryotic translation initiation factor 2-a |
| 460C4 | 151 | 635 | AW978361 | Hs.102630 | 0 | 2 | EST390470 cDNA /gb=AW978361 /gi=8169626 /ug= |
| 58E4 | 1 | 321 | BF970875 | Hs.102647 | 1.00E-177 | 2 | 602271536F1 cDNA, 5' end /clone=IMAGE:4359609 |
| 189G9 | 5473 | 6137 | NM_018489 | Hs.102652 | 0 | 2 | hypothetical protein ASH1 (ASH1), mRNA /cds=(|
| 111H5 | 3043 | 3331 | AK000354 | Hs.102669 | 1.00E-125 | 1 | cDNA FLJ20347 fis, clone HEP13790 /cds=(708,14 |
| 465B8 | 27 | 348 | AI707589 | Hs.102793 | 1.00E-164 | 1 | as30b05.x1 cDNA, 3' end /clone=IMAGE:2318673 |
| 126G11 | 1069 | 1431 | NM_016128 | Hs.102950 | 0 | 2 | coat protein gamma-cop (LOC51137), mRNA /cds= |
| 165H5 | 326 | 564 | BF698884 | Hs.103180 | 4.00E-71 | 1 | 602126455F1 cDNA, 5' end /clone=IMAGE:4283340 |
| 108H6 | 2135 | 2505 | AB023187 | Hs.103329 | 1.00E-59 | 1 | for KIAA0970 protein, complete cds /cds=(|
| 521C9 | 1440 | 1962 | AL136885 | Hs.103378 | 0 | 2 | mRNA; cDNA DKFZp434P116 (from clone DKFZp434P1 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|---|
| 458C9 | 3876 | 4415 | AF254411 | Hs.103521 | 0 | 1 | ser/arg-rich pre-mRNA splicing factor SR-A1 (|
| 99F6 | 349 | 767 | NM_018623 | Hs.103657 | 0 | 5 | hypothetical protein PRO2219 (PRO2219), mRNA |
| 162G11 | 1745 | 2161 | AF117829 | Hs.103755 | 1.00E-151 | 1 | 8q21.3: RICK gene /cds=(224,1846) /gb=AF11782 |
| 188G1 | 1757 | 2566 | NM_004501 | Hs.103804 | 0 | 2 | heterogeneous nuclear ribonucleoprotein U (|
| 470F7 | 56 | 302 | NM_024056 | Hs.103834 | 1.00E-137 | 1 | hypothetical protein MGC5576 (MGC5576), mRNA |
| 460A11 | 225 | 288 | BG033732 | Hs.103902 | 3.00E-29 | 1 | 602301101F1 cDNA, 5' end /clone=IMAGE:4402465 |
| 522H7 | 2157 | 2397 | NM_006342 | Hs.104019 | 1.00E-132 | 1 | transforming, acidic coiled-coil containing |
| 39E5 | 1007 | 2535 | L12168 | Hs.104125 | 0 | 10 | adenylyl cyclase-associated protein (CAP) mRNA |
| 98C11 | 1023 | 2558 | NM_006367 | Hs.104125 | 0 | 29 | adenylyl cyclase-associated protein (CAP), m |
| 461B2 | 88 | 221 | AW968823 | Hs.104157 | 1.00E-38 | 1 | EST380899 cDNA /gb=AW968823 /gi=8158664 /ug= |
| 110A4 | 4010 | 4306 | AB023143 | Hs.104305 | 1.00E-125 | 1 | for KIAA0926 protein, complete cds /cds=(|
| 122H5 | 4634 | 5232 | NM_014922 | Hs.104305 | 0 | 2 | KIAA0926 protein (KIAA0926), mRNA /cds=(522,4 |
| 105C2 | 1817 | 2174 | AB020669 | Hs.104315 | 0 | 1 | for KIAA0862 protein, complete cds /cds=(|
| 37G4 | 1321 | 2886 | AF016495 | Hs.104624 | 0 | 46 | small solute channel 1 (SSC1) mRNA, complete cd |
| 98D4 | 1578 | 2946 | NM_020980 | Hs.104624 | 0 | 71 | aquaporin 9 (AQP9), mRNA /cds=(286,1173) /gb= |
| 458E6 | 1007 | 1399 | NM_015898 | Hs.104640 | 0 | 1 | HIV-1 inducer of short transcripts binding pro |
| 462C11 | 1037 | 1532 | NM_018492 | Hs.104741 | 0 | 1 | PDZ-binding kinase; T-cell originated protein |
| 118G4 | 1940 | 2513 | BC002538 | Hs.104879 | 0 | 2 | serine (or cysteine) proteinase inhibitor, c |
| 496A7 | 1 | 618 | BG035120 | Hs.104893 | 0 | 4 | 602324815F1 cDNA, 5' end /clone=IMAGE:4413099 |
| 112G4 | 3421 | 3933 | NM_003633 | Hs.104925 | 0 | 2 | ectodermal-neural cortex (with BTB-like doma |
| 460E2 | 16 | 460 | AI479075 | Hs.104985 | 0 | 1 | tm30h01.x1 cDNA, 3' end /clone=IMAGE:2158129 |
| 461H4 | 1500 | 1781 | NM_020979 | Hs.105052 | 1.00E-148 | 1 | adaptor protein with pleckstrin homology and |
| 469C7 | 231 | 380 | NM_018331 | Hs.105216 | 1.00E-77 | 1 | hypothetical protein FLJ11125 (FLJ11125), mR |
| 461B6 | 84 | 489 | AA489227 | Hs.105230 | 0 | 1 | aa57f07.s1 cDNA, 3' end /clone=IMAGE:825061 / |
| 462D5 | 1735 | 2129 | NM_015393 | Hs.105460 | 0 | 1 | DKFZP564O0823 protein (DKFZP564O0823), mRNA |
| 465H7 | 1 | 624 | NM_017780 | Hs.105461 | 0 | 1 | hypothetical protein FLJ20357 (FLJ20357), mR |
| 471F3 | 819 | 1126 | AY007243 | Hs.105484 | 1.00E-160 | 1 | regenerating gene type IV mRNA, complete cds / |
| 473C1 | 42 | 479 | AW970759 | Hs.105621 | 0 | 1 | EST382842 cDNA /gb=AW970759 /gi=8160604 /ug= |
| 102A9 | 1 | 331 | AK025947 | Hs.105664 | 0 | 1 | FLJ22294 fis, clone HRC04426 /cds=(240,6 |
| 465G9 | 193 | 524 | AI475680 | Hs.105676 | 0 | 1 | tc93d12.x1 cDNA, 3' end /clone=IMAGE:2073719 |
| 469G2 | 1528 | 1625 | AK022481 | Hs.105779 | 8.00E-38 | 1 | cDNA FLJ12419 fis, clone MAMMA1003047, highly |
| 482A9 | 289 | 839 | NM_012483 | Hs.105806 | 0 | 3 | granulysin (GNLY), transcript variant 519, m |
| 595B11 | 918 | 1300 | NM_002343 | Hs.105938 | 0 | 1 | lactotransferrin (LTF), mRNA /cds=(294,2429) |
| 69B3 | 3649 | 4226 | Y13247 | Hs.106019 | 0 | 1 | fb19 mRNA /cds=(539,3361) /gb=Y13247 /gi=2117 |
| 459E8 | 106 | 563 | NM_013322 | Hs.106260 | 0 | 1 | sorting nexin 10 (SNX10), mRNA /cds=(128,733) |
| 459E2 | 1939 | 2361 | NM_003171 | Hs.106469 | 0 | 1 | suppressor of var1 (S.cerevisiae) 3-like 1 (S |
| 98H12 | 658 | 1040 | BC002748 | Hs.106650 | 0 | 2 | Similar to hypothetical protein FLJ20533, cl |
| 594H5 | 1418 | 1501 | NM_001568 | Hs.106673 | 6.00E-36 | 1 | eukaryotic translation initiation factor 3, |
| 194H12 | 751 | 1233 | NM_021626 | Hs.106747 | 0 | 1 | serine carboxypeptidase 1 precursor protein (|
| 138G6 | 2749 | 3214 | AF189723 | Hs.106778 | 0 | 3 | calcium transport ATPase ATP2C1 (ATP2C1A) mRN |
| 56A5 | 1 | 1089 | AL355722 | Hs.106875 | 0 | 2 | EST from clone 35214, full insert /cds=UNKNOWN |
| 67H8 | 844 | 1102 | X71490 | Hs.106876 | 1.00E-103 | 1 | vacuolar proton ATPase, subunit D /cds=(2 |
| 463G10 | 538 | 725 | AF035306 | Hs.106890 | 1.00E-102 | 1 | clone 23771 mRNA sequence /cds=UNKNOWN |
| 121H2 | 14 | 394 | NM_016619 | Hs.107139 | 0 | 1 | /gb=AF |
| 185D12 | 118 | 884 | NM_001564 | Hs.107153 | 0 | 3 | hypothetical protein (LOC51316), mRNA /cds=(|
| 186D6 | 1140 | 1507 | NM_017892 | Hs.107213 | 0 | 1 | inhibitor of growth family, member 1-like (ING |
| 462B10 | 192 | 541 | AI707896 | Hs.107369 | 1.00E-168 | 1 | hypothetical protein FLJ20585 (FLJ20585), mR |
| 59A10 | 1694 | 2335 | AJ270952 | Hs.107393 | 0 | 3 | as34a10.x1 cDNA, 3' end /clone=IMAGE:2319066 |
| 499G1 | 2987 | 4266 | AL035683 | Hs.107526 | 1.00E-104 | 2 | for putative membrane protein (GENX-3745 |
| 466F11 | 327 | 493 | AI391443 | Hs.107622 | 9.00E-90 | 1 | DNA sequence from clone RP5-1063B2 on |
| 182F9 | 153 | 649 | AF265439 | Hs.107707 | 0 | 1 | chromosome 20q1 |
| 481F9 | 1216 | 1609 | NM_016270 | Hs.107740 | 0 | 2 | tf96e06.x1 cDNA, 3' end /clone=IMAGE:2107138 |
| | | | | | | | DC37 mRNA, complete cds /cds=(5,856) /gb=AF26 |
| | | | | | | | Kruppel-like factor (LOC51713), mRNA /cds=(84 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | |
|--------|------|------|-----------|---------------------|----|--|
| 184H4 | 189 | 576 | AF081282 | Hs.107979 0 | 1 | small membrane protein 1 (SMP1) mRNA, complete |
| 103E11 | 1006 | 2137 | NM_014313 | Hs.107979 0 | 4 | small membrane protein 1 (SMP1), mRNA /cds=(99, |
| 596H7 | 1265 | 1771 | NM_004078 | Hs.108080 0 | 3 | cysteine and glycine-rich protein 1 (CSRP1), m |
| 46H8 | 777 | 914 | AF070640 | Hs.108112 2.00E-47 | 1 | clone 24781 mRNA sequence /cds=UNKNOWN /gb=AF |
| 53B4 | 1552 | 1967 | U32986 | Hs.108327 0 | 2 | xeroderma pigmentosum group E UV-damaged DNA binding |
| 124A10 | 1089 | 1733 | AK001428 | Hs.108332 0 | 3 | cDNA FLJ10566 fis, clone NT2RP2002959, highly |
| 127F8 | 428 | 746 | AL136941 | Hs.108338 0 | 1 | mRNA; cDNA DKFZp586C1924 (from clone DKFZp586 |
| 191G10 | 518 | 883 | AL136640 | Hs.108548 0 | 2 | mRNA; cDNA DKFZp564F163 (from clone DKFZp564F1 |
| 458G8 | 2374 | 5101 | NM_016227 | Hs.108636 0 | 2 | membrane protein CH1 (CH1), mRNA /cds=(124,434 |
| 58F11 | 735 | 798 | NM_006963 | Hs.108642 2.00E-28 | 1 | zinc finger protein 22 (KOX 15) (ZNF22), mRNA / |
| 118B5 | 2715 | 2797 | AK022874 | Hs.108779 2.00E-38 | 1 | cDNA FLJ12812 fis, clone NT2RP2002498 /cds=(3, |
| 110H2 | 18 | 661 | AF026292 | Hs.108809 0 | 1 | chaperonin containing t-complex polypeptide |
| 181G4 | 1008 | 1142 | NM_006429 | Hs.108809 2.00E-71 | 1 | chaperonin containing TCP1, subunit 7 (eta) (C |
| 189F11 | 415 | 615 | AK024569 | Hs.108854 2.00E-79 | 1 | cDNA: FLJ20916 fis, clone ADSE00738, highly s |
| 596F8 | 5958 | 6097 | AB011087 | Hs.108945 8.00E-48 | 1 | mRNA for KIAA0515 protein, partial cds /cds=(0, |
| 157D8 | 399 | 830 | NM_016145 | Hs.108969 0 | 1 | PTD008 protein (PTD008), /cds=(233,553) |
| 175E7 | 712 | 1849 | AL133111 | Hs.109150 0 | 2 | mRNA; cDNA DKFZp434H068 (from clone DKFZp434H0 |
| 514E1 | 66 | 613 | NM_012417 | Hs.109219 0 | 4 | retinal degeneration B beta (RDGBB), mRNA /cd |
| 106A4 | 1864 | 2220 | AJ011895 | Hs.109281 1.00E-111 | 1 | for HIV-1, Nef-associated factor 1 alpha |
| 169E1 | 938 | 1331 | AK024297 | Hs.109441 0 | 2 | FLJ14235 fis, clone NT2RP4000167 /cds=(82 |
| 100B8 | 1 | 191 | NM_012456 | Hs.109571 3.00E-85 | 1 | translocase of inner mitochondrial membrane 1 |
| 115B7 | 983 | 1193 | NM_007074 | Hs.109606 1.00E-116 | 1 | coronin, actin-binding protein, 1A (CORO1A), |
| 62H11 | 1 | 626 | BF245892 | Hs.109641 1.00E-154 | 10 | 601864070F1 cDNA, 5' end /clone=IMAGE:4082465 |
| 595B2 | 4976 | 5286 | AB040884 | Hs.109694 1.00E-142 | 1 | mRNA for KIAA1451 protein, partial cds /cds=(0 |
| 75H11 | 227 | 482 | BF244603 | Hs.109697 1.00E-129 | 1 | 601862620F1 cDNA, 5' end /clone=IMAGE:4080412 |
| 118G3 | 219 | 392 | NM_024292 | Hs.109701 2.00E-66 | 1 | ubiquitin-like 5 (UBL5), mRNA /cds=(65,286) / |
| 105A5 | 3271 | 3532 | AL117407 | Hs.109727 1.00E-147 | 2 | cDNA DKFZp434D2050 (from clone DKFZp434D |
| 481B7 | 1101 | 1201 | NM_006026 | Hs.109804 9.00E-42 | 1 | H1 histone family, member X (H1FX), mRNA /cds=(|
| 476H12 | 1018 | 1429 | NM_004310 | Hs.109918 0 | 3 | ras homolog gene family, member H (ARHH), mRNA |
| 144C8 | 1252 | 1429 | Z35227 | Hs.109918 7.00E-92 | 1 | TTF for small G protein /cds=(579,1154) /gb= |
| 141E10 | 630 | 1269 | AK001779 | Hs.110445 0 | 4 | FLJ10917 fis, clone OVARC1000321 /cds=(18 |
| 494D8 | 4102 | 4476 | NM_014918 | Hs.110488 0 | 1 | KIAA0990 protein (KIAA0990), mRNA /cds=(494,2 |
| 47C3 | 2298 | 2431 | D86974 | Hs.110613 1.00E-60 | 1 | KIAA0220 gene, partial cds /cds=(0,1661) /gb |
| 194C10 | 1210 | 1704 | AL157477 | Hs.110702 0 | 1 | mRNA; cDNA DKFZp761E212 (from clone DKFZp761E2 |
| 192F1 | 3254 | 3686 | NM_015726 | Hs.110707 1.00E-150 | 2 | H326 (H326), mRNA /cds=(176,1969) /gb=NM_0157 |
| 595B8 | 1148 | 1414 | NM_003472 | Hs.110713 1.00E-147 | 1 | DEK oncogene (DNA binding) (DEK), mRNA /cds=(3 |
| 459F3 | 3337 | 3915 | NM_001046 | Hs.110736 0 | 1 | solute carrier family 12 (sodium/potassium/ch |
| 195F5 | 1051 | 1482 | AK025557 | Hs.110771 0 | 2 | cDNA: FLJ21904 fis, clone HEP03585 /cds=UNKNOW |
| 53B10 | 163 | 742 | NM_020150 | Hs.110796 0 | 1 | SAR1 protein (SAR1), mRNA /cds=(100,696) /gb= |
| 164B11 | 122 | 932 | NM_016039 | Hs.110803 0 | 5 | CGI-99 protein (LOC51637), mRNA /cds=(161,895 |
| 594H4 | 982 | 1454 | AK026528 | Hs.111222 6.00E-95 | 3 | cDNA: FLJ22875 fis, clone KAT02879 /cds=(30,51 |
| 50A10 | 1688 | 2095 | AF119897 | Hs.111334 0 | 2 | PRO2760 mRNA, complete cds /cds=UNKNOWN /gb=A |
| 102H11 | 175 | 498 | AI436587 | Hs.111377 1.00E-148 | 1 | ti03d11.x1 cDNA, 3' end /clone=IMAGE:2129397 |
| 109G11 | 1324 | 1388 | AB016811 | Hs.111554 2.00E-29 | 1 | for ADP ribosylation factor-like protein, |
| 144E10 | 77 | 304 | BF219474 | Hs.111611 1.00E-122 | 2 | 601884269F1 5' end /clone=IMAGE:4102769 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|--|
| 583C9 | 4 | 272 | NM_000988 | Hs.111611 | 1.00E-148 | 10 | ribosomal protein L27 (RPL27), mRNA /cds=(17,4 |
| 111F4 | 31 | 380 | NM_014463 | Hs.111632 | 0 | 1 | Lsm3 protein (LSM3), mRNA /cds=(29,337) /gb=N |
| 106E6 | 2646 | 2892 | AL096723 | Hs.111801 | 1.00E-135 | 1 | cDNA DKFZp564H2023 (from clone DKFZp564H |
| 169A2 | 773 | 1015 | D14696 | Hs.111894 | 1.00E-135 | 2 | KIAA0108 gene, complete cds /cds=(146,847) / |
| 182D6 | 264 | 748 | NM_014713 | Hs.111894 | 0 | 1 | lysosomal-associated protein transmembrane |
| 460D11 | 205 | 452 | AI557431 | Hs.111973 | 4.00E-60 | 1 | PT2.1_7_C05.r cDNA, 3' end /clone_end=3' /gb= |
| 121A7 | 355 | 589 | NM_020382 | Hs.111988 | 1.00E-128 | 1 | PR/SET domain containing protein 07 (SET07), m |
| 476C12 | 254 | 463 | AA442585 | Hs.112071 | 1.00E-111 | 1 | zv57f09.r1 cDNA, 5' end /clone=IMAGE:757769 / |
| 172E7 | 469 | 736 | AF228422 | Hs.112242 | 1.00E-143 | 1 | normal mucosa of esophagus specific 1 (NMES1) |
| 108E10 | 4800 | 4901 | AF071076 | Hs.112255 | 6.00E-48 | 1 | cell-line HeLa Nup98-Nup96 precursor, mRNA, c |
| 47G12 | 1 | 301 | BF237710 | Hs.112318 | 1.00E-165 | 5 | 601842210F1 cDNA, 5' end /clone=IMAGE:4079930 |
| 599G7 | 38 | 455 | NM_019059 | Hs.112318 | 0 | 32 | 6.2 kd protein (LOC54543), mRNA /cds=(93,260) |
| 469F9 | 226 | 546 | NM_002638 | Hs.112341 | 1.00E-107 | 1 | protease inhibitor 3, skin-derived (SKALP) (P |
| 589G11 | 482 | 1336 | AK026396 | Hs.112497 | 0 | 2 | cDNA: FLJ22743 fis, clone HUV00901 |
| | | | | | | | /cds=UNKNOWN |
| 464F10 | 1686 | 1917 | NM_002978 | Hs.112842 | 1.00E-119 | 1 | sodium channel, nonvoltage-gated 1, delta (SC |
| 54B11 | 1 | 423 | BF025727 | Hs.113029 | 0 | 26 | 601670406F1 cDNA, 5' end /clone=IMAGE:3953425 |
| 591C5 | 31 | 469 | NM_001028 | Hs.113029 | 0 | 10 | ribosomal protein S25 (RPS25), mRNA /cds=(71,4 |
| 585F4 | 1882 | 3918 | AK027136 | Hs.113205 | 1.00E-130 | 3 | cDNA: FLJ23483 fis, clone KAIA04052 /cds=UNKNO |
| 61B12 | 1168 | 2386 | AF105253 | Hs.113368 | 0 | 5 | neuroendocrine secretory protein 55 mRNA, com |
| 163D9 | 3470 | 4109 | Y08890 | Hs.113503 | 0 | 1 | mRNA for Ran_GTP binding protein 5 |
| 466C4 | 276 | 946 | AL359916 | Hs.113872 | 0 | 1 | DNA sequence from clone RP11-55008 on |
| | | | | | | | chromosome 20 C |
| 592C12 | 2506 | 2696 | AF323540 | Hs.114309 | 2.00E-80 | 1 | apolipoprotein L-I mRNA, splice variant B, co |
| 476A11 | 121 | 528 | AA702108 | Hs.114931 | 0 | 1 | zi85e01.s1 cDNA, 3' end /clone=IMAGE:447576 / |
| 109F4 | 3123 | 3521 | D30783 | Hs.115263 | 0 | 1 | for epiregulin, complete cds /cds=(166,67 |
| 123D1 | 3123 | 3526 | NM_001432 | Hs.115263 | 0 | 1 | epiregulin (EREG), mRNA /cds=(166,675) /gb=N |
| 465D7 | 1 | 175 | BG288391 | Hs.115467 | 1.00E-94 | 1 | 602388053F1 cDNA, 5' end /clone=IMAGE:4517076 |
| 74H9 | 346 | 602 | AK027114 | Hs.115659 | 1.00E-108 | 1 | FLJ23461 fis, clone HSI07757 /cds=UNKNOWN |
| 585E4 | 384 | 1146 | NM_024061 | Hs.115659 | 0 | 3 | hypothetical protein MGC5521 (MGC5521), mRNA |
| 462C1 | 945 | 1222 | NM_024036 | Hs.115960 | 1.00E-152 | 1 | hypothetical protein MGC3103 (MGC3103), mRNA |
| 464E4 | 1276 | 1635 | AK023633 | Hs.116278 | 1.00E-138 | 1 | cDNA FLJ13571 fis, clone PLACE1008405 /cds=UNK |
| 43B10 | 1601 | 1798 | AF283777 | Hs.116481 | 9.00E-47 | 1 | clone TCBAPO702 mRNA sequence /cds=UNKNOWN |
| | | | | | | | /g |
| 465G1 | 374 | 654 | NM_001782 | Hs.116481 | 5.00E-85 | 2 | CD72 antigen (CD72), mRNA /cds=(108,1187) /gb |
| 51G8 | 29 | 203 | BF341330 | Hs.116567 | 6.00E-26 | 1 | 602013274F1 cDNA, 5' end /clone=IMAGE:4149066 |
| 40D10 | 2694 | 3430 | X68742 | Hs.116774 | 0 | 1 | integrin, alpha subunit /cds=UNKNOWN /g |
| 107D1 | 1778 | 1943 | U71383 | Hs.117005 | 1.00E-84 | 1 | OB binding protein-2 (OB-BP2) mRNA, complete cds |
| | | | | | | | /cds |
| 459D4 | 2882 | 3522 | AK025364 | Hs.117268 | 0 | 1 | cDNA: FLJ21711 fis, clone COL10156 /cds=UNKNOWN |
| 473E8 | 2104 | 2233 | AB029016 | Hs.117333 | 2.00E-65 | 3 | mRNA for KIAA1093 protein, partial cds /cds=(0 |
| 458E2 | 88 | 627 | AI825645 | Hs.117906 | 0 | 2 | wb75b09.x1 cDNA, 3' end /clone=IMAGE:2311481 |
| 163A7 | 1160 | 1420 | X53793 | Hs.117950 | 1.00E-109 | 1 | ADE2H1 mRNA showing homologies to SAICAR |
| | | | | | | | synthetase |
| 123B8 | 18 | 740 | NM_002799 | Hs.118065 | 0 | 1 | proteasome (prosome, macropain) subunit, bet |
| 583G3 | 924 | 1199 | AB011182 | Hs.118087 | 1.00E-155 | 4 | mRNA for KIAA0610 protein, partial cds /cds=(0, |
| 127A1 | 263 | 557 | NM_006441 | Hs.118131 | 1.00E-141 | 1 | 5,10-methenyltetrahydrofolate synthetase (|
| 459A10 | 188 | 817 | AL522477 | Hs.118142 | 0 | 1 | AL522477 cDNA /clone=CS0DB008YK14-(3-prime) |
| 584A10 | 8484 | 8875 | NM_003316 | Hs.118174 | 0 | 1 | tetratricopeptide repeat domain 3 (TTC3), mRN |
| 52D4 | 1287 | 1752 | AK026486 | Hs.118183 | 0 | 1 | FLJ22833 fis, clone KAIA4266 /cds=(479,8 |
| 470B6 | 68 | 532 | BF030930 | Hs.118303 | 0 | 1 | 601558648F1 cDNA, 5' end /clone=IMAGE:3828706 |
| 41B3 | 5041 | 5669 | M14648 | Hs.118512 | 0 | 1 | cell adhesion protein (vitronectin) receptor alpha s |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|--|
| 125B8 | 999 | 1573 | NM_003733 | Hs.118633 | 0 | 1 | 2'-5'oligoadenylate synthetase-like (OASL), oz07g04.x1 cDNA, 3' end /clone=IMAGE:1674678 |
| 459D3 | 3 | 427 | AI052447 | Hs.118659 | 0 | 1 | |
| 112F11 | 191 | 387 | NM_006923 | Hs.118684 | 1.00E-103 | 1 | stromal cell-derived factor 2 (SDF2), mRNA /c |
| 129E4 | 1727 | 1891 | AL050404 | Hs.118695 | 2.00E-86 | 1 | DNA sequence from clone 955M13 on chromosome 20. Conta |
| 126H2 | 1512 | 2209 | NM_000358 | Hs.118787 | 0 | 2 | transforming growth factor, beta-induced, 68 |
| 598D9 | 817 | 1106 | NM_001155 | Hs.118796 | 1.00E-108 | 1 | annexin A6 (ANXA6), transcript variant 1, mRNA |
| 331E6 | 89 | 475 | BE311727 | Hs.118857 | 0 | 1 | 601143334F1 cDNA, 5' end /clone=IMAGE:3507009 |
| 521C1 | 700 | 1180 | NM_006292 | Hs.118910 | 0 | 2 | tumor susceptibility gene 101 (TSG101), mRNA |
| 139E8 | 463 | 1198 | AJ012506 | Hs.118958 | 0 | 1 | activated in tumor suppression, clone TSA |
| 69H2 | 578 | 1117 | U05040 | Hs.118962 | 0 | 1 | FUSE binding protein mRNA, complete cds /cds=(26,1960 |
| 461F1 | 1241 | 1715 | AK024119 | Hs.118990 | 0 | 1 | cDNA FLJ14057 fis, clone HEMBB1000337 /cds=UNK |
| 481E1 | 1682 | 1969 | NM_017544 | Hs.119018 | 1.00E-129 | 1 | transcription factor NRF (NRF), mRNA /cds=(653 |
| 479B4 | 45 | 203 | AL109806 | Hs.119057 | 5.00E-43 | 1 | DNA sequence from clone RP5-1153D9 on chromosome 20 C |
| 520F1 | 177 | 672 | NM_012423 | Hs.119122 | 1.00E-148 | 8 | ribosomal protein L13a (RPL13A), mRNA /cds=(1 |
| 477E4 | 46 | 1565 | AL109786 | Hs.119155 | 0 | 3 | mRNA full length insert cDNA clone EUROIMAGE 81 |
| 166F10 | 304 | 814 | M37583 | Hs.119192 | 0 | 3 | histone (H2A.Z) mRNA, complete cds /cds=(106,492) /g |
| 592E5 | 302 | 814 | NM_002106 | Hs.119192 | 0 | 7 | H2A histone family, member Z (H2AFZ), mRNA /cd |
| 54B1 | 47 | 1144 | AJ400717 | Hs.119252 | 0 | 9 | TPT1 gene for translationally controlled tumo |
| 594H9 | 609 | 1013 | NM_000520 | Hs.119403 | 0 | 1 | hexosaminidase A (alpha polypeptide) (HEXA), |
| 492D9 | 30 | 272 | NM_001004 | Hs.119500 | 1.00E-135 | 2 | ribosomal protein, large P2 (RPLP2), mRNA /cd |
| 59H8 | 14 | 1890 | NM_016091 | Hs.119503 | 0 | 12 | HSPC025 (HSPC025), mRNA /cds=(33,1727) /gb=N |
| 525E8 | 12 | 446 | NM_006432 | Hs.119529 | 0 | 2 | epididymal secretory protein (19.5kD) (HE1), |
| 166G7 | 1323 | 2293 | M88108 | Hs.119537 | 0 | 3 | p62 mRNA, complete cds /cds=(106,1437) /gb=M88108 /g |
| 112D10 | 1054 | 1722 | NM_006559 | Hs.119537 | 0 | 1 | GAP-associated tyrosine phosphoprotein p62 |
| 158E9 | 847 | 1273 | AL022326 | Hs.119598 | 0 | 1 | DNA sequence from clone 333H23 on chromosome 22q12.1-1 |
| 161H7 | 738 | 1272 | NM_000967 | Hs.119598 | 0 | 1 | ribosomal protein L3 (RPL3), mRNA /cds=(6,1217 |
| 168F8 | 284 | 778 | M34671 | Hs.119663 | 0 | 1 | lymphocytic antigen CD59/MEM43 mRNA, complete cds /c |
| 585C9 | 285 | 783 | NM_000611 | Hs.119663 | 0 | 1 | CD59 antigen p18-20 (antigen identified by mo |
| 143G12 | 753 | 1329 | AK023975 | Hs.119908 | 0 | 4 | FLJ13913 fis, clone Y79AA1000231, highly |
| 55D12 | 1107 | 1365 | NM_015934 | Hs.119908 | 1.00E-119 | 1 | nucleolar protein NOP5/NOP58 (NOP5/NOP58), m |
| 467E7 | 37 | 419 | AI492066 | Hs.119923 | 0 | 1 | tg12b03.x1 cDNA, 3' end /clone=IMAGE:2108525 |
| 462C10 | 2669 | 3025 | NM_012318 | Hs.120165 | 0 | 1 | leucine zipper-EF-hand containing transmembr |
| 473F11 | 396 | 1006 | AK025068 | Hs.120170 | 0 | 1 | cDNA: FLJ21415 fis, clone COL04030 /cds=(138,7 |
| 98E11 | 211 | 458 | AW081455 | Hs.120219 | 1.00E-114 | 2 | xc31c07.x1 cDNA, 3' end /clone=IMAGE:2585868 |
| 471C8 | 60 | 301 | NM_014487 | Hs.120766 | 1.00E-120 | 1 | nucleolar cysteine-rich protein (HSA6591), m |
| 134C4 | 284 | 529 | AK000470 | Hs.120769 | 9.00E-98 | 1 | cDNA FLJ20463 fis, clone KAT06143 /cds=UNKNOWN |
| 469C10 | 1 | 441 | AA677952 | Hs.120891 | 0 | 1 | zi14a06.s1 cDNA, 3' end /clone=IMAGE:430738 / |
| 60C9 | 1022 | 1615 | AB011421 | Hs.120996 | 0 | 1 | for DRAK2, complete cds /cds=(261,1379) / |
| 461A7 | 738 | 1274 | NM_014205 | Hs.121025 | 0 | 1 | chromosome 11 open reading frame 5 (C11ORF5), m |
| 104A4 | 557 | 1942 | D89974 | Hs.121102 | 0 | 4 | for glycosylphosphatidyl inositol-anch |
| 196C9 | 557 | 1463 | NM_004665 | Hs.121102 | 0 | 9 | vanin 2 (VNN2), mRNA /cds=(11,1573) /gb=N004 |
| 467F4 | 4 | 328 | AW972196 | Hs.121210 | 1.00E-162 | 1 | EST384285 cDNA /gb=AW972196 /gi=8162042 /ug= |
| 587A12 | 224 | 367 | AW975541 | Hs.121572 | 1.00E-62 | 1 | EST387650 cDNA /gb=AW975541 /gi=8166755 /ug= |
| 36G5 | 13 | 604 | AL008729 | Hs.121591 | 0 | 1 | DNA sequence from PAC 257A7 on chromosome 6p24. Contai |
| 464C1 | 120 | 413 | AA772692 | Hs.121709 | 1.00E-120 | 1 | ai35b09.s1 cDNA, 3' end /clone=1358969 /clone |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | |
|--------|-------|-------|-----------|---------------------|---|---|
| 36E2 | 411 | 821 | AK025556 | Hs.121849 0 | 1 | FLJ21903 fis, clone HEP03579 /cds=(84,46 |
| 196A6 | 411 | 1113 | NM_022818 | Hs.121849 0 | 1 | Microtubule-associated proteins 1A and 1B, I |
| 471G2 | 176 | 333 | AW469546 | Hs.122116 2.00E-64 | 1 | hd19e09.x1 cDNA, 3' end /clone=IMAGE:2909992 |
| 462F5 | 218 | 611 | BF677944 | Hs.122406 1.00E-166 | 1 | 602084766F1 cDNA, 5' end /clone=IMAGE:4248905 |
| 465A6 | 376 | 478 | AV762642 | Hs.122431 2.00E-28 | 1 | AV762642 cDNA, 5' end /clone=MDSEMB08 /clone_ |
| 467G10 | 603 | 803 | AL040371 | Hs.122487 9.00E-96 | 1 | DKFZp434P0213_r1 cDNA, 5' end /clone=DKFZp434 |
| 465C12 | 66 | 260 | AI804629 | Hs.122848 3.00E-83 | 1 | tc81g03.x1 cDNA, 3' end /clone=IMAGE:2072596 |
| 98H6 | 442 | 591 | AI081246 | Hs.122983 5.00E-78 | 1 | oy67b06.x1 cDNA, 3' end /clone=IMAGE:1670867 |
| 52B4 | 123 | 236 | BE676541 | Hs.123254 8.00E-46 | 1 | 7f31g03.x1 cDNA, 3' end /clone=IMAGE:3296308 |
| 128C7 | 4875 | 5186 | AB020631 | Hs.123654 1.00E-131 | 1 | mRNA for KIAA0824 protein, partial cds /cds=(0 |
| 184B5 | 594 | 1187 | AL109865 | Hs.124186 0 | 1 | DNA sequence from clone GS1-120K12 on chromosome 1q25 |
| 106A6 | 1135 | 1456 | AK026776 | Hs.124292 9.00E-99 | 1 | FLJ23123 fis, clone LNG08039 /cds=UNKNOW |
| 525G12 | 314 | 503 | BF996704 | Hs.124344 1.00E-72 | 1 | MR1-GN0173-071100-009-g10 cDNA /gb=BF996704 |
| 466C3 | 120 | 496 | AA831838 | Hs.124391 1.00E-172 | 1 | oc85h06.s1 cDNA, 3' end /clone=IMAGE:1356539 |
| 48G4 | 1 | 568 | AA203497 | Hs.124601 0 | 1 | zx58g05.r1 cDNA, 5' end /clone=IMAGE:446744 / |
| 517G2 | 577 | 756 | AA858297 | Hs.124675 3.00E-61 | 1 | ob13b08.s1 cDNA, 3' end /clone=IMAGE:1323543 |
| 107H3 | 913 | 1220 | AK023013 | Hs.124762 1.00E-174 | 1 | FLJ12951 fis, clone NT2RP2005457, highly |
| 473A7 | 729 | 929 | NM_019062 | Hs.124835 4.00E-82 | 1 | hypothetical protein (FLJ20225), mRNA /cds=(|
| 108D12 | 3225 | 3531 | AF023142 | Hs.125134 1.00E-142 | 2 | pre-mRNA splicing SR protein rA4 mRNA, partial |
| 463E11 | 158 | 519 | AI380443 | Hs.125608 0 | 1 | tg02f04.x1 cDNA, 3' end /clone=IMAGE:2107615 |
| 104F6 | 1581 | 2028 | NM_019853 | Hs.125682 0 | 1 | protein phosphatase 4 regulatory subunit 2 (P |
| 462A5 | 5 | 282 | AW975851 | Hs.125815 1.00E-149 | 1 | EST387960 cDNA /gb=AW975851 /gi=8167072 /ug= |
| 462B1 | 534 | 702 | AI378032 | Hs.125892 1.00E-69 | 1 | te67g08.x1 cDNA, 3' end /clone=IMAGE:2091806 |
| 121A6 | 3074 | 3494 | AB028978 | Hs.126084 1.00E-174 | 1 | mRNA for KIAA1055 protein, partial cds /cds=(0 |
| 171G12 | 94 | 1240 | M15330 | Hs.126256 0 | 7 | interleukin 1-beta (IL1B) mRNA, complete cds /cds=(86 |
| 183D12 | 100 | 1275 | NM_000576 | Hs.126256 0 | 9 | interleukin 1, beta (IL1B), mRNA /cds=(86,895) |
| 458B2 | 6 | 415 | AI393205 | Hs.126265 0 | 1 | tg14b07.x1 cDNA, 3' end /clone=IMAGE:2108725 |
| 102G6 | 885 | 1906 | AJ271684 | Hs.126355 1.00E-171 | 2 | for myeloid DAP12-associating lectin (MD |
| 463E4 | 847 | 1015 | NM_013252 | Hs.126355 2.00E-89 | 1 | C-type (calcium dependent, carbohydrate-reco |
| 167B2 | 2468 | 2721 | AF195514 | Hs.126550 1.00E-142 | 1 | VPS4-2 ATPase (VPS42) mRNA, complete cds /cds= |
| 473D8 | 19 | 397 | BF445163 | Hs.126594 0 | 1 | nad21d12.x1 cDNA, 3' end /clone=IMAGE:3366191 |
| 143C9 | 333 | 551 | BE250027 | Hs.126701 1.00E-121 | 1 | 600943030F1 cDNA, 5' end /clone=IMAGE:2959639 |
| 471E10 | 806 | 945 | AK021519 | Hs.126707 2.00E-71 | 1 | cDNA FLJ11457 fis, clone HEMBA1001522 /cds=(1 |
| 462B4 | 159 | 572 | NM_017762 | Hs.126721 0 | 1 | hypothetical protein FLJ20313 (FLJ20313), mR |
| 41D8 | 1 | 2519 | AK023275 | Hs.126925 0 | 5 | FLJ13213 fis, clone NT2RP4001126, weakly |
| 463F5 | 2 | 563 | NM_014464 | Hs.127011 0 | 1 | tubulointerstitial nephritis antigen (TIN-A |
| 597C8 | 2662 | 2905 | AB046765 | Hs.127270 1.00E-136 | 1 | mRNA for KIAA1545 protein, partial cds /cds=(0 |
| 458F11 | 15 | 212 | BF508731 | Hs.127311 8.00E-81 | 1 | UI-H-BI4-aoq-b-08-0-UI.s1 cDNA, 3' end /clon |
| 462B3 | 76 | 389 | AW978753 | Hs.127327 1.00E-133 | 1 | EST390862 cDNA /gb=AW978753 /gi=8170027 /ug= |
| 463E2 | 176 | 787 | AI028267 | Hs.127514 0 | 1 | ow01d06.x1 cDNA, 3' end /clone=IMAGE:1645547 |
| 465G5 | 181 | 372 | AA953396 | Hs.127557 6.00E-78 | 1 | on63h10.s1 cDNA, 3' end /clone=IMAGE:1561411 |
| 463E10 | 11190 | 11634 | NM_016239 | Hs.127561 0 | 1 | unconventional myosin-15 (LOC51168), mRNA /c |
| 476A9 | 27 | 216 | AW384918 | Hs.127574 1.00E-101 | 1 | PM1-HT0422-291299-002-d01 cDNA /gb=AW384918 |
| 111B10 | 1825 | 2463 | NM_014007 | Hs.127649 0 | 1 | KIAA0414 protein (KIAA0414), mRNA /cds=(1132, |
| 499A7 | 2134 | 5198 | AF070674 | Hs.127799 0 | 8 | inhibitor of apoptosis protein-1 (MIHC) mRNA, |
| 331F5 | 4 | 460 | BF342439 | Hs.127863 0 | 1 | 602013944F1 cDNA, 5' end /clone=IMAGE:4149562 |
| 176A12 | 796 | 1351 | NM_022900 | Hs.128003 0 | 1 | hypothetical protein FLJ21213 (FLJ21213), mR |
| 462B5 | 1766 | 1949 | NM_014406 | Hs.128342 5.00E-82 | 1 | potassium large conductance calcium-activate |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|---|---|
| 467D5 | 157 | 279 | AI222805 | Hs.128630 | 6.00E-62 | 1 | qp39c07.x1 cDNA, 3' end /clone=IMAGE:1925388 |
| 465G3 | 1 | 529 | BE222032 | Hs.128675 | 0 | 1 | hr61g11.x1 cDNA, 3' end /clone=IMAGE:3133028 |
| 467C7 | 1172 | 1726 | AF118274 | Hs.128740 | 0 | 1 | DNb-5 mRNA, partial cds /cds=(0,1601) /gb=AF11 |
| 175G11 | 358 | 724 | AL110151 | Hs.128797 | 0 | 1 | mRNA; cDNA DKFZp586D0824 (from clone DKFZp586 |
| 472A12 | 402 | 782 | BE745645 | Hs.129135 | 1.00E-153 | 1 | 601578727F1 cDNA, 5' end /clone=IMAGE:3927535 |
| 473C7 | 46 | 217 | BE670584 | Hs.129192 | 3.00E-37 | 1 | 7a36h08.x1 cDNA, 3' end /clone=IMAGE:3284607 |
| 463G11 | 7 | 397 | AA746320 | Hs.129572 | 0 | 1 | ob08f01.s1 cDNA, 3' end /clone=IMAGE:3123097 |
| 63D8 | 18 | 1167 | D13748 | Hs.129673 | 0 | 4 | eukaryotic initiation factor 4A1 /cds=(16,12 |
| 57F3 | 19 | 1279 | NM_001416 | Hs.129673 | 0 | 4 | eukaryotic translation initiation factor 4A, |
| 144G5 | 1071 | 1192 | AF064090 | Hs.129708 | 3.00E-62 | 3 | ligand for herpesvirus entry mediator (HVEM-L) |
| 118A9 | 2684 | 3198 | AB046805 | Hs.129750 | 0 | 1 | mRNA for KIAA1585 protein, partial cds /cds=(2 |
| 50G5 | 1119 | 1440 | AK024068 | Hs.129872 | 1.00E-172 | 1 | FLJ14006 fis, clone Y79AA1002399, highly |
| 469D6 | 376 | 603 | D43968 | Hs.129914 | 1.00E-126 | 1 | AML1 mRNA for AML1b protein (alternatively spliced pr |
| 590G11 | 823 | 1571 | NM_003563 | Hs.129951 | 0 | 3 | speckle-type POZ protein (SPOP), mRNA /cds=(15 |
| 591C7 | 68 | 571 | NM_005243 | Hs.129953 | 0 | 1 | Ewing sarcoma breakpoint region 1 (EWSR1), tra |
| 459F5 | 579 | 768 | AI763262 | Hs.130059 | 1.00E-35 | 1 | wi66c04.x1 cDNA, 3' end /clone=IMAGE:2398278 |
| 479A10 | 259 | 448 | AI089359 | Hs.130232 | 1.00E-103 | 1 | qb05h03.x1 cDNA, 3' end /clone=IMAGE:1695413 |
| 461G5 | 193 | 347 | AW898615 | Hs.130729 | 2.00E-68 | 1 | RC1-NN0073-090500-012-f02 cDNA /gb=AW898615. |
| 466B1 | 373 | 569 | AI347054 | Hs.130879 | 1.00E-76 | 1 | qp60a04.x1 cDNA, 3' end /clone=IMAGE:1927374 |
| 463G3 | 3212 | 5430 | AJ404611 | Hs.130881 | 0 | 2 | mRNA for B-cell lymphoma/leukaemia 11A extra |
| 462C3 | 48 | 468 | AI421806 | Hs.131067 | 0 | 1 | tf44h11.x1 cDNA, 3' end /clone=IMAGE:2099109 |
| 596G10 | 39 | 491 | NM_006294 | Hs.131255 | 0 | 3 | ubiquinol-cytochrome c reductase binding pro |
| 469G10 | 189 | 361 | AI024984 | Hs.131580 | 1.00E-81 | 1 | ov39d11.x1 cDNA, 3' end /clone=IMAGE:1639701 |
| 458B7 | 169 | 659 | AW978870 | Hs.131828 | 0 | 1 | EST390979 cDNA /gb=AW978870 /gi=8170147 /ug= |
| 63D1 | 185 | 500 | AF176706 | Hs.131859 | 1.00E-133 | 1 | F-box protein FBX11 mRNA, partial cds /cds=(0, |
| 58C10 | 4188 | 4313 | NM_014913 | Hs.131915 | 2.00E-65 | 1 | KIAA0863 protein (KIAA0863), mRNA /cds=(185,3 |
| 117H2 | 282 | 569 | NM_003608 | Hs.131924 | 1.00E-143 | 1 | G protein-coupled receptor 65 (GPR65), mRNA / |
| 462D11 | 441 | 683 | AW976422 | Hs.132064 | 1.00E-118 | 1 | EST388531 cDNA /gb=AW976422 /gi=8167649 /ug= |
| 586F11 | 161 | 1094 | NM_017830 | Hs.132071 | 0 | 2 | hypothetical protein FLJ20455 (FLJ20455), mR |
| 466A8 | 118 | 224 | AI042377 | Hs.132156 | 2.00E-44 | 1 | ox62c03.x1 cDNA, 3' end /clone=IMAGE:1660900 |
| 472F6 | 979 | 1431 | AK022463 | Hs.132221 | 0 | 1 | cDNA FLJ12401 fis, clone MAMMA1002796 /cds=(3, |
| 462E4 | 19 | 567 | AI031656 | Hs.132237 | 0 | 1 | ow48e06.x1 cDNA, 3' end /clone=IMAGE:1650082 |
| 462E2 | 4 | 539 | AI829569 | Hs.132238 | 0 | 1 | wf28e02.x1 cDNA, 3' end /clone=IMAGE:2356922 |
| 461H9 | 453 | 618 | BG037042 | Hs.132555 | 4.00E-57 | 1 | 602288311F1 cDNA, 5' end /clone=IMAGE:4374122 |
| 467D10 | 4518 | 4689 | AK024449 | Hs.132569 | 2.00E-55 | 1 | mRNA for FLJ00041 protein, partial cds /cds=(0 |
| 463H7 | 162 | 438 | AI346336 | Hs.132594 | 1.00E-132 | 1 | qp50b04.x1 cDNA, 3' end /clone=IMAGE:1926415 |
| 592B8 | 2415 | 2957 | NM_005337 | Hs.132834 | 0 | 1 | hematopoietic protein 1 (HEM1), mRNA /cds=(158 |
| 70H2 | 6370 | 6718 | AF047033 | Hs.132904 | 1.00E-175 | 1 | sodium bicarbonate cotransporter 3 (SLC4A7) m |
| 50G10 | 1167 | 2041 | AL121985 | Hs.132906 | 0 | 4 | DNA sequence from clone RP11-404F10 on chromosome 1q2 |
| 123C10 | 1323 | 1570 | NM_015071 | Hs.132942 | 1.00E-136 | 1 | GTPase regulator associated with the focal adh |
| 121B10 | 92 | 503 | AA504269 | Hs.133032 | 0 | 1 | aa61c09.s1 cDNA, 3' end /clone=IMAGE:825424 / |
| 171A12 | 696 | 909 | AL050035 | Hs.133130 | 6.00E-83 | 1 | mRNA; cDNA DKFZp566H0124 (from clone DKFZp566 |
| 463B5 | 123 | 449 | AI051673 | Hs.133175 | 1.00E-176 | 1 | oy77g06.x1 cDNA, 3' end /clone=IMAGE:1671898 |
| 463B7 | 966 | 1103 | AL044498 | Hs.133262 | 3.00E-46 | 1 | DKFZp434I082_s1 cDNA, 3' end /clone=DKFZp434I |
| 463B8 | 1 | 322 | AV661783 | Hs.133333 | 1.00E-176 | 1 | AV661783 cDNA, 3' end /clone=GLCGXE12 /clone_ |
| 463A10 | 431 | 694 | AW966876 | Hs.133543 | 1.00E-110 | 1 | EST378950 cDNA /gb=AW966876 /gi=8156712 /ug= |
| 464B10 | 63 | 547 | BF965766 | Hs.133864 | 0 | 1 | 602276890F1 cDNA, 5' end /clone=IMAGE:4364495 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|---|
| 460C6 | 454 | 653 | AW009671 | Hs.134272 | 8.00E-70 | 1 | ws85g09.x1 cDNA, 3' end /clone=IMAGE:2504800 |
| 459C12 | 3337 | 3745 | AJ278245 | Hs.134342 | 1.00E-121 | 1 | mRNA for LanC-like protein 2 (lanc12 gene) /cds |
| 462G1 | 33 | 454 | AI074016 | Hs.134473 | 0 | 1 | oy66g02.x1 cDNA, 3' end /clone=IMAGE:1670834 |
| 462G6 | 260 | 597 | BE676210 | Hs.134648 | 1.00E-156 | 1 | 7f25c05.x1 cDNA, 3' end /clone=IMAGE:3295688 |
| 466H12 | 505 | 662 | AV706481 | Hs.134829 | 3.00E-65 | 1 | AV706481 cDNA, 5' end /clone=ADBBYF02 |
| 148H11 | 16 | 474 | BE786820 | Hs.135056 | 0 | 1 | 601477630F1 5' end /clone=IMAGE:3880471 |
| 462E1 | 139 | 487 | BF109873 | Hs.135106 | 0 | 1 | 7I70e11.x1 cDNA, 3' end /clone=IMAGE:3526772 |
| 147E6 | 11 | 364 | AV712376 | Hs.135167 | 0 | 2 | AV712376 cDNA, 5' end /clone=DCAAND12 /clone_ |
| 465B4 | 1993 | 2237 | AJ271326 | Hs.135187 | 1.00E-92 | 1 | mRNA for unc-93 related protein (UNC93 gene) / |
| 463B4 | 185 | 352 | AI051664 | Hs.135339 | 4.00E-48 | 1 | oy77f06.x1 cDNA, 3' end /clone=IMAGE:1671875 |
| 478H4 | 2126 | 2458 | AK024921 | Hs.135570 | 1.00E-170 | 1 | cDNA: FLJ21268 fis, clone COL01718 /cds=UNKNOWN |
| 148B6 | 119 | 444 | AI004582 | Hs.135764 | 3.00E-82 | 8 | ou04a11.x1 3' end /clone=IMAGE:1625276 |
| 598E9 | 1948 | 2184 | NM_022117 | Hs.136164 | 3.00E-93 | 1 | cutaneous T-cell lymphoma-associated tumor a |
| 514C10 | 398 | 840 | AL049597 | Hs.136309 | 0 | 2 | DNA sequence from clone RP4-612B15 on chromosome 1p22 |
| 461C6 | 18 | 219 | BF513274 | Hs.136375 | 1.00E-101 | 1 | UI-H-BW1-amo-d-11-0-UI.s1 cDNA, 3' end /clon |
| 482E4 | 291 | 699 | BF526066 | Hs.136537 | 1.00E-142 | 1 | 602071176F1 cDNA, 5' end /clone=IMAGE:4214059 |
| 461G7 | 43 | 466 | NM_013378 | Hs.136713 | 0 | 1 | pre-B lymphocyte gene 3 (VPREB3), mRNA /cds=(4 |
| 119B10 | 10 | 677 | NM_013269 | Hs.136748 | 0 | 2 | lectin-like NK cell receptor (LLT1), mRNA /cd |
| 462A10 | 1233 | 1727 | AK024426 | Hs.137354 | 0 | 1 | mRNA for FLJ00015 protein, partial cds /cds=(3 |
| 41F2 | 2684 | 3000 | AJ223324 | Hs.137548 | 1.00E-156 | 1 | for MAX.3 cell surface antigen /cds=(44,10 |
| 74E8 | 16 | 2000 | D10923 | Hs.137555 | 0 | 15 | HM74 /cds=(60,1223) /gb=D10923 /gi=219866 / |
| 58D10 | 8 | 2000 | NM_006018 | Hs.137555 | 0 | 9 | putative chemokine receptor; GTP-binding pro |
| 120E2 | 210 | 814 | NM_002027 | Hs.138381 | 0 | 1 | farnesyltransferase, CAAX box, alpha (FNTA), |
| 168E12 | 1953 | 2522 | D38524 | Hs.138593 | 0 | 1 | 5'-nucleotidase /cds=(83,1768) /gb=D38524 |
| 178F7 | 573 | 824 | NM_006413 | Hs.139120 | 1.00E-115 | 1 | ribonuclease P (30kD) (RPP30), mRNA /cds=(27,8 |
| 473D1 | 1635 | 1767 | AL049942 | Hs.139240 | 6.00E-50 | 1 | mRNA; cDNA DKFZp564F1422 (from clone DKFZp564F |
| 188A8 | 924 | 1038 | NM_017523 | Hs.139262 | 1.00E-56 | 2 | XIAP associated factor-1 (HSXIAPAF1), mRNA /c |
| 168F7 | 933 | 1038 | X99699 | Hs.139262 | 1.00E-53 | 1 | for XIAP associated factor-1 /cds=(0,953) / |
| 181B10 | 1556 | 2517 | NM_005816 | Hs.142023 | 0 | 3 | T cell activation, increased late expression (|
| 514E7 | 2052 | 2339 | NM_003150 | Hs.142258 | 1.00E-114 | 1 | signal transducer and activator of transcripti |
| 196C7 | 355 | 524 | NM_016123 | Hs.142295 | 9.00E-92 | 1 | putative protein kinase NY-REN-64 antigen (LO |
| 585B10 | 3261 | 3465 | AK023129 | Hs.142442 | 1.00E-100 | 1 | cDNA FLJ13067 fis, clone NT2RP3001712, highly |
| 458F2 | 283 | 413 | BE293343 | Hs.142737 | 3.00E-68 | 1 | 601143756F1 cDNA, 5' end /clone=IMAGE:3051493 |
| 134C6 | 289 | 572 | BE886127 | Hs.142838 | 1.00E-160 | 1 | 601509912F1 cDNA, 5' end /clone=IMAGE:3911451 |
| 110A11 | 345 | 584 | AI126688 | Hs.143049 | 1.00E-102 | 1 | qb94a06.x1 cDNA, 3' end /clone=IMAGE:1707730 |
| 472G7 | 127 | 452 | AW976331 | Hs.143254 | 0 | 1 | EST388440 cDNA /gb=AW976331 /gi=8167557 /ug= |
| 464G11 | 425 | 547 | AI357640 | Hs.143314 | 1.00E-56 | 1 | qy15b06.x1 cDNA, 3' end /clone=IMAGE:2012051 |
| 463F11 | 257 | 640 | BF446017 | Hs.143389 | 0 | 1 | 7p18a11.x1 cDNA, 3' end /clone=IMAGE:3646004 |
| 463H2 | 107 | 443 | AA825245 | Hs.143410 | 1.00E-151 | 1 | oe59g09.s1 cDNA, 3' end /clone=IMAGE:1415968 |
| 48B7 | 1 | 3366 | NM_005813 | Hs.143460 | 0 | 2 | protein kinase C, nu (PRKCN), mRNA /cds=(555,32 |
| 463C9 | 290 | 405 | AW173163 | Hs.143525 | 5.00E-41 | 1 | xj84b08.x1 cDNA, 3' end /clone=IMAGE:2663895 |
| 463C8 | 330 | 473 | AI095189 | Hs.143534 | 5.00E-57 | 2 | oy83b06.s1 cDNA, 3' end /clone=IMAGE:1672403 |
| 464G5 | 94 | 189 | BG033028 | Hs.143554 | 1.00E-38 | 1 | 602300135F1 cDNA, 5' end /clone=IMAGE:4401776 |
| 463D7 | 120 | 563 | NM_006777 | Hs.143604 | 0 | 1 | Kaiso (ZNF-kaiso), mRNA /cds=(0,2018) /gb=NM |
| 471A10 | 132 | 586 | AK026372 | Hs.143631 | 0 | 1 | cDNA: FLJ22719 fis, clone HSI14307 /cds=UNKNOWN |
| 74G2 | 5129 | 5285 | AF073310 | Hs.143648 | 2.00E-79 | 2 | insulin receptor substrate-2 (IRS2) mRNA, com |
| 471G11 | 7 | 320 | AI568622 | Hs.143951 | 1.00E-154 | 2 | tn41e10.x1 cDNA, 3' end /clone=IMAGE:2170218 |
| 478H12 | 963 | 1532 | NM_018270 | Hs.143954 | 0 | 1 | hypothetical protein FLJ10914 (FLJ10914), mR |
| 462G3 | 100 | 529 | AI074020 | Hs.144114 | 0 | 1 | oy66g06.x1 cDNA, 3' end /clone=IMAGE:1670842 |
| 463C1 | 52 | 151 | AI090305 | Hs.144119 | 1.00E-42 | 1 | oy81b01.s1 cDNA, 3' end /clone=IMAGE:1672201 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|-------|-----------|-----------|-----------|----|---|
| 472H8 | 157 | 485 | BF509758 | Hs.144265 | 1.00E-178 | 1 | UI-H-BI4-apg-d-04-0-UI.s1 cDNA, 3' end /clon |
| 166E1 | 23 | 443 | D63874 | Hs.144321 | 0 | 1 | HMG-1, complete cds /cds=(76,723) /gb=D63874 |
| 145G8 | 125 | 1606 | NM_018548 | Hs.144477 | 0 | 2 | hypothetical protein PRO2975 (PRO2975), mRNA |
| 191H8 | 46 | 624 | BF036686 | Hs.144559 | 0 | 1 | 601459771F1 cDNA, 5' end /clone=IMAGE:3863248 |
| 151B1 | 1983 | 2561 | M93651 | Hs.145279 | 0 | 2 | set gene, complete cds /cds=(3,836) /gb=M93651 /gi=33 |
| 514B2 | 115 | 1583 | NM_003011 | Hs.145279 | 0 | 4 | SET translocation (myeloid leukemia-associat |
| 596D4 | 89 | 734 | AA631938 | Hs.145668 | 0 | 8 | fmfc5 cDNA /clone=CR6-21 /gb=AA631938 /gi=25 |
| 492B3 | 512 | 2226 | NM_004902 | Hs.145696 | 0 | 2 | splicing factor (CC1.3) (CC1.3), mRNA /cds=(14 |
| 192E4 | 1483 | 1837 | AF246126 | Hs.145956 | 0 | 1 | zinc finger protein mRNA, complete cds /cds=(1 |
| 480B9 | 1094 | 1426 | AL136874 | Hs.146037 | 1.00E-111 | 1 | mRNA; cDNA DKFZp434C135 (from clone DKFZp434C1 |
| 49H1 | 1761 | 2182 | NM_022894 | Hs.146123 | 0 | 1 | hypothetical protein FLJ12972 (FLJ12972), mR |
| 129C6 | 517 | 603 | BE220959 | Hs.146215 | 6.00E-21 | 1 | hu02b06.x1 cDNA, 3' end /clone=IMAGE:3165395 |
| 583D9 | 249 | 646 | NM_003641 | Hs.146360 | 0 | 1 | interferon induced transmembrane protein 1 (|
| 589D9 | 125 | 1866 | NM_002139 | Hs.146381 | 0 | 5 | RNA binding motif protein, X chromosome (RBMX) |
| 68H11 | 122 | 1567 | Z23064 | Hs.146381 | 0 | 2 | mRNA gene for hnRNP G protein /cds=(11,1186) /gb= |
| 174A8 | 461 | 1008 | NM_004757 | Hs.146401 | 0 | 1 | small inducible cytokine subfamily E, member 1 |
| 171A6 | 461 | 686 | U10117 | Hs.146401 | 1.00E-100 | 1 | endothelial-monocyte activating polypeptide II mRN |
| 465C4 | 53 | 342 | AI141004 | Hs.146627 | 3.00E-89 | 1 | oy68f02.x1 cDNA, 3' end /clone=IMAGE:1671003 |
| 190H7 | 1306 | 3107 | AB033079 | Hs.146668 | 0 | 3 | mRNA for KIAA1253 protein, partial cds /cds=(0 |
| 102E9 | 412 | 1022 | AF054187 | Hs.146763 | 0 | 3 | alpha NAC mRNA, complete cds /cds=(309,956) /g |
| 179B1 | 364 | 843 | D16481 | Hs.146812 | 0 | 1 | mitochondrial 3-ketoacyl-CoA thiolas |
| 126H12 | 1 | 358 | NM_000183 | Hs.146812 | 0 | 1 | hydroxyacyl-Coenzyme A dehydrogenase/3-keto |
| 476C9 | 20 | 249 | AI187423 | Hs.147040 | 1.00E-128 | 2 | qf31d04.x1 cDNA, 3' end /clone=IMAGE:1751623 |
| 70H11 | 47 | 1593 | AF272148 | Hs.147644 | 0 | 7 | KRAB zinc finger protein (RITA) mRNA, complete |
| 51F1 | 635 | 1039 | NM_018555 | Hs.147644 | 0 | 3 | C2H2-like zinc finger protein (ZNF361), mRNA |
| 72H1 | 948 | 5026 | AF000982 | Hs.147916 | 0 | 7 | dead box, X isoform (DBX) mRNA, alternative tra |
| 37F10 | 3128 | 3652 | X63563 | Hs.148027 | 0 | 1 | RNA polymerase II 140 kDa /cds=(43,3567) |
| 64C11 | 163 | 279 | AA908367 | Hs.148288 | 6.00E-29 | 1 | og76c11.s1 cDNA, 3' end /clone=IMAGE:1454228 |
| 463G2 | 52 | 473 | AI335004 | Hs.148558 | 0 | 1 | tb21e09.x1 cDNA, 3' end /clone=IMAGE:2055016 |
| 471F8 | 17 | 463 | AI471866 | Hs.149095 | 0 | 1 | ti67d04.x1 cDNA, 3' end /clone=IMAGE:2137063 |
| 169C12 | 449 | 1711 | L06132 | Hs.149155 | 0 | 2 | voltage-dependent anion channel isoform 1 (VDAC) |
| 189G6 | 1353 | 1711 | NM_003374 | Hs.149155 | 0 | 5 | mRN |
| 481E3 | 501 | 669 | NM_007022 | Hs.149443 | 5.00E-84 | 1 | voltage-dependent anion channel 1 (VDAC1), mR |
| 472B3 | 93 | 182 | BF029894 | Hs.149595 | 6.00E-44 | 1 | putative tumor suppressor (101F6), mRNA /cds= |
| 173D1 | 3719 | 3877 | AB037901 | Hs.149918 | 3.00E-83 | 1 | 601557056F1 cDNA, 5' end /clone=IMAGE:3827172 |
| 153G12 | 1429 | 1787 | M31627 | Hs.149923 | 0 | 2 | GASC-1 mRNA, complete cds /cds=(150,3320) /gb |
| 116B10 | 1435 | 1787 | NM_005080 | Hs.149923 | 1.00E-180 | 1 | X box binding protein-1 (XBP-1) mRNA, complete cds |
| 111G4 | 480 | 1891 | L12052 | Hs.150395 | 0 | 2 | /cd |
| 461D6 | 1407 | 1904 | NM_000790 | Hs.150403 | 0 | 1 | X-box binding protein 1 (XBP1), mRNA /cds=(12,7 |
| 73B3 | 896 | 1779 | AL050005 | Hs.150580 | 0 | 23 | cAMP phosphodiesterase PDE7 (PDE7A1) mRNA, co |
| 465G12 | 1 | 549 | AJ272212 | Hs.150601 | 0 | 1 | dopa decarboxylase (aromatic L-amino acid dec |
| 140G12 | 2 | 195 | BF028489 | Hs.150675 | 1.00E-100 | 1 | cDNA DKFZp564A153 (from clone DKFZp564A1 |
| 496E10 | 17 | 1686 | BC000167 | Hs.151001 | 0 | 5 | mRNA for protein serine kinase (PSKH1 gene) /c |
| 597G7 | 623 | 1488 | NM_005015 | Hs.151134 | 0 | 2 | 601763692F1 cDNA, 5' end /clone=IMAGE:3995950 |
| 50C9 | 1051 | 1467 | X80695 | Hs.151134 | 0 | 1 | clone IMAGE:2900671, mRNA, partial cds /cds= |
| 125H7 | 3154 | 3957 | NM_001421 | Hs.151139 | 0 | 3 | oxidase (cytochrome c) assembly 1-like (OXA1L |
| 111F2 | 306 | 638 | BG286500 | Hs.151239 | 1.00E-149 | 1 | OXA1Hs mRNA /cds=(6,1313) /gb=X80695 /gi=619490 |
| 177A4 | 9686 | 10035 | AF075587 | Hs.151411 | 0 | 1 | E74-like factor 4 (ets domain transcription fa |
| 185C7 | 6934 | 13968 | NM_015057 | Hs.151411 | 0 | 3 | 602382992F1 cDNA, 5' end /clone=IMAGE:4500527 |
| 115E7 | 3406 | 4005 | NM_004124 | Hs.151413 | 0 | 1 | protein associated with Myc mRNA, complete cds |
| | | | | | | | KIAA0916 protein (KIAA0916), mRNA /cds=(146,1 |
| | | | | | | | glia maturation factor, beta (GMFB), mRNA /cds |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|--|
| 182H7 | 234 | 833 | AF099032 | Hs.151461 | 0 | 1 | embryonic ectoderm development protein short |
| 169C10 | 4247 | 4727 | U38847 | Hs.151518 | 0 | 1 | TAR RNA loop binding protein (TRP-185) mRNA, complete |
| 167D6 | 1013 | 1197 | NM_002870 | Hs.151536 | 6.00E-83 | 1 | RAB13, member RAS oncogene family (RAB13), mRNA |
| 588G11 | 1249 | 1898 | AK023362 | Hs.151604 | 1.00E-157 | 9 | cDNA FLJ13300 fis, clone OVARC1001342, highly |
| 479G10 | 1 | 277 | NM_007210 | Hs.151678 | 1.00E-103 | 1 | UDP-N-acetyl-alpha-D-galactosamine:polype |
| 178B7 | 2664 | 3033 | NM_004247 | Hs.151787 | 0 | 4 | U5 snRNP-specific protein, 116 kD (U5-116KD), |
| 59A6 | 382 | 860 | D42054 | Hs.151791 | 0 | 1 | KIAA0092 gene, complete cds /cds=(53,1477) / |
| 521B6 | 2017 | 2205 | NM_014679 | Hs.151791 | 2.00E-93 | 1 | KIAA0092 gene product (KIAA0092), mRNA /cds=(|
| 59C10 | 37 | 697 | AF070525 | Hs.151903 | 0 | 5 | clone 24706 mRNA sequence /cds=UNKNOWN /gb=AF |
| 519A7 | 165 | 686 | NM_005792 | Hs.152720 | 0 | 1 | M-phase phosphoprotein 6 (MPHOSPH6), mRNA /c |
| 481E11 | 3990 | 4280 | NM_005154 | Hs.152818 | 1.00E-135 | 1 | ubiquitin specific protease 8 (USP8), mRNA /cd |
| 110F2 | 1210 | 1841 | L25931 | Hs.152931 | 0 | 2 | lamin B receptor (LBR) mRNA, complete cds /cds=(75,192 |
| 516F8 | 1217 | 1708 | NM_002296 | Hs.152931 | 0 | 1 | lamin B receptor (LBR), mRNA /cds=(75,1922) /g |
| 462B2 | 93 | 2385 | AF244129 | Hs.153042 | 0 | 2 | cell-surface molecule Ly-9 mRNA, complete cds |
| 41F4 | 617 | 905 | X14046 | Hs.153053 | 1.00E-162 | 1 | leukocyte antigen CD37 /cds=(63,908) /gb=X14 |
| 462G8 | 2312 | 2843 | AF311312 | Hs.153057 | 0 | 1 | infertility-related sperm protein mRNA, comp |
| 142H5 | 17 | 221 | M94856 | Hs.153179 | 1.00E-92 | 1 | fatty acid binding protein homologue (PA-FABP) mRNA, |
| 486G9 | 3 | 431 | NM_001444 | Hs.153179 | 0 | 1 | fatty acid binding protein 5 (psoriasis-associ |
| 40A1 | 2158 | 2716 | X79201 | Hs.153221 | 0 | 1 | SYT /cds=(3,1178) /gb=X79201 /gi=531105 |
| 101D9 | 1524 | 2060 | AB014601 | Hs.153293 | 0 | 1 | for KIAA0701 protein, partial cds /cds=(0 |
| 460F10 | 1457 | 6107 | AB032972 | Hs.153489 | 0 | 2 | mRNA for KIAA1146 protein, partial cds /cds=(0 |
| 106A5 | 445 | 547 | AI761622 | Hs.153523 | 2.00E-37 | 1 | wg66f05.x1 cDNA, 3' end /clone=IMAGE:2370081 |
| 482A6 | 49 | 369 | AI859076 | Hs.153551 | 1.00E-106 | 1 | wl33b04.x1 cDNA, 3' end /clone=IMAGE:2426671 |
| 589B2 | 1054 | 1556 | AF261091 | Hs.153612 | 0 | 1 | iron inhibited ABC transporter 2 mRNA, complet |
| 57A3 | 1586 | 1757 | NM_004073 | Hs.153640 | 9.00E-87 | 1 | cytokine-inducible kinase (CNK), mRNA /cds=(3 |
| 466H3 | 2 | 257 | NM_003866 | Hs.153687 | 1.00E-133 | 1 | inositol polyphosphate-4-phosphatase, type |
| 483B6 | 3337 | 3544 | NM_002526 | Hs.153952 | 2.00E-72 | 1 | 5' nucleotidase (CD73) (NT5), mRNA /cds=(49,17 |
| 41F1 | 2749 | 3371 | X55740 | Hs.153952 | 0 | 1 | placental cDNA coding for 5'nucleotidase (EC 3.1.3.5) |
| 44C3 | 1319 | 1574 | X82206 | Hs.153961 | 1.00E-130 | 1 | alpha-centractin /cds=(66,1196) /gb=X8 |
| 64F12 | 2578 | 2713 | NM_022790 | Hs.154057 | 1.00E-26 | 1 | matrix metalloproteinase 19 (MMP19), transcri |
| 72E11 | 1886 | 2717 | U38320 | Hs.154057 | 0 | 15 | clone rasi-3 matrix metalloproteinase RASI-1 |
| 165H12 | 414 | 663 | AW970676 | Hs.154172 | 2.00E-22 | 1 | EST382759 cDNA /gb=AW970676 /gi=8160521 /ug= |
| 37A4 | 1151 | 2746 | M31210 | Hs.154210 | 0 | 2 | endothelial differentiation protein (edg-1) gene mR |
| 597F4 | 1125 | 2395 | NM_001400 | Hs.154210 | 0 | 11 | endothelial differentiation, sphingolipid G |
| 106F2 | 24 | 1657 | U22897 | Hs.154230 | 0 | 2 | nuclear domain 10 protein (ndp52) mRNA, comple |
| 466E2 | 116 | 373 | AB023149 | Hs.154296 | 1.00E-131 | 2 | mRNA for KIAA0932 protein, partial cds /cds=(0 |
| 107F11 | 1386 | 1743 | AL117566 | Hs.154320 | 0 | 1 | cDNA DKFZp566J164 (from clone DKFZp566J1 |
| 166E12 | 4490 | 4894 | D86967 | Hs.154332 | 0 | 1 | KIAA0212 gene, complete cds /cds=(58,2031) / |
| 188D12 | 5148 | 5666 | NM_014674 | Hs.154332 | 0 | 2 | KIAA0212 gene product (KIAA0212), mRNA /cds=(|
| 66A1 | 88 | 615 | M82882 | Hs.154365 | 0 | 1 | cis-acting sequence /cds=UNKNOWN /gb=M82882 /gi=180 |
| 37C1 | 4320 | 4776 | AB028999 | Hs.154525 | 0 | 1 | for KIAA1076 protein, partial cds /cds=(0 |
| 98D2 | 2317 | 4907 | NM_000104 | Hs.154654 | 0 | 6 | cytochrome P450, subfamily I (dioxin-inducibl |
| 37C4 | 4445 | 4907 | U03688 | Hs.154654 | 0 | 3 | dioxin-inducible cytochrome P450 (CYP1B1) mRNA, comp |
| 464A5 | 1418 | 2027 | NM_006636 | Hs.154672 | 0 | 3 | methylene tetrahydrofolate dehydrogenase (N |
| 36C5 | 615 | 1689 | X16396 | Hs.154672 | 0 | 7 | NAD-dependent methylene tetrahydrofolate d |
| 67C8 | 1 | 397 | U85773 | Hs.154695 | 0 | 1 | phosphomannomutase (PMM2) mRNA, complete cds /cds=(|
| 525D3 | 2084 | 2533 | NM_002651 | Hs.154846 | 0 | 1 | phosphatidylinositol 4-kinase, catalytic, b |
| 109A7 | 1979 | 3148 | D10040 | Hs.154890 | 0 | 2 | for long-chain acyl-CoA synthetase, compl |
| 167F6 | 1817 | 3359 | NM_021122 | Hs.154890 | 0 | 8 | fatty-acid-Coenzyme A ligase, long-chain 2 (|

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|-------|-------|-----------|-----------|-----------|---|--|
| 182A1 | 344 | 793 | NM_021825 | Hs.154938 | 0 | 1 | hypothetical protein MDS025 (MDS025), mRNA / |
| 104E2 | 1254 | 1762 | D87450 | Hs.154978 | 0 | 1 | KIAA0261 gene, partial cds /cds=(0,3865) /gb |
| 519G10 | 4912 | 5303 | NM_003489 | Hs.155017 | 0 | 1 | nuclear receptor interacting protein 1 (NRIP1 |
| 595C6 | 4067 | 4631 | NM_006526 | Hs.155040 | 0 | 2 | zinc finger protein 217 (ZNF217), mRNA /cds=(2 |
| 105D4 | 1768 | 2418 | L42373 | Hs.155079 | 0 | 1 | phosphatase 2A B56-alpha (PP2A) mRNA, complete |
| 174B7 | 1768 | 2320 | NM_006243 | Hs.155079 | 0 | 1 | protein phosphatase 2, regulatory subunit B (|
| 75G4 | 920 | 1775 | X59066 | Hs.155101 | 0 | 2 | mitochondrial ATP synthase (F1-ATPase) alpha |
| 523G12 | 20 | 848 | NM_004681 | Hs.155103 | 0 | 3 | eukaryotic translation initiation factor 1A, |
| 74D7 | 292 | 1094 | M16942 | Hs.155122 | 0 | 3 | MHC class II HLA-DRw53-associated glycoprotein beta- |
| 137D4 | 2500 | 2822 | AL049761 | Hs.155140 | 1.00E-176 | 1 | DNA sequence from clone RP5-863C7 on chromosome 20p12 |
| 471B5 | 908 | 1168 | AK023379 | Hs.155160 | 1.00E-141 | 1 | cDNA FLJ13317 fis, clone OVARC1001577, highly |
| 176C9 | 2104 | 2635 | NM_003664 | Hs.155172 | 0 | 1 | adaptor-related protein complex 3, beta 1 sub |
| 99F5 | 212 | 671 | NM_005642 | Hs.155188 | 0 | 1 | TATA box binding protein (TBP)-associated fac |
| 166E9 | 1215 | 1637 | U18062 | Hs.155188 | 0 | 1 | TFIID subunit TAFII55 (TAFII55) mRNA, complete cds /c |
| 163A11 | 60 | 3052 | AL162086 | Hs.155191 | 0 | 8 | cDNA DKFZp762H157 (from clone DKFZp762H1 |
| 71E4 | 44 | 558 | NM_003379 | Hs.155191 | 1.00E-175 | 4 | villin 2 (ezrin) (VIL2), mRNA /cds=(117,1877) |
| 145D8 | 2135 | 2669 | L47345 | Hs.155202 | 0 | 1 | elongin A mRNA, complete cds /cds=(32,2350) /g |
| 477H9 | 357 | 2812 | NM_014670 | Hs.155291 | 0 | 2 | KIAA0005 gene product (KIAA0005), mRNA /cds=(|
| 58D8 | 38 | 336 | NM_000518 | Hs.155376 | 1.00E-100 | 1 | hemoglobin, beta (HBB), mRNA /cds=(50,493) /g |
| 48F11 | 576 | 2131 | NM_006164 | Hs.155396 | 0 | 2 | nuclear factor (erythroid-derived 2)-like 2 |
| 65G11 | 426 | 1179 | S74017 | Hs.155396 | 0 | 1 | Nrf2=NF-E2-like basic leucine zipper transcriptional act |
| 480G12 | 852 | 1246 | NM_001352 | Hs.155402 | 0 | 1 | D site of albumin promoter (albumin D-box) bind |
| 182B12 | 245 | 592 | NM_006899 | Hs.155410 | 0 | 1 | isocitrate dehydrogenase 3 (NAD+) beta (IDH3B |
| 599C9 | 3188 | 3487 | NM_021643 | Hs.155418 | 1.00E-163 | 1 | GS3955 protein (GS3955), mRNA /cds=(1225,2256 |
| 68H2 | 563 | 1749 | AF037448 | Hs.155489 | 0 | 2 | RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA |
| 173F6 | 1243 | 1811 | AF208043 | Hs.155530 | 0 | 2 | IFI16b (IFI16b) mRNA, complete cds /cds=(264,2 |
| 170B3 | 1061 | 1342 | D50063 | Hs.155543 | 1.00E-139 | 1 | proteasome subunit p40_ / Mov34 protein, comp |
| 590E9 | 494 | 1323 | NM_002811 | Hs.155543 | 0 | 2 | proteasome (prosome, macropain) 26S subunit, |
| 522D11 | 1463 | 1710 | AB029003 | Hs.155546 | 1.00E-138 | 2 | mRNA for KIAA1080 protein, partial cds /cds=(0 |
| 587A8 | 3514 | 3923 | NM_001746 | Hs.155560 | 0 | 1 | calnexin (CANX), mRNA /cds=(89,1867) /gb=NM_0 |
| 39A6 | 830 | 1474 | D63878 | Hs.155595 | 0 | 1 | KIAA0158 gene, complete cds /cds=(258,1343) |
| 167F5 | 745 | 2735 | NM_004404 | Hs.155595 | 0 | 3 | neural precursor cell expressed, developmenta |
| 106E10 | 1922 | 2340 | U15173 | Hs.155596 | 1.00E-179 | 2 | BCL2/adenovirus E1B 19kD-interacting protein |
| 524A8 | 1639 | 2229 | NM_014666 | Hs.155623 | 0 | 1 | KIAA0171 gene product (KIAA0171), mRNA /cds=(|
| 166D6 | 12177 | 12974 | U47077 | Hs.155637 | 0 | 3 | DNA-dependent protein kinase catalytic subuni |
| 488A10 | 1961 | 2426 | NM_002827 | Hs.155894 | 0 | 3 | protein tyrosine phosphatase, non-receptor t |
| 65D6 | 696 | 1107 | S68271 | Hs.155924 | 0 | 3 | cyclic AMP-responsive element modulator (CRE |
| 113E8 | 682 | 1435 | NM_004054 | Hs.155935 | 0 | 1 | complement component 3a receptor 1 (C3AR1), mR |
| 105F10 | 119 | 1591 | U62027 | Hs.155935 | 0 | 3 | anaphylatoxin C3a receptor (HNFA09) mRNA, complete |
| 111C1 | 4122 | 4779 | NM_005541 | Hs.155939 | 0 | 5 | inositol polyphosphate-5-phosphatase, 145kD |
| 40A9 | 1727 | 2300 | D76444 | Hs.155968 | 0 | 1 | hkf-1 mRNA, complete cds /cds=(922,2979) /gb= |
| 124F1 | 1464 | 2121 | NM_005667 | Hs.155968 | 0 | 1 | zinc finger protein homologous to Zfp103 in mo |
| 481E12 | 2237 | 2691 | NM_003588 | Hs.155976 | 0 | 1 | cullin 4B (CUL4B), mRNA /cds=(78,2231) /gb=NM |
| 109H3 | 36 | 440 | NM_020414 | Hs.155986 | 0 | 1 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide |
| 193B10 | 1103 | 1892 | AK024974 | Hs.156110 | 1.00E-180 | 5 | cDNA: FLJ21321 fis, clone COL02335, highly sim |
| 463H6 | 26 | 149 | AI337347 | Hs.156339 | 5.00E-57 | 1 | tb98e10.x1 cDNA, 3' end /clone=IMAGE:2062410 |
| 107H5 | 34 | 253 | AI146787 | Hs.156601 | 7.00E-93 | 1 | qb83f02.x1 cDNA, 3' end /clone=IMAGE:1706715 |
| 517E8 | 209 | 822 | NM_015646 | Hs.156764 | 0 | 3 | RAP1B, member of RAS oncogene family (RAP1B), |
| 478H11 | 456 | 768 | NM_005819 | Hs.157144 | 1.00E-172 | 1 | syntaxin 6 (STX6), mRNA /cds=(0,767) /gb=NM_0 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|-------|-------|-----------|-----------|-----------|----|--|
| 463G12 | 44 | 283 | AI351144 | Hs.157213 | 3.00E-95 | 1 | qt23f10.x1 cDNA, 3' end /clone=IMAGE:1948459 |
| 520A2 | 2359 | 2565 | BC001913 | Hs.157236 | 1.00E-95 | 2 | Similar to membrane protein of cholinergic sy |
| 473A8 | 2944 | 3570 | AK026394 | Hs.157240 | 0 | 1 | cDNA: FLJ22741 fis, clone HUV00774 /cds=UNKNOWN |
| 464D5 | 433 | 601 | AW207701 | Hs.157315 | 8.00E-37 | 1 | UI-H-BI2-age-e-03-0-UI.s1 cDNA, 3' end /clon |
| 464B8 | 288 | 633 | BF184881 | Hs.157396 | 2.00E-99 | 1 | 601843756F1 cDNA, 5' end /clone=IMAGE:4064508 |
| 463A6 | 225 | 554 | AW976630 | Hs.157447 | 1.00E-169 | 1 | EST388739 cDNA /gb=AW976630 /gi=8167861 /ug= |
| 464G10 | 423 | 661 | AI356405 | Hs.157556 | 1.00E-103 | 1 | qz26g04.x1 cDNA, 3' end /clone=IMAGE:2028054 |
| 464H3 | 396 | 642 | AI568755 | Hs.157564 | 1.00E-123 | 1 | th15f03.x1 cDNA, 3' end /clone=IMAGE:2118365 |
| 466C1 | 110 | 384 | AI760026 | Hs.157569 | 1.00E-135 | 1 | wh83c05.x1 cDNA, 3' end /clone=IMAGE:2387336 |
| 465A2 | 11 | 178 | AI823541 | Hs.157710 | 1.00E-79 | 1 | wh55c11.x1 cDNA, 3' end /clone=IMAGE:2384660 |
| 464A8 | 2000 | 2248 | AK023779 | Hs.157777 | 1.00E-134 | 1 | cDNA FLJ13717 fis, clone PLACE2000425 /cds=UNK |
| 464G1 | 122 | 447 | AI361761 | Hs.157813 | 1.00E-163 | 2 | qz19a07.x1 cDNA, 3' end /clone=IMAGE:2021940 |
| 464G7 | 293 | 395 | AI361849 | Hs.157815 | 4.00E-30 | 1 | qz19h11.x1 cDNA, 3' end /clone=IMAGE:2022021 |
| 145B8 | 238 | 598 | BF303931 | Hs.157850 | 1.00E-179 | 3 | 601886564F2 cDNA, 5' end /clone=IMAGE:4120574 |
| 115D1 | 111 | 712 | NM_000661 | Hs.157850 | 1.00E-159 | 2 | ribosomal protein L9 (RPL9), mRNA /cds=(29,607 |
| 102F8 | 4161 | 4818 | AB023198 | Hs.158135 | 0 | 1 | for KIAA0981 protein, partial cds /cds=(0 |
| 597H12 | 1253 | 2625 | NM_000593 | Hs.158164 | 0 | 5 | ATP-binding cassette, sub-family B (MDR/TAP), |
| 465A3 | 172 | 342 | T78173 | Hs.158193 | 5.00E-64 | 1 | yd79c05.r1 cDNA, 5' end /clone=IMAGE:114440 / |
| 465H8 | 740 | 1171 | NM_006354 | Hs.158196 | 1.00E-149 | 1 | transcriptional adaptor 3 (ADA3, yeast homolo |
| 59H12 | 1646 | 6883 | NM_002313 | Hs.158203 | 0 | 4 | actin-binding LIM protein (ABLIM), transcript |
| 464A2 | 32 | 549 | NM_004571 | Hs.158225 | 0 | 1 | PBX/knotted 1 hoemobox 1 (PKNOX1), mRNA /cds=(|
| 124F12 | 6603 | 6907 | AB007915 | Hs.158286 | 1.00E-172 | 1 | mRNA for KIAA0446 protein, partial cds /cds=(3 |
| 519F5 | 80 | 268 | AI199223 | Hs.158289 | 1.00E-86 | 1 | qi47c06.x1 cDNA, 3' end /clone=IMAGE:1859626 |
| 463F8 | 33 | 286 | BF433857 | Hs.158501 | 1.00E-123 | 1 | 7q71b07.x1 cDNA /clone=IMAGE /gb=BF433857 /g |
| 137A8 | 204 | 452 | AI370965 | Hs.158653 | 5.00E-32 | 1 | ta29b11.x1 cDNA, 3' end /clone=IMAGE:2045469 |
| 466A11 | 1 | 565 | BE676408 | Hs.158714 | 0 | 1 | 7f29b11.x1 cDNA, 3' end /clone=IMAGE:3296061 |
| 73C2 | 5 | 396 | AW362008 | Hs.158794 | 0 | 1 | PM2-CT0265-211099-002-d04 /gb=AW362008 |
| 465C6 | 242 | 433 | AI378113 | Hs.158877 | 2.00E-95 | 1 | tc80c12.x1 cDNA, 3' end /clone=IMAGE:2072470 |
| 465C2 | 29 | 153 | AI378457 | Hs.158894 | 4.00E-60 | 2 | tc79d10.x1 cDNA, 3' end /clone=IMAGE:2072371 |
| 465C10 | 47 | 442 | AI379953 | Hs.158943 | 0 | 1 | tc81a07.x1 cDNA, 3' end /clone=IMAGE:2072532 |
| 477B9 | 151 | 396 | AI380220 | Hs.158965 | 1.00E-109 | 2 | tf94a04.x1 cDNA, 3' end /clone=IMAGE:2106894 |
| 477B10 | 1 | 414 | AI380236 | Hs.158966 | 0 | 2 | tf94b10.x1 cDNA, 3' end /clone=IMAGE:2106907 |
| 466F8 | 128 | 233 | AI380388 | Hs.158975 | 4.00E-30 | 1 | tf96a03.x1 cDNA, 3' end /clone=IMAGE:2107084 |
| 467E12 | 109 | 350 | AI799909 | Hs.158989 | 1.00E-82 | 1 | wc46c08.x1 cDNA, 3' end /clone=IMAGE:2321678 |
| 469G6 | 169 | 470 | AI631850 | Hs.158992 | 1.00E-119 | 1 | wa36h07.x1 cDNA, 3' end /clone=IMAGE:2300221 |
| 467H4 | 17 | 292 | BF508694 | Hs.158999 | 1.00E-117 | 1 | UI-H-BI4-aop-f-09-0-UI.s1 cDNA, 3' end /clon |
| 469B2 | 179 | 388 | AI568751 | Hs.159014 | 4.00E-94 | 1 | th15d09.x1 cDNA, 3' end /clone=IMAGE:2118353 |
| 464E8 | 742 | 945 | AL538276 | Hs.159065 | 1.00E-110 | 1 | AL538276 cDNA /clone=CS0DF027YC09-(5-prime) |
| 469D9 | 1 | 413 | AI431873 | Hs.159103 | 0 | 1 | ti26b11.x1 cDNA, 3' end /clone=IMAGE:2131581 |
| 122C7 | 1916 | 2375 | NM_003266 | Hs.159239 | 0 | 1 | toll-like receptor 4 (TLR4), mRNA /cds=(284,26 |
| 462H4 | 79 | 239 | BF307871 | Hs.159336 | 7.00E-66 | 1 | 601890687F1 cDNA, 5' end /clone=IMAGE:4132028 |
| 179C1 | 428 | 734 | AJ225093 | Hs.159386 | 3.00E-88 | 1 | single-chain antibody, complete cds |
| 473D11 | 267 | 339 | AI380255 | Hs.159424 | 5.00E-34 | 1 | tf94d08.x1 cDNA, 3' end /clone=IMAGE:2106927 |
| 107B2 | 1 | 617 | BE783628 | Hs.159441 | 1.00E-160 | 2 | 601471696F1 cDNA, 5' end /clone=IMAGE:3874823 |
| 590E12 | 52 | 654 | BG290141 | Hs.159441 | 0 | 6 | 602385221F1 cDNA, 5' end /clone=IMAGE:4514380 |
| 70E1 | 2095 | 2333 | AK027194 | Hs.159483 | 1.00E-119 | 1 | FLJ23541 fis, clone LNG08276, highly sim |
| 58A5 | 10448 | 12675 | AF193556 | Hs.159492 | 0 | 10 | saccin (SACS) gene, complete cds /cds=(76,1156 |
| 482E11 | 2064 | 2559 | NM_000061 | Hs.159494 | 0 | 1 | Bruton agammaglobulinemia tyrosine kinase (B |
| 147A11 | 755 | 2415 | AF001622 | Hs.159523 | 0 | 7 | class-I MHC-restricted T cell associated mole |
| 486H6 | 1164 | 1382 | NM_019604 | Hs.159523 | 1.00E-117 | 2 | class-I MHC-restricted T cell associated mole |
| 465A5 | 2693 | 3039 | NM_000033 | Hs.159546 | 1.00E-148 | 1 | ATP-binding cassette, sub-family D (ALD), mem |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|---|--|
| 60C4 | 1102 | 1962 | AK024833 | Hs.159557 | 1.00E-147 | 4 | FLJ21180 fis, clone CAS11176, highly sim |
| 465B11 | 457 | 1126 | NM_016952 | Hs.159565 | 0 | 1 | surface glycoprotein, Ig superfamily member (|
| 477A12 | 89 | 581 | AI797788 | Hs.159577 | 0 | 5 | wh78b11.x1 cDNA, 3' end /clone=IMAGE:2386845 |
| 595H8 | 19 | 912 | NM_004632 | Hs.159627 | 0 | 2 | death associated protein 3 (DAP3), mRNA /cds=(|
| 74D2 | 7 | 2119 | AF153609 | Hs.159640 | 0 | 9 | serine/threonine protein kinase sgk mRNA, com |
| 71B2 | 8 | 533 | NM_005627 | Hs.159640 | 0 | 1 | serum/glucocorticoid regulated kinase (SGK) |
| 467G8 | 310 | 488 | AW006352 | Hs.159643 | 2.00E-92 | 1 | wt04d12.x1 cDNA, 3' end /clone=IMAGE:2506487 |
| 467B8 | 11 | 363 | AI392893 | Hs.159655 | 1.00E-173 | 1 | tg05d07.x1 cDNA, 3' end /clone=IMAGE:2107885 |
| 471F11 | 16 | 303 | AI827950 | Hs.159659 | 1.00E-162 | 1 | wk31a11.x1 cDNA, 3' end /clone=IMAGE:2413916 |
| 467C11 | 18 | 501 | BF508053 | Hs.159673 | 0 | 1 | UI-H-BI4-apx-b-11-0-UI.s1 cDNA, 3' end /clon |
| 477F4 | 3 | 405 | AI394671 | Hs.159678 | 0 | 2 | tg24a07.x1 cDNA, 3' end /clone=IMAGE:2109684 |
| 472F5 | 194 | 366 | NM_018490 | Hs.160271 | 1.00E-93 | 1 | G protein-coupled receptor 48 (GPR48), mRNA / |
| 468B11 | 72 | 481 | AI393041 | Hs.160273 | 0 | 1 | tg25b10.x1 cDNA, 3' end /clone=IMAGE:2109787 |
| 477D3 | 5 | 484 | AI393906 | Hs.160401 | 0 | 2 | tg05f08.x1 cDNA, 3' end /clone=IMAGE:2107911 |
| 477D12 | 11 | 389 | AI393962 | Hs.160405 | 1.00E-178 | 1 | tg11d08.x1 cDNA, 3' end /clone=IMAGE:2108463 |
| 477D5 | 15 | 262 | AI393992 | Hs.160408 | 1.00E-138 | 1 | tg06c05.x1 cDNA, 3' end /clone=IMAGE:2107976 |
| 65A9 | 4106 | 5547 | AF137030 | Hs.160417 | 0 | 5 | transmembrane protein 2 (TMEM2) mRNA, complete |
| 513A2 | 4109 | 5547 | NM_013390 | Hs.160417 | 0 | 5 | transmembrane protein 2 (TMEM2), mRNA /cds=(14 |
| 463F12 | 688 | 1425 | AF218032 | Hs.160422 | 0 | 1 | clone PP902 unknown mRNA /cds=(693,1706) /gb= |
| 165C1 | 2625 | 2987 | X85116 | Hs.160483 | 0 | 1 | H.sapiens epb72 gene exon 1 /cds=(61,927) /gb=X85116 /gi=1 |
| 469G4 | 145 | 550 | AI634652 | Hs.160795 | 0 | 1 | wa07e10.x1 cDNA, 3' end /clone=IMAGE:2297418 |
| 472C7 | 343 | 565 | AI760020 | Hs.160951 | 1.00E-105 | 1 | wh83b05.x1 cDNA, 3' end /clone=IMAGE:2387313 |
| 466F12 | 485 | 662 | BF207290 | Hs.160954 | 2.00E-62 | 1 | 601870777F1 cDNA, 5' end /clone=IMAGE:4100850 |
| 477C10 | 5 | 290 | BF437585 | Hs.160980 | 1.00E-149 | 1 | 7p74d12.x1 cDNA, 3' end /clone=IMAGE:3651526 |
| 61E8 | 4435 | 6593 | U83115 | Hs.161002 | 0 | 3 | non-lens beta gamma-crystallin like protein (AIM1) m |
| 458E5 | 1 | 462 | R84314 | Hs.161043 | 1.00E-159 | 1 | yq23a02.r1 cDNA, 5' end /clone=IMAGE:274443 / |
| 466E12 | 117 | 447 | BF001821 | Hs.161075 | 0 | 1 | 7g93g02.x1 cDNA, 3' end /clone=IMAGE:3314066 |
| 102H4 | 7 | 219 | AW963155 | Hs.161786 | 1.00E-111 | 1 | EST375228 /gb=AW963155 /gi=8152991 /ug= |
| 118B6 | 2050 | 2260 | NM_022570 | Hs.161786 | 2.00E-75 | 1 | C-type (calcium dependent, carbohydrate-reco |
| 593C4 | 3863 | 4092 | U86453 | Hs.162808 | 9.00E-92 | 1 | phosphatidylinositol 3-kinase catalytic subunit p1 |
| 467B7 | 129 | 455 | AI023714 | Hs.163442 | 1.00E-164 | 1 | ow91h05.x1 cDNA, 3' end /clone=IMAGE:1654233 |
| 107G8 | 592 | 1016 | AK023670 | Hs.163495 | 0 | 1 | FLJ13608 fis, clone PLACE1010628 /cds=UNK |
| 74F3 | 229 | 449 | AA627122 | Hs.163787 | 4.00E-77 | 1 | nq70g02.s1 cDNA, 3' end /clone=IMAGE:1157714 |
| 68B3 | 1094 | 1771 | AK023494 | Hs.164005 | 0 | 5 | FLJ13432 fis, clone PLACE1002537 /cds=UNK |
| 469H10 | 420 | 850 | NM_002993 | Hs.164021 | 0 | 1 | small inducible cytokine subfamily B (Cys-X-C |
| 464E9 | 86 | 424 | AA811244 | Hs.164168 | 1.00E-166 | 1 | ob58h11.s1 cDNA, 3' end /clone=IMAGE:1335621 |
| 467E11 | 788 | 1330 | NM_007063 | Hs.164170 | 0 | 1 | vascular Rab-GAP/TBC-containing (VRP), mRNA |
| 597C5 | 59 | 1251 | AY007135 | Hs.164280 | 1.00E-126 | 3 | clone CDABP0051 mRNA sequence /cds=(89,985) / |
| 464H11 | 2 | 202 | BF689700 | Hs.164675 | 9.00E-65 | 1 | 602186609F1 cDNA, 5' end /clone=IMAGE:4298402 |
| 459D5 | 6 | 496 | AI248204 | Hs.165051 | 0 | 1 | qh64h11.x1 cDNA, 3' end /clone=IMAGE:1849509 |
| 120F12 | 23 | 502 | NM_001017 | Hs.165590 | 1.00E-159 | 5 | ribosomal protein S13 (RPS13), mRNA /cds=(32,4 |
| 469C11 | 301 | 613 | AW364833 | Hs.165681 | 1.00E-136 | 1 | QV3-DT0043-211299-044-d03 cDNA /gb=AW364833 |
| 465D3 | 289 | 481 | AI766638 | Hs.165693 | 2.00E-62 | 1 | wi02a10.x1 cDNA, 3' end /clone=IMAGE:2389050 |
| 465D6 | 107 | 238 | AW850041 | Hs.165695 | 3.00E-61 | 1 | IL3-CT0216-170300-097-C07 cDNA /gb=AW850041 |
| 466C7 | 166 | 421 | AI538546 | Hs.165696 | 1.00E-122 | 1 | td08b07.x1 cDNA, 3' end /clone=IMAGE:2075029 |
| 469C4 | 351 | 691 | AI436561 | Hs.165703 | 1.00E-148 | 1 | ti03b03.x1 cDNA, 3' end /clone=IMAGE:2129357 |
| 62A12 | 32 | 256 | AV727063 | Hs.165980 | 1.00E-120 | 4 | AV727063 cDNA, 5' end /clone=HTCCED11 /clone_ |
| 107C2 | 2427 | 2613 | AJ250865 | Hs.165986 | 1.00E-82 | 1 | for TESS 2 protein (TESS /cds=(128,1393) / |
| 461D5 | 1762 | 1935 | NM_004031 | Hs.166120 | 8.00E-81 | 1 | interferon regulatory factor 7 (IRF7), transc |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|-------|-------|-----------|-----------|-----------|----|--|
| 147D11 | 38 | 1283 | AL022097 | Hs.166203 | 0 | 5 | DNA sequence from PAC 256G22 on chromosome 6p24 |
| 595H12 | 1321 | 1597 | NM_002636 | Hs.166204 | 1.00E-135 | 2 | PHD finger protein 1 (PHF1), mRNA /cds=(56,1429 |
| 58H7 | 41 | 2036 | AL136711 | Hs.166254 | 0 | 2 | mRNA; cDNA DKFZp566I133 (from clone DKFZp566I1 |
| 98D12 | 5559 | 6110 | NM_014646 | Hs.166318 | 0 | 1 | lipin 2 (LPIN2), mRNA /cds=(239,2929) /gb=NM_0 |
| 468G1 | 146 | 509 | AW873324 | Hs.166338 | 1.00E-168 | 2 | hl92a07.x1 cDNA, 3' end /clone=IMAGE:3009396 |
| 477D7 | 2900 | 3748 | L14922 | Hs.166563 | 0 | 1 | DNA-binding protein (PO-GA) mRNA, complete cd |
| 177E7 | 3265 | 3595 | L23320 | Hs.166563 | 0 | 1 | replication factor C large subunit mRNA, complete cds |
| 584H2 | 206 | 1613 | NM_006925 | Hs.166975 | 1.00E-112 | 5 | splicing factor, arginine/serine-rich 5 (SFR |
| 481F5 | 647 | 917 | NM_002643 | Hs.166982 | 1.00E-128 | 1 | phosphatidylinositol glycan, class F (PIGF), |
| 598E4 | 112 | 538 | NM_002788 | Hs.167106 | 1.00E-174 | 1 | proteasome (prosome, macropain) subunit, alp |
| 466D8 | 46 | 470 | AI805131 | Hs.167206 | 0 | 1 | td11f04.x1 cDNA, 3' end /clone=IMAGE:2075359 |
| 464C8 | 342 | 469 | BE674762 | Hs.167208 | 4.00E-50 | 1 | 7e98d05.x1 cDNA, 3' end /clone=IMAGE:3293193 |
| 468A6 | 1177 | 1417 | NM_003658 | Hs.167218 | 4.00E-85 | 1 | BarH-like homeobox 2 (BARX2), mRNA /cds=(96,93 |
| 74H10 | 1 | 1271 | AF107405 | Hs.167460 | 0 | 12 | pre-mRNA splicing factor (SFRS3) mRNA, comple |
| 60E9 | 3154 | 3926 | U43185 | Hs.167503 | 1.00E-143 | 2 | signal transducer and activator of transcription Sta |
| 517G3 | 1129 | 2787 | NM_006994 | Hs.167741 | 0 | 3 | butyrophilin, subfamily 3, member A3 (BTN3A3), |
| 175H2 | 2261 | 2467 | U90548 | Hs.167741 | 2.00E-86 | 1 | butyrophilin (BTF3) mRNA, complete cds /cds=(171,192 |
| 588H5 | 1324 | 1735 | NM_002901 | Hs.167791 | 0 | 1 | reticulocalbin 1, EF-hand calcium binding dom |
| 331D7 | 53 | 625 | AF116909 | Hs.167827 | 4.00E-22 | 1 | clone HH419 unknown mRNA /cds=(189,593) /gb=A |
| 39C11 | 938 | 1672 | AF026402 | Hs.168103 | 0 | 1 | U5 snRNP 100 kD protein mRNA, cds /cds=(39,2501 |
| 583C8 | 906 | 1669 | NM_004818 | Hs.168103 | 0 | 5 | prp28, U5 snRNP 100 kd protein (U5-100K), mRNA |
| 43B1 | 1156 | 1224 | AF031167 | Hs.168132 | 1.00E-22 | 1 | interleukin 15 precursor (IL-15) mRNA, complet |
| 479A7 | 424 | 801 | NM_000585 | Hs.168132 | 1.00E-149 | 1 | interleukin 15 (IL15), mRNA /cds=(316,804) /g |
| 67D6 | 1783 | 2336 | AK024030 | Hs.168232 | 0 | 1 | FLJ13968 fis, clone Y79AA1001493, weakly |
| 122H3 | 1646 | 2894 | NM_023079 | Hs.168232 | 0 | 2 | hypothetical protein FLJ13855 (FLJ13855), mR |
| 459H3 | 9 | 504 | AI392830 | Hs.168287 | 0 | 1 | tg10b09.x1 cDNA, 3' end /clone=IMAGE:2103345 |
| 463G5 | 103 | 851 | NM_003002 | Hs.168289 | 0 | 1 | succinate dehydrogenase complex, subunit D, |
| 144G9 | 5588 | 5937 | AL049935 | Hs.168350 | 0 | 2 | DKFZp564O1116 (from clone DKFZp564O |
| 459A9 | 2293 | 2727 | NM_000201 | Hs.168383 | 0 | 2 | intercellular adhesion molecule 1 (CD54), hum |
| 123G3 | 2194 | 2675 | AB046801 | Hs.168640 | 0 | 2 | mRNA for KIAA1581 protein, partial cds /cds=(0 |
| 112H10 | 505 | 864 | AF007155 | Hs.168694 | 1.00E-175 | 2 | clone 23763 unknown mRNA, partial cds /cds=(0, |
| 60H7 | 223 | 897 | AF083420 | Hs.168913 | 0 | 1 | brain-specific STE20-like protein kinase 3 (|
| 105C12 | 1698 | 2052 | AK026671 | Hs.169078 | 1.00E-176 | 1 | FLJ23018 fis, clone LNG00903 /cds=(27,14 |
| 181B9 | 1148 | 1610 | NM_003937 | Hs.169139 | 0 | 1 | kynureninase (L-kynurenine hydrolase) (KYNU) |
| 462B7 | 13 | 478 | AA977148 | Hs.169168 | 0 | 1 | oq24g08.s1 cDNA, 3' end /clone=IMAGE:1587326 |
| 41H5 | 197 | 624 | U58913 | Hs.169191 | 0 | 1 | chemokine (hmrp-2a) mRNA, complete cds /cds=(71,484) |
| 69G6 | 11 | 552 | BF214508 | Hs.169248 | 1.00E-160 | 4 | 601845758F1 cDNA, 5' end /clone=IMAGE:4076510 |
| 460B2 | 904 | 2904 | NM_003202 | Hs.169294 | 1.00E-161 | 2 | transcription factor 7 (T-cell specific, HMG- |
| 464G12 | 543 | 994 | D26121 | Hs.169303 | 0 | 1 | mRNA for ZFM1 protein alternatively spliced product, |
| 464B5 | 163 | 762 | NM_013259 | Hs.169330 | 0 | 1 | neuronal protein (NP25), mRNA /cds=(49,897) / |
| 593G4 | 787 | 1353 | Z97989 | Hs.169370 | 0 | 2 | DNA sequence from PAC 66H14 on chromosome 6q21-22. Con |
| 165F12 | 1177 | 1751 | AK001725 | Hs.169407 | 0 | 1 | cDNA FLJ10863 fis, clone NT2RP4001575, highly |
| 483B12 | 10871 | 11349 | NM_004010 | Hs.169470 | 0 | 1 | dystrophin (muscular dystrophy, Duchenne and |
| 518B3 | 22 | 1257 | NM_002046 | Hs.169476 | 0 | 5 | glyceraldehyde-3-phosphate dehydrogenase (|
| 67E7 | 1289 | 1597 | U34995 | Hs.169476 | 3.00E-88 | 1 | normal keratinocyte subtraction library mRNA, clon |
| 47E9 | 2148 | 2452 | NM_005461 | Hs.169487 | 1.00E-172 | 1 | Kreisler (mouse) maf-related leucine zipper h |
| 69C3 | 846 | 3195 | U41387 | Hs.169531 | 0 | 24 | Gu protein mRNA, partial cds /cds=(0,2405) /gb=U41387 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|---|
| 468G7 | 73 | 450 | AI523598 | Hs.169541 | 1.00E-178 | 1 | th08g11.x1 cDNA, 3' end /clone=IMAGE:2117732 |
| 72E12 | 490 | 3074 | AJ251595 | Hs.169610 | 0 | 29 | for transmembrane glycoprotein (CD44 gen |
| 471F2 | 97 | 533 | AW172306 | Hs.169738 | 0 | 1 | xj37a08.x1 cDNA, 3' end /clone=IMAGE:2659382 |
| 589D4 | 96 | 488 | NM_000994 | Hs.169793 | 1.00E-163 | 2 | ribosomal protein L32 (RPL32), mRNA /cds=(34,4 |
| 105B6 | 1590 | 2215 | AK027212 | Hs.169854 | 0 | 1 | FLJ23559 fis, clone LNG09844 /cds=UNKNOWN |
| 462A8 | 1043 | 1529 | NM_000305 | Hs.169857 | 0 | 1 | paraoxonase 2 (PON2), mRNA /cds=(32,1096) /gb |
| 175D11 | 390 | 929 | AF061736 | Hs.169895 | 1.00E-132 | 2 | ubiquitin-conjugating enzyme RIG-B mRNA, com |
| 149A2 | 2442 | 2942 | U75686 | Hs.169900 | 0 | 1 | polyadenylate binding protein mRNA, complete |
| 524B9 | 2484 | 2709 | NM_007049 | Hs.169963 | 1.00E-125 | 2 | butyrophilin, subfamily 2, member A1 (BTN2A1), |
| 169G8 | 1192 | 1684 | U90543 | Hs.169963 | 0 | 1 | butyrophilin (BTF1) mRNA, complete cds /cds=(210,179 |
| 129E9 | 686 | 1227 | X70340 | Hs.170009 | 0 | 1 | transforming growth factor alpha /cds=(3 |
| 589C1 | 1893 | 3451 | NM_004350 | Hs.170019 | 0 | 5 | runt-related transcription factor 3 (RUNX3), |
| 331E1 | 5084 | 5496 | NM_001621 | Hs.170087 | 0 | 1 | aryl hydrocarbon receptor (AHR) mRNA /cds=(643 |
| 595H7 | 659 | 4185 | NM_002838 | Hs.170121 | 0 | 34 | protein tyrosine phosphatase, receptor type, |
| 184G8 | 1083 | 3762 | Y00062 | Hs.170121 | 0 | 10 | T200 leukocyte common antigen (CD45, LC-A) /c |
| 109D4 | 4529 | 4876 | AF032885 | Hs.170133 | 0 | 1 | forkhead protein (FKHR) mRNA, complete cds /cd |
| 98A12 | 4529 | 4882 | NM_002015 | Hs.170133 | 1.00E-160 | 1 | forkhead box O1A (rhabdomyosarcoma) (FOXO1A), |
| 99E3 | 2098 | 2334 | NM_004761 | Hs.170160 | 1.00E-125 | 1 | RAB2, member RAS oncogene family-like (RAB2L), |
| 498F10 | 3472 | 4909 | AL161952 | Hs.170171 | 0 | 28 | mRNA; cDNA DKFZp434M0813 (from clone DKFZp434M |
| 465G7 | 390 | 462 | AI475666 | Hs.170288 | 2.00E-31 | 1 | tc93c08.x1 cDNA, 3' end /clone=IMAGE:2073710 |
| 467E6 | 68 | 482 | AK025743 | Hs.170296 | 0 | 1 | cDNA: FLJ22090 fis, clone HEP16084 /cds=UNKNOWN |
| 459H9 | 4659 | 5168 | NM_014636 | Hs.170307 | 0 | 1 | Ral guanine nucleotide exchange factor RalGPS |
| 38D9 | 618 | 992 | D89678 | Hs.170311 | 0 | 25 | for A+U-rich element RNA binding factor, |
| 589F11 | 1033 | 2022 | NM_005463 | Hs.170311 | 0 | 13 | heterogeneous nuclear ribonucleoprotein D-I |
| 469B9 | 127 | 573 | AI436418 | Hs.170326 | 0 | 1 | ti01h02.x1 cDNA, 3' end /clone=IMAGE:2129235 |
| 183E4 | 2725 | 3777 | NM_002444 | Hs.170328 | 0 | 7 | moesin (MSN), mRNA /cds=(100,1833) /gb=NM_002 |
| 170G2 | 1693 | 3305 | Z98946 | Hs.170328 | 0 | 4 | DNA sequence from clone 376D21 on chromosome Xq11.1-12 |
| 464F6 | 162 | 534 | AI492865 | Hs.170331 | 1.00E-163 | 1 | th78a05.x1 cDNA, 3' end /clone=IMAGE:2124752 |
| 472F8 | 412 | 554 | AI373163 | Hs.170333 | 1.00E-75 | 1 | qz13a07.x1 cDNA, 3' end /clone=IMAGE:2021364 |
| 473C3 | 376 | 610 | AW291507 | Hs.170381 | 1.00E-123 | 1 | UI-H-BI2-aga-g-11-0-UI.s1 cDNA, 3' end /clon |
| 465E5 | 421 | 547 | BE676049 | Hs.170584 | 3.00E-54 | 1 | 7f21a03.x1 cDNA, 3' end /clone=IMAGE:3295276 |
| 477A3 | 25 | 202 | AI475884 | Hs.170587 | 4.00E-92 | 2 | tc95c12.x1 cDNA, 3' end /clone=IMAGE:2073910 |
| 477A4 | 34 | 489 | AI475905 | Hs.170588 | 0 | 1 | tc95f06.x1 cDNA, 3' end /clone=IMAGE:2073923 |
| 469F2 | 238 | 490 | AI478556 | Hs.170777 | 2.00E-84 | 1 | tm53e03.x1 cDNA, 3' end /clone=IMAGE:2161852 |
| 472C5 | 357 | 474 | AI479022 | Hs.170784 | 1.00E-53 | 1 | tm30a05.x1 cDNA, 3' end /clone=IMAGE:2158064 |
| 477D6 | 23 | 407 | AI492034 | Hs.170909 | 0 | 2 | tg06f12.x1 cDNA, 3' end /clone=IMAGE:2108015 |
| 471D4 | 187 | 416 | AI492181 | Hs.170913 | 1.00E-106 | 1 | tg07e06.x1 cDNA, 3' end /clone=IMAGE:2108098 |
| 464F8 | 14 | 142 | AI492651 | Hs.170934 | 7.00E-53 | 1 | qz18b10.x1 cDNA, 3' end /clone=IMAGE:2021851 |
| 466D3 | 173 | 461 | AI540204 | Hs.170935 | 1.00E-131 | 1 | td10h12.x1 cDNA, 3' end /clone=IMAGE:2075303 |
| 478F10 | 314 | 461 | AI761144 | Hs.171004 | 4.00E-45 | 1 | wh97h01.x1 cDNA, 3' end /clone=IMAGE:2388721 |
| 476E2 | 187 | 253 | AI494612 | Hs.171009 | 2.00E-30 | 2 | qz17a03.x1 cDNA, 3' end /clone=IMAGE:2021740 |
| 107G12 | 2413 | 2929 | AK024436 | Hs.171118 | 0 | 1 | for FLJ00026 protein, partial cds /cds=(0 |
| 478H3 | 1237 | 1509 | AL161725 | Hs.171118 | 1.00E-107 | 1 | DNA sequence from clone RP11-165F24 on chromosome 9. |
| 477H10 | 252 | 489 | BE674709 | Hs.171120 | 3.00E-87 | 1 | 7e94f05.x1 cDNA, 3' end /clone=IMAGE:3292833 |
| 477H11 | 18 | 521 | AI524202 | Hs.171122 | 0 | 1 | th10d11.x1 cDNA, 3' end /clone=IMAGE:2117877 |
| 466C10 | 24 | 216 | BE816212 | Hs.171261 | 8.00E-81 | 1 | MR1-BN0212-280600-001-c06 cDNA /gb=BE816212 |
| 470A4 | 22 | 562 | AI628893 | Hs.171262 | 0 | 1 | ty95h02.x1 cDNA, 3' end /clone=IMAGE:2286867 |
| 477C4 | 216 | 464 | AI540161 | Hs.171264 | 1.00E-112 | 2 | td10c10.x1 cDNA, 3' end /clone=IMAGE:2075250 |
| 519E12 | 1 | 321 | NM_016468 | Hs.171566 | 1.00E-167 | 2 | hypothetical protein (LOC51241), mRNA /cds=(|
| 44C11 | 5363 | 5829 | AF012872 | Hs.171625 | 0 | 1 | phosphatidylinositol 4-kinase 230 (pi4K230) |
| 517D4 | 19 | 559 | NM_003197 | Hs.171626 | 0 | 3 | transcription elongation factor B (SIII), pol |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|---|
| 48E9 | 1563 | 1809 | NM_004417 | Hs.171695 | 1.00E-138 | 2 | dual specificity phosphatase 1 (DUSP1), mRNA |
| 520H5 | 941 | 3667 | NM_002719 | Hs.171734 | 0 | 2 | protein phosphatase 2, regulatory subunit B (|
| 106G2 | 1 | 308 | BF243010 | Hs.171774 | 1.00E-167 | 2 | 601877795F1 cDNA, 5' end /clone=IMAGE:4106303 |
| 524A7 | 14 | 359 | NM_015933 | Hs.171774 | 0 | 14 | hypothetical protein (HSPC016), mRNA /cds=(3 |
| 117A11 | 311 | 614 | BF966361 | Hs.171802 | 1.00E-143 | 2 | 602286929F1 cDNA, 5' end /clone=IMAGE:4375783 |
| 38H11 | 885 | 2087 | M55543 | Hs.171862 | 0 | 6 | guanylate binding protein isoform II (GBP-2) mRNA, co |
| 512F8 | 232 | 1971 | NM_004120 | Hs.171862 | 0 | 12 | guanylate binding protein 2, interferon-induc |
| 111B9 | 3748 | 4161 | NM_004941 | Hs.171872 | 0 | 1 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide |
| 192H11 | 5738 | 5903 | NM_000937 | Hs.171880 | 2.00E-68 | 1 | polymerase (RNA) II (DNA directed) polypeptide |
| 176F11 | 1322 | 4789 | AL109935 | Hs.171917 | 0 | 3 | DNA sequence from clone RP5-1022P6 on chromosome 20 C |
| 596G12 | 2472 | 3152 | NM_001110 | Hs.172028 | 0 | 5 | a disintegrin and metalloproteinase domain 10 |
| 170A5 | 2438 | 2767 | AK023154 | Hs.172035 | 0 | 1 | FLJ13092 fis, clone NT2RP3002147 /cds=(34 |
| 469D11 | 71 | 535 | AI474074 | Hs.172070 | 0 | 1 | ti68h11.x1 cDNA, 3' end /clone=IMAGE:2137221 |
| 100G4 | 5574 | 5662 | U02882 | Hs.172081 | 3.00E-24 | 1 | rolipram-sensitive 3',5'-cyclic AMP phosphodiester |
| 524A11 | 1 | 2517 | AL110202 | Hs.172089 | 0 | 20 | mRNA; cDNA DKFZp586I2022 (from clone DKFZp586 |
| 49A2 | 929 | 2845 | NM_002568 | Hs.172182 | 0 | 30 | poly(A)-binding protein, cytoplasmic 1 (PABP |
| 54C5 | 929 | 2484 | Y00345 | Hs.172182 | 0 | 9 | polyA binding protein /cds=(502,2403) /gb=Y0 |
| 586B1 | 1042 | 1504 | NM_002408 | Hs.172195 | 0 | 1 | mannosyl (alpha-1,6-)-glycoprotein beta-1,2 |
| 169H6 | 5576 | 5958 | D25538 | Hs.172199 | 0 | 1 | KIAA0037 gene, complete cds /cds=(265,3507) |
| 115G7 | 4531 | 4976 | NM_001114 | Hs.172199 | 0 | 1 | adenylate cyclase 7 (ADCY7), mRNA /cds=(265,35 |
| 120F2 | 1 | 2496 | NM_007363 | Hs.172207 | 0 | 11 | non-POU-domain-containing, octamer-binding |
| 74A3 | 860 | 1364 | Y11289 | Hs.172207 | 0 | 1 | p54nrb gene, exon 3 (and joined /cds=(136,1551) |
| 60B7 | 695 | 1160 | NM_000202 | Hs.172458 | 0 | 1 | iduronate 2-sulfatase (Hunter syndrome) (IDS |
| 479D10 | 4059 | 4347 | NM_000632 | Hs.172631 | 1.00E-125 | 1 | integrin, alpha M (complement component recep |
| 167B10 | 1 | 389 | NM_003761 | Hs.172684 | 0 | 4 | vesicle-associated membrane protein 8 (endob |
| 189E11 | 1773 | 2038 | NM_001345 | Hs.172690 | 1.00E-149 | 2 | diacylglycerol kinase, alpha (80kD) (DGKA), m |
| 177C2 | 983 | 1489 | X62535 | Hs.172690 | 0 | 1 | diacylglycerol kinase /cds=(103,2310) |
| 458B12 | 535 | 1002 | NM_012326 | Hs.172740 | 0 | 1 | microtubule-associated protein, RP/EB family |
| 53A11 | 69 | 430 | W26908 | Hs.172762 | 1.00E-180 | 1 | 16b3 /gb=W26908 /gi=1306136 /ug=Hs.17276 |
| 151H2 | 2016 | 2572 | M80359 | Hs.172766 | 0 | 1 | protein p78 mRNA, complete cds /cds=(171,2312) /gb=M8 |
| 100G10 | 3983 | 4302 | AB037808 | Hs.172789 | 1.00E-149 | 1 | for KIAA1387 protein, partial cds /cds=(0 |
| 515D9 | 354 | 548 | NM_004182 | Hs.172791 | 3.00E-65 | 1 | ubiquitously-expressed transcript (UXT), mR |
| 193D9 | 2282 | 2757 | AL109669 | Hs.172803 | 0 | 3 | mRNA full length insert cDNA clone EUROIMAGE 31 |
| 460H10 | 12 | 490 | NM_016466 | Hs.172918 | 0 | 1 | hypothetical protein (LOC51239), mRNA /cds=(|
| 483D3 | 3473 | 3941 | AB011102 | Hs.173081 | 0 | 1 | mRNA for KIAA0530 protein, partial cds /cds=(0, |
| 195B9 | 380 | 854 | NM_005729 | Hs.173125 | 0 | 2 | peptidylprolyl isomerase F (cyclophilin F) (|
| 173H6 | 6008 | 6412 | NM_006283 | Hs.173159 | 0 | 1 | transforming, acidic coiled-coil containing |
| 113E6 | 142 | 240 | AI554733 | Hs.173182 | 3.00E-49 | 1 | tn27f08.x1 cDNA, 3' end /clone=IMAGE:2168871 |
| 56G8 | 140 | 630 | AK002009 | Hs.173203 | 0 | 2 | FLJ11147 fis, clone PLACE1006678, weakly |
| 69E6 | 1 | 463 | BF131656 | Hs.173205 | 1.00E-147 | 8 | 601820483F1 cDNA, 5' end /clone=IMAGE:4052348 |
| 44A2 | 6 | 196 | X06347 | Hs.173255 | 1.00E-94 | 1 | U1 small nuclear RNP-specific A protein /cds= |
| 149G1 | 79 | 498 | AY007165 | Hs.173274 | 1.00E-117 | 2 | clone CDABP0163 mRNA sequence /cds=UNKNOWN /g |
| 464F3 | 53 | 500 | AW005376 | Hs.173280 | 0 | 1 | ws94a12.x1 cDNA, 3' end /clone=IMAGE:2505598 |
| 587H5 | 3299 | 4083 | NM_014633 | Hs.173288 | 0 | 2 | KIAA0155 gene product (KIAA0155), mRNA /cds=(|
| 499B9 | 1032 | 1923 | NM_012081 | Hs.173334 | 0 | 2 | ELL-RELATED RNA POLYMERASE II, ELONGATION FAC |
| 54F11 | 368 | 1923 | U88629 | Hs.173334 | 0 | 2 | RNA polymerase II elongation factor ELL2, complete cd |
| 459A4 | 2170 | 2775 | AK001362 | Hs.173374 | 0 | 1 | cDNA FLJ10500 fis, clone NT2RP2000369 /cds=UNK |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|---|
| 124B1 | 2566 | 3019 | AB046825 | Hs.173422 | 0 | 1 | mRNA for KIAA1605 protein, partial cds /cds=(3 |
| 126H6 | 1080 | 1626 | NM_006363 | Hs.173497 | 0 | 1 | Sec23 (S. cerevisiae) homolog B (SEC23B), mRNA |
| 596D5 | 1233 | 1365 | NM_004550 | Hs.173611 | 8.00E-63 | 5 | NADH dehydrogenase (ubiquinone) Fe-S protein |
| 108C5 | 1709 | 1864 | AK022681 | Hs.173685 | 2.00E-83 | 1 | FLJ12619 fis, clone NT2RM4001682 /cds=(39 |
| 583D12 | 3 | 1960 | AK025703 | Hs.173705 | 0 | 4 | cDNA: FLJ22050 fis, clone HEP09454 /cds=UNKNOWN |
| 70B6 | 579 | 1140 | AL049610 | Hs.173714 | 0 | 2 | DNA sequence from clone 1055C14 on chromosome Xq22.1- |
| 46D7 | 590 | 1150 | NM_012286 | Hs.173714 | 0 | 1 | MORF-related gene X (KIAA0026), mRNA /cds=(305 |
| 467G5 | 17 | 283 | AA534537 | Hs.173720 | 1.00E-104 | 1 | nf80h10.s1 cDNA, 3' end /clone=IMAGE:926275 / |
| 168H5 | 1 | 1066 | D25274 | Hs.173737 | 0 | 5 | mRNA, clone:PO2ST9 /cds=UNKNOWN /gb=D25274 / |
| 471B8 | 5347 | 5922 | NM_014832 | Hs.173802 | 0 | 1 | KIAA0603 gene product (KIAA0603), mRNA /cds=(|
| 177F4 | 1053 | 1622 | U51166 | Hs.173824 | 0 | 1 | G/T mismatch-specific thymine DNA glycosylase mRNA, |
| 471C3 | 396 | 719 | AF277292 | Hs.173840 | 1.00E-176 | 1 | C4orf1 mRNA /cds=(0,281) /gb=AF277292 /gi=96 |
| 477F7 | 2053 | 2694 | U80735 | Hs.173854 | 0 | 3 | CAGF28 mRNA, partial cds /cds=(0,2235) /gb=U80 |
| 41F3 | 3595 | 3890 | M37435 | Hs.173894 | 1.00E-143 | 1 | macrophage-specific colony-stimulating factor (CSF |
| 460C8 | 1542 | 1939 | NM_014225 | Hs.173902 | 0 | 1 | protein phosphatase 2 (formerly 2A), regulator |
| 458A9 | 292 | 414 | AI763121 | Hs.173904 | 4.00E-57 | 1 | wi06d12.x1 cDNA, 3' end /clone=IMAGE:2389463 |
| 170B10 | 1230 | 3510 | AL137681 | Hs.173912 | 1.00E-176 | 5 | cDNA DKFZp434M0326 (from clone DKFZp434M |
| 126E10 | 1061 | 1795 | Z17227 | Hs.173936 | 1.00E-111 | 2 | mRNA for transmembrane receptor protein /cds=(4 |
| 72H7 | 1210 | 1907 | U08316 | Hs.173965 | 0 | 2 | insulin-stimulated protein kinase 1 (ISPK-1) mRNA, c |
| 123G7 | 554 | 858 | NM_005777 | Hs.173993 | 1.00E-168 | 1 | RNA binding motif protein 6 (RBM6), mRNA /cds=(|
| 469C8 | 261 | 528 | BE674902 | Hs.174010 | 1.00E-113 | 1 | 7e97a04.x1 cDNA, 3' end /clone=IMAGE:3293070 |
| 117G6 | 2450 | 2657 | NM_003089 | Hs.174051 | 1.00E-112 | 1 | small nuclear ribonucleoprotein 70kD polypept |
| 103A5 | 4907 | 5011 | NM_002209 | Hs.174103 | 1.00E-48 | 1 | integrin, alpha L (antigen CD11A (p180), lymph |
| 159F4 | 333 | 925 | AF261087 | Hs.174131 | 0 | 7 | DNA-binding protein TAXREB107 mRNA, complete |
| 588F9 | 333 | 926 | NM_000970 | Hs.174131 | 0 | 8 | ribosomal protein L6 (RPL6), mRNA /cds=(26,892 |
| 187A2 | 2993 | 3464 | NM_001096 | Hs.174140 | 0 | 2 | ATP citrate lyase (ACLY), mRNA /cds=(84,3401) |
| 41C6 | 3652 | 3992 | X03663 | Hs.174142 | 0 | 1 | c-fms proto-oncogene /cds=(300,3218) /gb=X0 |
| 465G10 | 199 | 489 | BE674951 | Hs.174144 | 1.00E-152 | 1 | 7e97g10.x1 cDNA, 3' end /clone=IMAGE:3293154 |
| 468H10 | 28 | 159 | AI524263 | Hs.174193 | 6.00E-62 | 1 | th11g07.x1 cDNA, 3' end /clone=IMAGE:2118012 |
| 99C7 | 402 | 733 | NM_006435 | Hs.174195 | 1.00E-179 | 2 | interferon induced transmembrane protein 2 (|
| 467E4 | 162 | 516 | BF062628 | Hs.174215 | 1.00E-157 | 1 | 7h62h05.x1 cDNA, 3' end /clone=IMAGE:3320601 |
| 74E5 | 2 | 485 | D63789 | Hs.174228 | 0 | 15 | DNA for SCM-1beta precursor, complete cds /cd |
| 470F11 | 108 | 305 | AI590337 | Hs.174258 | 1.00E-104 | 1 | tn49c03.x1 cDNA, 3' end /clone=IMAGE:2171716 |
| 463D2 | 1 | 194 | AV734916 | Hs.175971 | 1.00E-94 | 1 | AV734916 cDNA, 5' end /clone=cdaAHE11 /clone_ |
| 477E5 | 75 | 222 | AI380955 | Hs.176374 | 2.00E-33 | 1 | tg18b08.x1 cDNA, 3' end /clone=IMAGE:2109111 |
| 473A9 | 1 | 296 | AI708327 | Hs.176430 | 1.00E-162 | 1 | at04c02.x1 cDNA, 3' end /clone=IMAGE:2354114 |
| 468C3 | 24 | 235 | AW081098 | Hs.176498 | 6.00E-91 | 1 | xc29a12.x1 cDNA, 3' end /clone=IMAGE:2585662 |
| 479D11 | 595 | 1810 | J04162 | Hs.176663 | 0 | 14 | leukocyte IgG receptor (Fc-gamma-R) mRNA, complete c |
| 108G2 | 388 | 579 | AI638800 | Hs.176920 | 6.00E-78 | 4 | tt32e01.x1 cDNA, 3' end /clone=IMAGE:2242488 |
| 467A10 | 98 | 170 | AI865603 | Hs.177045 | 6.00E-27 | 1 | wk47g03.x1 cDNA, 3' end /clone=IMAGE:2418580 |
| 117A6 | 1179 | 1403 | AF116606 | Hs.177415 | 1.00E-112 | 2 | PRO0890 mRNA, complete cds /cds=(1020,1265) / |
| 73F2 | 236 | 919 | NM_016406 | Hs.177507 | 0 | 4 | hypothetical protein (HSPC155), mRNA /cds=(2 |
| 516D8 | 24 | 340 | NM_006886 | Hs.177530 | 1.00E-179 | 1 | ATP synthase, H+ transporting, mitochondrial |
| 479F4 | 163 | 676 | NM_002414 | Hs.177543 | 0 | 1 | antigen identified by monoclonal antibodies 1 |
| 126A9 | 906 | 2105 | NM_005534 | Hs.177559 | 0 | 35 | interferon gamma receptor 2 (interferon gamma |
| 41H6 | 905 | 1826 | U05875 | Hs.177559 | 0 | 10 | clone pSK1 interferon gamma receptor accessory factor |
| 37G1 | 1690 | 2420 | U62961 | Hs.177584 | 0 | 1 | succinyl CoA:3-oxoacid CoA transferase precursor (O |
| 597H7 | 1764 | 2520 | AF218002 | Hs.177596 | 0 | 7 | clone PP2464 unknown mRNA /cds=(675,2339) /gb |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|--|
| 520B8 | 1036 | 1202 | NM_006888 | Hs.177656 | 4.00E-90 | 3 | calmodulin 1 (phosphorylase kinase, delta) (C |
| 151G7 | 2439 | 3048 | J03473 | Hs.177766 | 0 | 1 | poly(ADP-ribose) synthetase mRNA, complete cds /cds= |
| 116C6 | 318 | 834 | BC001980 | Hs.177781 | 1.00E-144 | 4 | clone MGC:5618, mRNA, complete cds /cds=(156, |
| 179C11 | 211 | 737 | X07834 | Hs.177781 | 0 | 3 | manganese superoxide dismutase (EC 1.15.1.1) |
| 98A9 | 213 | 648 | M73547 | Hs.178112 | 0 | 4 | polyposis locus (DP1 gene) mRNA, complete cds /cds=(82 |
| 459E10 | 149 | 789 | AK023719 | Hs.178357 | 0 | 1 | cDNA FLJ13657 fis, clone PLACE1011563 /cds=(8 |
| 120H6 | 137 | 404 | NM_021029 | Hs.178391 | 1.00E-136 | 1 | ribosomal protein L44 (RPL44), mRNA /cds=(37,3 |
| 589E9 | 371 | 596 | NM_000973 | Hs.178551 | 1.00E-125 | 1 | ribosomal protein L8 (RPL8), mRNA /cds=(43,816 |
| 142F5 | 1848 | 2210 | D21090 | Hs.178658 | 1.00E-179 | 1 | XP-C repair complementing protein (p58/HHR23 |
| 120H11 | 402 | 532 | AV716627 | Hs.178703 | 9.00E-69 | 1 | AV716627 cDNA, 5' end /clone=DCBBCH05 /clone_ |
| 98G11 | 3287 | 6017 | NM_004859 | Hs.178710 | 0 | 5 | clathrin, heavy polypeptide (Hc) (CLTC), mRNA |
| 177H1 | 142 | 421 | BF130300 | Hs.178732 | 1.00E-139 | 1 | 601818357F1 cDNA, 5' end /clone=IMAGE:4041902 |
| 472A10 | 421 | 562 | AI681868 | Hs.178784 | 4.00E-63 | 1 | tx50a12.x1 cDNA, 3' end /clone=IMAGE:2272990 |
| 467G6 | 194 | 292 | AW138461 | Hs.179003 | 1.00E-49 | 1 | UI-H-B11-adg-e-06-0-UI.s1 cDNA, 3' end /clon |
| 465C11 | 3312 | 3606 | NM_016562 | Hs.179152 | 1.00E-166 | 1 | toll-like receptor 7 (LOC51284), mRNA /cds=(13 |
| 469F7 | 268 | 405 | AI568459 | Hs.179419 | 3.00E-45 | 1 | tn39e07.x1 cDNA, 3' end /clone=IMAGE:2170020 |
| 99F11 | 750 | 2687 | NM_006472 | Hs.179526 | 0 | 73 | upregulated by 1,25-dihydroxyvitamin D-3 (VD |
| 39G9 | 526 | 2687 | S73591 | Hs.179526 | 0 | 17 | brain-expressed HHCPA78 homolog VDUP1 (Gene) |
| 102A1 | 2235 | 2659 | AL034343 | Hs.179565 | 0 | 1 | DNA sequence from clone RP1-108C2 on |
| 492B2 | 1074 | 2126 | NM_002717 | Hs.179574 | 1.00E-131 | 3 | chromosome 6p12. |
| 143F2 | 242 | 457 | NM_005771 | Hs.179608 | 1.00E-117 | 1 | protein phosphatase 2 (formerly 2A), regulator |
| 111G7 | 626 | 898 | NM_002659 | Hs.179657 | 1.00E-153 | 1 | retinol dehydrogenase homolog (RDHL) mRNA / |
| 585D2 | 61 | 3189 | AL162068 | Hs.179662 | 0 | 6 | plasminogen activator, urokinase receptor (P |
| 125G4 | 1159 | 1627 | NM_000389 | Hs.179665 | 1.00E-130 | 2 | mRNA; cDNA DKFZp762G106 (from clone |
| 331A1 | 51 | 377 | AK026642 | Hs.179666 | 1.00E-161 | 2 | DKFZp762G1 |
| 516H12 | 19 | 362 | NM_000997 | Hs.179779 | 1.00E-180 | 3 | cyclin-dependent kinase inhibitor 1A (p21, Ci |
| 170A11 | 1390 | 2087 | L20298 | Hs.179881 | 0 | 1 | FLJ22989 fis, clone KAT11824, highly sim |
| 195H8 | 1732 | 2110 | NM_001755 | Hs.179881 | 1.00E-173 | 1 | ribosomal protein L37 (RPL37), mRNA /cds=(28,3 |
| 127G6 | 2406 | 2924 | AK022499 | Hs.179882 | 0 | 2 | transcription factor (CBFB) mRNA, 3' end /cds=(|
| 461E6 | 610 | 1148 | NM_014153 | Hs.179898 | 0 | 1 | core-binding factor, beta subunit (CBFB), tra |
| 516B3 | 4 | 584 | NM_000975 | Hs.179943 | 1.00E-136 | 2 | cDNA FLJ12437 fis, clone NT2RM1000118, weakly |
| 62F8 | 24 | 537 | X79234 | Hs.179943 | 1.00E-175 | 1 | HSPC055 protein (HSPC055), mRNA /cds=(1400,19 |
| 471B11 | 1990 | 2496 | NM_005802 | Hs.179982 | 0 | 1 | ribosomal protein L11 (RPL11), mRNA /cds=(0,53 |
| 194B4 | 693 | 956 | NM_004159 | Hs.180062 | 1.00E-112 | 1 | ribosomal protein L11 /cds=(0,536) /gb= |
| 49D4 | 1002 | 1259 | NM_002690 | Hs.180107 | 1.00E-125 | 1 | tumor protein p53-binding protein (TP53BPL), |
| 184A11 | 26 | 515 | AK024823 | Hs.180139 | 0 | 2 | proteasome (prosome, macropain) subunit, bet |
| 593A8 | 43 | 535 | NM_006937 | Hs.180139 | 0 | 13 | polymerase (DNA directed), beta (POLB), mRNA |
| 61D10 | 102 | 722 | AF161415 | Hs.180145 | 0 | 1 | FLJ21170 fis, clone CAS10946, highly sim |
| 178A4 | 131 | 628 | NM_017924 | Hs.180201 | 0 | 2 | SMT3 (suppressor of mif two 3, yeast) homolog 2 |
| 463H9 | 54 | 171 | NM_005507 | Hs.180370 | 1.00E-60 | 1 | HSPC297 mRNA, partial cds /cds=(0,438) /gb=AF |
| 162B9 | 2139 | 2386 | AB013382 | Hs.180383 | 1.00E-124 | 1 | hypothetical protein FLJ20671 (FLJ20671), mR |
| 190B7 | 1743 | 2386 | NM_001946 | Hs.180383 | 1.00E-124 | 2 | cofilin 1 (non-muscle) (CFL1), mRNA /cds=(51,5 |
| 589B11 | 21 | 1566 | NM_006597 | Hs.180414 | 0 | 11 | for DUSP6, complete cds /cds=(351,1496) / |
| 73G2 | 21 | 1567 | Y00371 | Hs.180414 | 0 | 16 | dual specificity phosphatase 6 (DUSP6), trans |
| 62G1 | 985 | 1559 | X89602 | Hs.180433 | 0 | 1 | heat shock 70kD protein 8 (HSPA8), mRNA /cds=(8 |
| 98F9 | 1479 | 3653 | L38951 | Hs.180446 | 0 | 9 | hsc70 gene for 71 kd heat shock protein |
| 590F12 | 283 | 614 | NM_001026 | Hs.180450 | 0 | 1 | /cds=(83,2023) |
| 597F2 | 2670 | 3046 | AF187554 | Hs.180532 | 0 | 47 | rTS beta protein /cds=(17,1267) /gb=X896 |
| 482E2 | 85 | 366 | AL571386 | Hs.180546 | 1.00E-106 | 1 | importin beta subunit mRNA, complete cds /cds=(|
| | | | | | | | ribosomal protein S24 (RPS24), mRNA /cds=(142, |
| | | | | | | | sperm antigen-36 mRNA, complete cds /cds=(234, |
| | | | | | | | AL571386 cDNA /clone=CS0DI009YL09-(3-prime) |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|-----|--|
| 109C2 | 324 | 682 | BE540238 | Hs.180549 | 1.00E-143 | 1 | 601059809F1 cDNA, 5' end /clone=IMAGE:3446283 |
| 68G8 | 1447 | 3594 | AF123094 | Hs.180566 | 0 | 3 | API2-MLT fusion protein (API2-MLT) mRNA, comp |
| 180B9 | 1851 | 2142 | NM_002087 | Hs.180577 | 1.00E-160 | 2 | granulin (GRN), mRNA /cds=(62,1843) /gb=NM_00 |
| 51E4 | 880 | 2466 | NM_005066 | Hs.180610 | 0 | 6 | splicing factor proline/glutamine rich (poly |
| 50G4 | 880 | 1280 | X70944 | Hs.180610 | 0 | 1 | PTB-associated splicing factor /cds=(85 |
| 127C8 | 317 | 3175 | AK023143 | Hs.180638 | 0 | 5 | cDNA FLJ13081 fis, clone NT2RP3002033 /cds=(17 |
| 125E2 | 287 | 1692 | AL117621 | Hs.180777 | 0 | 2 | mRNA; cDNA DKFZp564M0264 (from clone DKFZp564 |
| 521F11 | 1969 | 2431 | AF126964 | Hs.180799 | 0 | 1 | C3HC4-type zinc finger protein (LZK1) mRNA, co |
| 479C11 | 1186 | 2245 | AK000271 | Hs.180804 | 1.00E-155 | 2 | cDNA FLJ20264 fis, clone COLF7912 /cds=UNKNOWN |
| 479C2 | 732 | 911 | NM_001242 | Hs.180841 | 3.00E-62 | 1 | tumor necrosis factor receptor superfamily, m |
| 596D2 | 67 | 942 | NM_000977 | Hs.180842 | 0 | 11 | ribosomal protein L13 (RPL13), mRNA /cds=(51,6 |
| 41E9 | 884 | 1779 | AL050337 | Hs.180866 | 0 | 2 | DNA sequence from clone 503F13 on chromosome 6q24.1-25 |
| 196C10 | 679 | 1338 | NM_000416 | Hs.180866 | 0 | 2 | interferon gamma receptor 1 (IFNGR1), mRNA /cd |
| 99A10 | 1 | 1655 | AF218029 | Hs.180877 | 0 | 11 | clone PP781 unknown mRNA /cds=(113,523) /gb=A |
| 65H9 | 1 | 1320 | Z48950 | Hs.180877 | 0 | 6 | hH3.3B gene for histone H3.3 /cds=(10,420) /gb=Z |
| 160G1 | 2065 | 2538 | AF045555 | Hs.180900 | 0 | 2 | wbscr1 (WBSR1) and wbscr5 (WBSR5) genes, com |
| 596B1 | 5 | 860 | NM_001008 | Hs.180911 | 0 | 5 | ribosomal protein S4, Y-linked (RPS4Y), mRNA |
| 192F11 | 1857 | 2521 | AK000299 | Hs.180952 | 0 | 1 | cDNA FLJ20292 fis, clone HEP05374 /cds=(21,140 |
| 75D10 | 94 | 1656 | AY007118 | Hs.181013 | 0 | 8 | clone CDABP0006 mRNA sequence /cds=(20,784) / |
| 46H2 | 105 | 1661 | NM_002629 | Hs.181013 | 0 | 5 | phosphoglycerate mutase 1 (brain) (PGAM1), mR |
| 107G10 | 4869 | 5527 | AK024391 | Hs.181043 | 0 | 1 | FLJ14329 fis, clone PLACE4000259, highly |
| 179A1 | 22 | 908 | AK001934 | Hs.181112 | 0 | 2 | FLJ11072 fis, clone PLACE1004982 /cds=(2 |
| 118D5 | 610 | 1130 | NM_014166 | Hs.181112 | 0 | 1 | HSPC126 protein (HSPC126), mRNA /cds=(25,837) |
| 483D9 | 659 | 915 | X57809 | Hs.181125 | 1.00E-123 | 1 | rearranged immunoglobulin lambda light chain mRNA /c |
| 596B10 | 499 | 1198 | NM_005517 | Hs.181163 | 0 | 2 | high-mobility group (nonhistone chromosomal) |
| 74A12 | 34 | 1674 | AK026650 | Hs.181165 | 0 | 192 | FLJ22997 fis, clone KAT11962, highly sim |
| 99H8 | 1079 | 2742 | BC001412 | Hs.181165 | 0 | 260 | eukaryotic translation elongation factor 1 |
| 70F10 | 144 | 840 | AB015798 | Hs.181195 | 0 | 1 | HSJ2 mRNA for DnaJ homolog, complete cds /cds= |
| 64E10 | 72 | 856 | BC002446 | Hs.181195 | 0 | 2 | MRJ gene for a member of protein family, clone |
| 597F6 | 1119 | 1767 | NM_001675 | Hs.181243 | 0 | 3 | activating transcription factor 4 (tax-respon |
| 109D8 | 825 | 1233 | D32129 | Hs.181244 | 0 | 1 | HLA class-I (HLA-A26) heavy chain, complete c |
| 593H10 | 465 | 1222 | NM_016057 | Hs.181271 | 0 | 3 | CGI-120 protein (LOC51644), mRNA /cds=(37,570 |
| 127H10 | 4782 | 5154 | AB020335 | Hs.181300 | 0 | 1 | Pancreas-specific TSA305 mRNA, complete cds |
| 150F7 | 509 | 1238 | M11353 | Hs.181307 | 1.00E-175 | 5 | H3.3 histone class C mRNA, complete cds /cds=(374,784) |
| 127F7 | 895 | 1057 | NM_002107 | Hs.181307 | 3.00E-85 | 2 | H3 histone, family 3A (H3F3A), mRNA /cds=(374,7 |
| 39H10 | 6 | 416 | BF676042 | Hs.181357 | 0 | 7 | 602084011F1 cDNA, 5' end /clone=IMAGE:4248195 |
| 99G12 | 193 | 842 | NM_002295 | Hs.181357 | 0 | 28 | laminin receptor 1 (67kD, ribosomal protein SA |
| 66A12 | 312 | 1084 | M20430 | Hs.181366 | 0 | 4 | MHC class II HLA-DR-beta (DR2-DQw1/DR4 DQw3) mRNA, co |
| 71H11 | 748 | 1096 | NM_002125 | Hs.181366 | 1.00E-176 | 1 | major histocompatibility complex, class II, |
| 56E4 | 272 | 521 | AI827911 | Hs.181400 | 1.00E-126 | 1 | wf34e11.x1 cDNA, 3' end /clone=IMAGE:2357516 |
| 170F6 | 5255 | 5724 | D63486 | Hs.181418 | 0 | 1 | KIAA0152 gene, complete cds /cds=(128,1006) |
| 464A11 | 5981 | 6322 | NM_014730 | Hs.181418 | 1.00E-159 | 1 | KIAA0152 gene product (KIAA0152), mRNA /cds=(|
| 514F6 | 1 | 232 | AW955745 | Hs.181426 | 1.00E-117 | 1 | EST367815 cDNA /gb=AW955745 /gi=8145428 /ug= |
| 177E2 | 690 | 947 | U81002 | Hs.181466 | 1.00E-130 | 2 | TRAF4 associated factor 1 mRNA, partial cds /c |
| 99B5 | 260 | 1660 | NM_001549 | Hs.181874 | 0 | 6 | interferon-induced protein with tetratricope |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|--|
| 595H9 | 104 | 645 | M90356 | Hs.181967 | 0 | 1 | BTF3 protein homologue gene, complete cds /cds=(0,644 |
| 67E2 | 1057 | 1782 | AK026664 | Hs.182225 | 4.00E-85 | 3 | FLJ23011 fis, clone LNG00572 /cds=(288,7 |
| 190A3 | 319 | 1615 | NM_014052 | Hs.182238 | 0 | 7 | GW128 protein (GW128), mRNA /cds=(698,889) /g |
| 140B10 | 1770 | 2034 | U46751 | Hs.182248 | 2.00E-92 | 1 | phosphotyrosine independent ligand p62 for the Lck S |
| 158H11 | 371 | 597 | D50420 | Hs.182255 | 1.00E-126 | 1 | OTK27, complete cds /cds=(94,480) /gb |
| 584A12 | 95 | 1397 | NM_005008 | Hs.182255 | 0 | 3 | non-histone chromosome protein 2 (S. cerevisia |
| 40G2 | 735 | 908 | Y00503 | Hs.182265 | 7.00E-41 | 1 | keratin 19 /cds=(32,1234) /gb=Y00503 /gi=340 |
| 596E7 | 1 | 886 | NM_001743 | Hs.182278 | 0 | 3 | calmodulin 2 (phosphorylase kinase, delta) (C |
| 129E10 | 36 | 350 | L29348 | Hs.182378 | 1.00E-174 | 2 | granulocyte-macrophage colony-stimulating |
| 487G1 | 184 | 934 | NM_002952 | Hs.182426 | 0 | 3 | ribosomal protein S2 (RPS2), mRNA /cds=(240,90 |
| 517G6 | 126 | 1497 | NM_005742 | Hs.182429 | 0 | 4 | protein disulfide isomerase-related protein |
| 60E12 | 10 | 1329 | M16342 | Hs.182447 | 0 | 4 | nuclear ribonucleoprotein particle (hnRNP) C protein |
| 98E9 | 10 | 1184 | NM_004500 | Hs.182447 | 0 | 8 | heterogeneous nuclear ribonucleoprotein C (|
| 496A4 | 87 | 1835 | NM_014394 | Hs.182470 | 0 | 2 | PTD010 protein (PTD010), mRNA /cds=(129,1088) |
| 110F11 | 947 | 1571 | AF061738 | Hs.182579 | 0 | 2 | leucine aminopeptidase mRNA, complete cds /cd |
| 124E1 | 1330 | 1889 | NM_005739 | Hs.182591 | 0 | 2 | RAS guanyl releasing protein 1 (calcium and DA |
| 143B2 | 32 | 565 | Z47087 | Hs.182643 | 0 | 1 | RNA polymerase II elongation factor-like |
| 103D2 | 161 | 538 | NM_001015 | Hs.182740 | 8.00E-97 | 5 | ribosomal protein S11 (RPS11), mRNA /cds=(15,4 |
| 331C2 | 1310 | 1585 | D64015 | Hs.182741 | 1.00E-136 | 1 | for T-cluster binding protein, complete c |
| 59E9 | 27 | 269 | BF245224 | Hs.182825 | 1.00E-105 | 1 | 601863885F1 cDNA, 5' end /clone=IMAGE:4082396 |
| 525E3 | 12 | 261 | NM_007209 | Hs.182825 | 1.00E-135 | 2 | ribosomal protein L35 (RPL35), mRNA /cds=(27,3 |
| 70C9 | 189 | 625 | BE963551 | Hs.182928 | 1.00E-129 | 1 | 601657346R1 cDNA, 3' end /clone=IMAGE:3866266 |
| 177B9 | 14 | 561 | BF242969 | Hs.182937 | 0 | 2 | 601877739F1 cDNA, 5' end /clone=IMAGE:4106289 |
| 519H3 | 34 | 526 | NM_021130 | Hs.182937 | 0 | 1 | peptidylprolyl isomerase A (cyclophilin A) (|
| 159A5 | 3163 | 3579 | AK026491 | Hs.182979 | 1.00E-141 | 2 | FLJ22838 fis, clone KAI44494, highly sim |
| 106G11 | 2956 | 3527 | AF204231 | Hs.182982 | 1.00E-138 | 2 | 88-kDa Golgi protein (GM88) mRNA, complete cds |
| 169A3 | 2117 | 2495 | M33336 | Hs.183037 | 1.00E-105 | 3 | cAMP-dependent protein kinase type I-alpha subunit (|
| 124H9 | 2767 | 2955 | NM_002734 | Hs.183037 | 7.00E-91 | 1 | protein kinase, cAMP-dependent, regulatory, |
| 107B3 | 2877 | 3182 | U17989 | Hs.183105 | 1.00E-170 | 1 | nuclear autoantigen GS2NA mRNA, complete cds / |
| 476A6 | 538 | 893 | NM_016523 | Hs.183125 | 0 | 1 | killer cell lectin-like receptor F1 (KLRF1), m |
| 75A1 | 629 | 1222 | AK001433 | Hs.183297 | 0 | 1 | FLJ10571 fis, clone NT2RP2003121, weakly |
| 597E11 | 97 | 1656 | AF248966 | Hs.183434 | 0 | 5 | HT028 mRNA, complete cds /cds=(107,1159) /gb= |
| 124A2 | 2015 | 2756 | AK024275 | Hs.183506 | 0 | 1 | cDNA FLJ14213 fis, clone NT2RP3003572 /cds=(11 |
| 74F2 | 2082 | 2418 | U53347 | Hs.183556 | 1.00E-177 | 2 | neutral amino acid transporter B mRNA, complete cds / |
| 482C5 | 1211 | 1688 | NM_018399 | Hs.183656 | 0 | 1 | VNN3 protein (HSA238982), mRNA /cds=(45,1550) |
| 594H12 | 1718 | 3458 | NM_001418 | Hs.183684 | 0 | 4 | eukaryotic translation initiation factor 4 g |
| 61H11 | 1457 | 2024 | U73824 | Hs.183684 | 0 | 2 | p97 mRNA, complete cds /cds=(306,3029) /gb=U73824 /g |
| 75H7 | 342 | 2258 | M26880 | Hs.183704 | 0 | 7 | ubiquitin mRNA, complete cds /cds=(135,2192) /gb=M26 |
| 599E7 | 2306 | 3111 | D44640 | Hs.183706 | 0 | 6 | HUMSUPY040 cDNA /clone=035-00-1 /gb=D44640 / |
| 518H4 | 1554 | 1973 | NM_002078 | Hs.183773 | 0 | 1 | golgi autoantigen, golgin subfamily a, 4 (GOL |
| 520C3 | 98 | 255 | NM_018955 | Hs.183842 | 3.00E-64 | 1 | ubiquitin B (UBB), mRNA /cds=(94,783) /gb=N |
| 102C11 | 1730 | 1808 | M15182 | Hs.183868 | 8.00E-33 | 2 | beta-glucuronidase mRNA, complete cds /cds=(26,1981 |
| 523D3 | 1730 | 2183 | NM_000181 | Hs.183868 | 0 | 2 | glucuronidase, beta (GUSB), mRNA /cds=(26,198 |
| 187A12 | 122 | 828 | NM_003589 | Hs.183874 | 0 | 1 | cullin 4A (CUL4A), mRNA /cds=(160,2139) /gb=N |
| 156F4 | 228 | 907 | AF119665 | Hs.184011 | 0 | 4 | inorganic pyrophosphatase complete cds |
| 525B8 | 225 | 791 | NM_021129 | Hs.184011 | 0 | 2 | pyrophosphatase (inorganic) (PP), nuclear ge |
| 589B1 | 3 | 394 | NM_000993 | Hs.184014 | 0 | 10 | ribosomal protein L31 (RPL31), mRNA /cds=(7,38 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|--|
| 99D6 | 3909 | 4308 | NM_004985 | Hs.184050 | 1.00E-145 | 1 | v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene |
| 166B3 | 12 | 345 | BE964596 | Hs.184052 | 1.00E-90 | 1 | 601658521R1 cDNA, 3' end /clone=IMAGE:3885796 |
| 591G6 | 1348 | 1958 | NM_022152 | Hs.184052 | 0 | 3 | PP1201 protein (PP1201), mRNA /cds=(66,1001) |
| 114E11 | 1780 | 1942 | AK025645 | Hs.184062 | 4.00E-59 | 1 | cDNA: FLJ21992 fis, clone HEP06554 /cds=(60,84 |
| 597E4 | 8 | 407 | NM_000982 | Hs.184108 | 1.00E-114 | 6 | ribosomal protein L21 (gene or pseudogene) (RP |
| 162C5 | 295 | 1062 | L41887 | Hs.184167 | 0 | 3 | splicing factor, arginine/serine-rich 7 (SFR |
| 109F6 | 151 | 749 | AF054182 | Hs.184211 | 0 | 1 | mitochondrial processing peptidase beta-subu |
| 462C6 | 4590 | 5087 | NM_015001 | Hs.184245 | 0 | 1 | KIAA0929 protein Mx2 interacting nuclear tar |
| 517D1 | 1510 | 1936 | NM_004252 | Hs.184276 | 1.00E-162 | 7 | solute carrier family 9 (sodium/hydrogen exch |
| 55E3 | 174 | 427 | NM_018370 | Hs.184465 | 1.00E-107 | 1 | hypothetical protein FLJ11259 (FLJ11259), mR |
| 50F9 | 2484 | 3108 | AB023182 | Hs.184523 | 0 | 1 | for KIAA0965 protein, partial cds /cds=(0 |
| 100A4 | 297 | 1941 | AK025730 | Hs.184542 | 1.00E-149 | 3 | FLJ22077 fis, clone HEP12728, highly sim |
| 113D4 | 950 | 1623 | NM_016061 | Hs.184542 | 0 | 1 | CGI-127 protein (LOC51646), mRNA /cds=(125,49 |
| 145D11 | 41 | 339 | BE730026 | Hs.184582 | 1.00E-111 | 1 | 601562642F1 cDNA, 5' end /clone=IMAGE:3832258 |
| 595F4 | 69 | 548 | NM_000986 | Hs.184582 | 0 | 1 | ribosomal protein L24 (RPL24), mRNA /cds=(39,5 |
| 108H10 | 250 | 701 | U00946 | Hs.184592 | 0 | 1 | clone A9A2BRB5 (CAC)n/(GTG)n repeat-containing mRN |
| 43B5 | 4399 | 4488 | AF104032 | Hs.184601 | 3.00E-24 | 1 | L-type amino acid transporter subunit LAT1 mRNA |
| 104F12 | 298 | 1713 | NM_014999 | Hs.184627 | 0 | 2 | KIAA0118 protein (KIAA0118), mRNA /cds=(255,9 |
| 122E8 | 513 | 995 | AF035307 | Hs.184697 | 0 | 2 | clone 23785 mRNA sequence /cds=UNKNOWN /gb=AF |
| 40H2 | 66 | 2605 | M37197 | Hs.184760 | 1.00E-177 | 4 | CCAAT-box-binding factor (CBF) mRNA, complete cds /c |
| 514E4 | 29 | 519 | NM_000984 | Hs.184776 | 0 | 3 | ribosomal protein L23a (RPL23A), mRNA /cds=(2 |
| 589A7 | 736 | 983 | AK025533 | Hs.184793 | 1.00E-138 | 1 | cDNA: FLJ21880 fis, clone HEP02743 /cds=UNKNOW |
| 142G5 | 1918 | 2157 | AL049782 | Hs.184938 | 8.00E-83 | 3 | Novel human gene mapping to chromosome 13 /cds=UNKNOWN /gb=A |
| 462G9 | 178 | 398 | AI085568 | Hs.185062 | 1.00E-76 | 1 | oy68b05.x1 cDNA, 3' end /clone=IMAGE:1670961 |
| 470C12 | 81 | 333 | T98171 | Hs.185675 | 1.00E-105 | 1 | ye56c12.s1 cDNA, 3' end /clone=IMAGE:121750 / |
| 463F2 | 3175 | 3359 | NM_014686 | Hs.186840 | 1.00E-72 | 1 | KIAA0355 gene product (KIAA0355), mRNA /cds=(|
| 461E4 | 907 | 1118 | NM_018519 | Hs.186874 | 4.00E-91 | 1 | hypothetical protein PRO2266 (PRO2266), mRNA |
| 155A1 | 53 | 379 | AI619574 | Hs.187362 | 1.00E-109 | 1 | ty50c09.x1 cDNA, 3' end /clone=IMAGE:2282512 |
| 461C9 | 2948 | 3458 | NM_014504 | Hs.187660 | 0 | 1 | putative Rab5 GDP/GTP exchange factor homologu |
| 470F2 | 5 | 331 | BE646499 | Hs.187872 | 1.00E-156 | 1 | 7e87h02.x1 cDNA, 3' end /clone=IMAGE:3292179 |
| 68D12 | 590 | 740 | AW963239 | Hs.187908 | 4.00E-66 | 1 | EST375312 /gb=AW963239 /gi=8153075 /ug= |
| 75H12 | 2012 | 2585 | AL110269 | Hs.187991 | 0 | 1 | cDNA DKFZp564A122 (from clone DKFZp564A1 |
| 167G4 | 1474 | 1958 | NM_015626 | Hs.187991 | 0 | 1 | DKFZP564A122 protein (DKFZP564A122), mRNA /c |
| 137G3 | 54 | 197 | AI625368 | Hs.188365 | 2.00E-34 | 46 | ts37c10.x1 cDNA, 3' end /clone=IMAGE:2230770 |
| 464C12 | 183 | 404 | AA432364 | Hs.188777 | 7.00E-94 | 1 | zw76a09.s1 cDNA, 3' end /clone=IMAGE:782104 / |
| 467E9 | 29 | 183 | AA576947 | Hs.188886 | 1.00E-63 | 1 | nm82b04.s1 cDNA, 3' end /clone=IMAGE:1074703 |
| 467B4 | 349 | 459 | AI392805 | Hs.189031 | 2.00E-49 | 1 | tg04h03.x1 cDNA, 3' end /clone=IMAGE:2107829 |
| 461E2 | 242 | 473 | BE674964 | Hs.190065 | 1.00E-109 | 1 | 7f11b09.x1 cDNA, 3' end /clone=IMAGE:3294329 |
| 466F4 | 58 | 295 | BG326781 | Hs.190219 | 1.00E-132 | 1 | 602425659F1 cDNA, 5' end /clone=IMAGE:4563471 |
| 465H4 | 111 | 558 | AA582958 | Hs.190229 | 0 | 1 | nn80d08.s1 cDNA, 3' end /clone=IMAGE:1090191 |
| 470F9 | 26 | 529 | AI763206 | Hs.190453 | 0 | 1 | wh95e09.x1 cDNA, 3' end /clone=IMAGE:2388520 |
| 66H12 | 1 | 3459 | D00099 | Hs.190703 | 0 | 5 | for Na,K-ATPase alpha-subunit, complete |
| 472E1 | 338 | 540 | AW294083 | Hs.190904 | 2.00E-46 | 1 | UI-H-BI2-ahg-b-05-0-UI.s1 cDNA, 3' end /clon |
| 522G10 | 433 | 970 | NM_003757 | Hs.192023 | 0 | 2 | eukaryotic translation initiation factor 3, |
| 54G8 | 29 | 410 | AW838827 | Hs.192123 | 0 | 1 | CM1-LT0059-280100-108-e02 /gb=AW838827 |
| 465G4 | 261 | 515 | BF224348 | Hs.192463 | 1.00E-104 | 1 | 7q86c05.x1 cDNA /clone=IMAGE /gb=BF224348 /g |
| 468F9 | 392 | 487 | AI524039 | Hs.192524 | 2.00E-36 | 1 | tg99h02.x1 cDNA, 3' end /clone=IMAGE:2116947 |
| 466C6 | 111 | 392 | AW972048 | Hs.192534 | 1.00E-153 | 1 | EST384032 cDNA /gb=AW972048 /gi=8161789 /ug= |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | |
|--------|-------|-------|-----------|---------------------|----|--|
| 184F12 | 1 | 677 | AF090927 | Hs.192705 0 | 1 | clone HQ0457 PRO0457 mRNA, complete cds /cds=(|
| 464C11 | 1 | 65 | BE298181 | Hs.192755 3.00E-23 | 1 | 601118566F1 cDNA, 5' end /clone=IMAGE:3028193 |
| 465H3 | 108 | 706 | BG036938 | Hs.192965 0 | 1 | 602287708F1 cDNA, 5' end /clone=IMAGE:4375153 |
| 169F9 | 4138 | 4890 | D87454 | Hs.192966 0 | 1 | KIAA0265 gene, partial cds /cds=(0,1205) /gb |
| 118H10 | 1104 | 1858 | AK024263 | Hs.193063 1.00E-132 | 2 | cDNA FLJ14201 fis, clone NT2RP3002955 /cds=UNK |
| 472F3 | 28 | 405 | BF062295 | Hs.193237 0 | 1 | 7k76b11.x1 cDNA, 3' end /clone=IMAGE:3481293 |
| 40A5 | 1933 | 2611 | X12830 | Hs.193400 0 | 1 | interleukin-6 (IL-6) receptor /cds=(437,184 |
| 63B5 | 327 | 582 | AW959162 | Hs.193669 1.00E-103 | 1 | EST371232 /gb=AW959162 /gi=8148846 /ug= |
| 52G10 | 803 | 1173 | M57627 | Hs.193717 0 | 1 | interleukin 10 (IL10) mRNA, complete cds /cds=(30,566 |
| 469F5 | 2088 | 2438 | AL110204 | Hs.193784 1.00E-179 | 1 | mRNA; cDNA DKFZp586K1922 (from clone DKFZp586K |
| 598H7 | 1428 | 1715 | NM_014828 | Hs.194035 1.00E-119 | 1 | KIAA0737 gene product (KIAA0737), mRNA /cds=(|
| 462B6 | 103 | 546 | BE618004 | Hs.194362 1.00E-165 | 1 | 601462354F1 cDNA, 5' end /clone=IMAGE:3865861 |
| 472F12 | 1177 | 1667 | AB036737 | Hs.194369 0 | 2 | mRNA for RERE, complete cds /cds=(636,5336) /g |
| 182E10 | 11785 | 13486 | U82828 | Hs.194382 0 | 5 | ataxia telangiectasia (ATM) gene, complete cd |
| 458F4 | 258 | 408 | NM_022739 | Hs.194477 2.00E-62 | 1 | E3 ubiquitin ligase SMURF2 (SMURF2), mRNA /cd |
| 583D2 | 1425 | 1732 | NM_014232 | Hs.194534 1.00E-136 | 1 | vesicle-associated membrane protein 2 (synapt |
| 38H8 | 1198 | 1620 | U89387 | Hs.194638 0 | 1 | RNA polymerase II subunit hRPB4 gene, complete cds / |
| 122H10 | 5292 | 5481 | NM_023005 | Hs.194688 4.00E-80 | 1 | bromodomain adjacent to zinc finger domain, 1B |
| 186G9 | 1 | 1908 | AL136945 | Hs.194718 0 | 2 | mRNA; cDNA DKFZp586O012 (from clone DKFZp586O0 |
| 113F3 | 1852 | 2375 | NM_000634 | Hs.194778 0 | 1 | interleukin 8 receptor, alpha (IL8RA), mRNA / |
| 106A3 | 35 | 404 | U11870 | Hs.194778 0 | 1 | interleukin-8 receptor type A (IL8RA) gene, promote |
| 473B8 | 1001 | 1314 | AF319438 | Hs.194976 1.00E-172 | 1 | SH2 domain-containing phosphatase anchor pro |
| 57F9 | 442 | 1934 | Y14039 | Hs.195175 0 | 27 | mRNA for CASH alpha protein /cds=(481,1923) /g |
| 49E5 | 2314 | 2512 | NM_018666 | Hs.195292 2.00E-37 | 1 | putative tumor antigen (SAGE), mRNA /cds=(167, |
| 473B10 | 406 | 532 | BE671815 | Hs.195374 1.00E-54 | 1 | 7a47c12.x1 cDNA, 3' end /clone=IMAGE:3221878 |
| 595B5 | 59 | 311 | AI653766 | Hs.195378 6.00E-46 | 1 | ty01b06.x1 cDNA, 3' end /clone=IMAGE:2277779 |
| 60G4 | 42 | 1554 | D13642 | Hs.195614 0 | 2 | KIAA0017 gene, complete cds /cds=(136,1335) |
| 473B9 | 739 | 927 | AF241534 | Hs.196015 2.00E-73 | 1 | hydattidiform mole associated and imprinted (H |
| 99C10 | 1075 | 1424 | NM_000294 | Hs.196177 1.00E-115 | 1 | phosphorylase kinase, gamma 2 (testis) (PHKG2 |
| 45H9 | 956 | 1405 | AF283645 | Hs.196270 0 | 1 | folate transporter/carrier mRNA, complete cd |
| 54F9 | 2567 | 2954 | U04636 | Hs.196384 0 | 1 | cyclooxygenase-2 (hCox-2) gene, complete cds /cds=(1 |
| 38F12 | 401 | 606 | AI984074 | Hs.196398 1.00E-104 | 1 | wz56c02.x1 cDNA, 3' end /clone=IMAGE:2562050 |
| 157G1 | 403 | 551 | AJ006835 | Hs.196769 7.00E-77 | 2 | RNA transcript from U17 small nucleolar RNA ho |
| 163F4 | 1 | 402 | AI650871 | Hs.197028 0 | 1 | wa95f03.x1 cDNA, 3' end /clone=IMAGE:2303933 |
| 160B3 | 408 | 476 | AI832038 | Hs.197091 5.00E-27 | 1 | wj99e02.x1 3' end /clone=IMAGE:2410970 |
| 105E8 | 1299 | 3674 | AB020657 | Hs.197298 0 | 6 | for KIAA0850 protein, complete cds /cds=(|
| 178G12 | 2097 | 3593 | AF205218 | Hs.197298 0 | 8 | NS1-binding protein-like protein mRNA, compl |
| 585F1 | 284 | 1711 | NM_001469 | Hs.197345 0 | 4 | thyroid autoantigen 70kD (Ku antigen) (G22P1) |
| 39C10 | 545 | 1984 | Z83840 | Hs.197345 0 | 2 | DNA sequence from clone CTA-216E10 on chromosome 22 C |
| 58E12 | 2162 | 3013 | NM_001530 | Hs.197540 0 | 2 | hypoxia-inducible factor 1, alpha subunit (ba |
| 125G11 | 3673 | 4059 | D29805 | Hs.198248 0 | 1 | mRNA for beta-1,4-galactosyltransferase, complete |
| 41H10 | 6 | 821 | M33906 | Hs.198253 1.00E-156 | 2 | MHC class II HLA-DQA1 mRNA, complete cds /cds=(43,810) |
| 186A11 | 551 | 1031 | NM_004544 | Hs.198271 0 | 2 | NADH dehydrogenase (ubiquinone) 1 alpha subco |
| 126D8 | 993 | 1381 | NM_021105 | Hs.198282 0 | 1 | phospholipid scramblase 1 (PLSCR1), mRNA /cds |
| 174C12 | 4824 | 5257 | NM_003070 | Hs.198296 0 | 1 | SWI/SNF related, matrix associated, actin dep |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|---|
| 109C6 | 128 | 833 | X04327 | Hs.198365 | 0 | 1 | erythrocyte 2,3-bisphosphoglycerate mutase mRNA EC |
| 64B12 | 4383 | 5289 | NM_000189 | Hs.198427 | 0 | 2 | hexokinase 2 (HK2), mRNA /cds=(1490,4243) /gb |
| 70B4 | 3267 | 5289 | Z46376 | Hs.198427 | 0 | 4 | HK2 mRNA for hexokinase II /cds=(1490,4243) /gb=Z |
| 478H6 | 186 | 475 | AI978581 | Hs.198694 | 1.00E-129 | 1 | wq72d08.x1 cDNA, 3' end /clone=IMAGE:2476815 |
| 587G1 | 767 | 1143 | NM_006837 | Hs.198767 | 1.00E-170 | 1 | COP9 (constitutive photomorphogenic, Arabido |
| 465F12 | 373 | 554 | BE621611 | Hs.198802 | 2.00E-77 | 1 | 601493754T1 cDNA, 3' end /clone=IMAGE:3895836 |
| 123B3 | 310 | 3608 | AB011108 | Hs.198891 | 0 | 3 | mRNA for KIAA0536 protein, partial cds /cds=(0, |
| 157H3 | 3457 | 5268 | D50929 | Hs.198899 | 0 | 2 | KIAA0139 gene, complete cds /cds=(128,4276) |
| 477H1 | 35 | 592 | NM_002229 | Hs.198951 | 0 | 1 | jun B proto-oncogene (JUNB), mRNA /cds=(253,12 |
| 53C5 | 979 | 1296 | X51345 | Hs.198951 | 1.00E-160 | 1 | jun-B mRNA for JUN-B protein /cds=(253,1296) /gb=X513 |
| 54H8 | 350 | 501 | AW450874 | Hs.199014 | 5.00E-81 | 1 | UI-H-BI3-all-a-11-0-UI.s1 cDNA, 3' end /clon |
| 520E12 | 3506 | 3878 | L04731 | Hs.199160 | 0 | 1 | translocation T(4:11) of ALL-1 gene to chromoso |
| 57F4 | 5941 | 6266 | NM_006267 | Hs.199179 | 1.00E-158 | 1 | RAN binding protein 2 (RANBP2), mRNA /cds=(127, |
| 50B10 | 5 | 3645 | D86984 | Hs.199243 | 0 | 2 | KIAA0231 gene, partial cds /cds=(0,1430) /gb |
| 68E12 | 1757 | 2052 | L25124 | Hs.199248 | 1.00E-156 | 2 | prostaglandin E2 receptor mRNA, complete cds / |
| 484H3 | 1879 | 1958 | NM_000958 | Hs.199248 | 3.00E-33 | 1 | prostaglandin E receptor 4 (subtype EP4) (PTGE |
| 466G6 | 368 | 3287 | NM_013233 | Hs.199263 | 0 | 2 | Ste-20 related kinase (SPAK), mRNA /cds=(173,1 |
| 464B9 | 633 | 1068 | AF015041 | Hs.199291 | 0 | 1 | NUMB-R protein (NUMB-R) mRNA, complete cds /c |
| 522F9 | 2 | 116 | AI669591 | Hs.200442 | 5.00E-59 | 1 | tw34b09.x1 cDNA, 3' end /clone=IMAGE:2261561 |
| 60F11 | 4945 | 5114 | AB040942 | Hs.201500 | 7.00E-92 | 1 | for KIAA1509 protein, partial cds /cds=(0 |
| 72D12 | 819 | 1293 | AF104398 | Hs.201673 | 0 | 1 | cornichon mRNA, complete cds /cds=(56,490) /g |
| 105G6 | 1629 | 2130 | AF091263 | Hs.201675 | 0 | 1 | RNA binding motif protein 5 (RBM5) mRNA, comple |
| 116G3 | 1637 | 2854 | NM_005778 | Hs.201675 | 0 | 2 | RNA binding motif protein 5 (RBM5), mRNA /cds=(|
| 40A10 | 254 | 431 | AI693179 | Hs.201789 | 5.00E-85 | 1 | wd68d12.x1 cDNA, 3' end /clone=IMAGE:2336759 |
| 473D4 | 421 | 547 | BE551203 | Hs.201792 | 3.00E-49 | 1 | 7b55h12.x1 cDNA, 3' end /clone=IMAGE:3232199 |
| 472D8 | 313 | 623 | AW390251 | Hs.202402 | 1.00E-123 | 1 | CM4-ST0182-051099-021-b06 cDNA /gb=AW390251 |
| 66H5 | 176 | 482 | AI271437 | Hs.203041 | 1.00E-173 | 1 | qj19c05.x1 cDNA, 3' end /clone=IMAGE:1856936 |
| 594C2 | 35 | 368 | AW131782 | Hs.203606 | 1.00E-147 | 2 | xf34e08.x1 cDNA, 3' end /clone=IMAGE:2619974 |
| 138B12 | 101 | 420 | AW194379 | Hs.203755 | 1.00E-93 | 3 | xm08h07.x1 3' end /clone=IMAGE:2683645 |
| 473D3 | 1 | 234 | AI538474 | Hs.203784 | 1.00E-117 | 1 | td06h08.x1 cDNA, 3' end /clone=IMAGE:2074911 |
| 471A5 | 113 | 442 | AI393908 | Hs.203829 | 1.00E-153 | 1 | tg05f10.x1 cDNA, 3' end /clone=IMAGE:2107915 |
| 40A4 | 1621 | 2037 | AF004230 | Hs.204040 | 0 | 1 | monocyte/macrophage lg-related receptor MIR |
| 463H1 | 7 | 319 | AW977671 | Hs.204214 | 1.00E-161 | 1 | EST389900 cDNA /gb=AW977671 /gi=8169049 /ug= |
| 478E7 | 25 | 434 | AI762023 | Hs.204610 | 0 | 2 | wh89f04.x1 cDNA, 3' end /clone=IMAGE:2387935 |
| 55E11 | 324 | 469 | AI741246 | Hs.204656 | 1.00E-58 | 12 | wg26g09.x1 cDNA, 3' end /clone=IMAGE:2366272 |
| 478G10 | 345 | 476 | AI760901 | Hs.204703 | 9.00E-34 | 1 | wi09h06.x1 cDNA, 3' end /clone=IMAGE:2389787 |
| 470E11 | 374 | 507 | AI762741 | Hs.204707 | 2.00E-49 | 1 | wh93h02.x1 cDNA, 3' end /clone=IMAGE:2388339 |
| 478F5 | 179 | 437 | AI086035 | Hs.204873 | 1.00E-110 | 1 | oy70h04.x1 cDNA, 3' end /clone=IMAGE:1671223 |
| 464G4 | 33 | 320 | AI749444 | Hs.204929 | 5.00E-50 | 1 | at24c03.x1 cDNA, 3' end /clone=IMAGE:2356036 |
| 472D2 | 88 | 198 | AI760018 | Hs.205071 | 4.00E-54 | 1 | wh83b02.x1 cDNA, 3' end /clone=IMAGE:2387307 |
| 470D9 | 5 | 422 | AW976641 | Hs.205079 | 0 | 1 | EST388750 cDNA /gb=AW976641 /gi=8167872 /ug= |
| 470D4 | 122 | 500 | AA885473 | Hs.205175 | 0 | 1 | am10c12.s1 cDNA, 3' end /clone=IMAGE:1466422 |
| 473C5 | 285 | 525 | BF679831 | Hs.205319 | 2.00E-96 | 1 | 602154415F1 cDNA, 5' end /clone=IMAGE:4295595 |
| 470E7 | 295 | 521 | AI762557 | Hs.205327 | 9.00E-95 | 2 | wh92f07.x1 cDNA, 3' end /clone=IMAGE:2388229 |
| 478F11 | 11 | 447 | AI761141 | Hs.205452 | 0 | 3 | wh97g08.x1 cDNA, 3' end /clone=IMAGE:2388734 |
| 459A12 | 111 | 323 | N72600 | Hs.205555 | 9.00E-96 | 1 | za46f08.s1 cDNA, 3' end /clone=IMAGE:295623 / |
| 470F4 | 214 | 481 | AW977820 | Hs.205675 | 1.00E-131 | 1 | EST389824 cDNA /gb=AW977820 /gi=8168971 /ug= |
| 102G3 | 1 | 249 | BF680988 | Hs.205696 | 2.00E-78 | 1 | 602156272F1 cDNA, 5' end /clone=IMAGE:4297216 |
| 472B2 | 312 | 700 | BF794256 | Hs.206761 | 0 | 1 | 602255454F1 cDNA, 5' end /clone=IMAGE:4338949 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|--|
| 470C1 | 1113 | 1643 | AK024118 | Hs.206868 | 0 | 1 | cDNA FLJ14056 fis, clone HEMBB1000335 /cds=UNK |
| 469H7 | 1076 | 1215 | U15177 | Hs.206984 | 3.00E-69 | 1 | cosmid CRI-JC2015 at D10S289 in 10sp13 /cds=(0,1214) |
| 61F9 | 5 | 181 | AW340421 | Hs.207995 | 4.00E-94 | 1 | hc96h02.x1 cDNA, 3' end /clone=IMAGE:2907891 |
| 473C2 | 239 | 551 | BF439675 | Hs.208854 | 1.00E-151 | 1 | nab69e11.x1 cDNA /clone=IMAGE /gb=BF439675 / |
| 62G11 | 159 | 292 | BE781611 | Hs.208985 | 1.00E-60 | 1 | 601467463F1 cDNA, 5' end /clone=IMAGE:3870902 |
| 472E2 | 258 | 554 | AI343473 | Hs.209203 | 1.00E-135 | 1 | tb97a08.x1 cDNA, 3' end /clone=IMAGE:2062262 |
| 471C10 | 148 | 498 | AI768880 | Hs.209511 | 0 | 1 | wh71e04.x1 cDNA, 3' end /clone=IMAGE:2386206 |
| 470G9 | 416 | 561 | AI798144 | Hs.209609 | 4.00E-63 | 1 | wh81g12.x1 cDNA, 3' end /clone=IMAGE:2387206 |
| 478C10 | 120 | 447 | AI809310 | Hs.210385 | 1.00E-158 | 2 | wh75h08.x1 cDNA, 3' end /clone=IMAGE:2386623 |
| 476B7 | 64 | 341 | AI075288 | Hs.210727 | 1.00E-151 | 2 | oy69h10.x1 cDNA, 3' end /clone=IMAGE:1671139 |
| 477G4 | 915 | 1541 | AB040919 | Hs.210958 | 0 | 1 | mRNA for KIAA1486 protein, partial cds /cds=(1 |
| 468C2 | 215 | 498 | AI832182 | Hs.210995 | 1.00E-145 | 1 | td13h11.x1 cDNA, 3' end /clone=IMAGE:2075589 |
| 472D11 | 1 | 300 | AI860120 | Hs.211024 | 1.00E-126 | 1 | wh39e01.x1 cDNA, 3' end /clone=IMAGE:2383128 |
| 470D3 | 30 | 317 | AW362304 | Hs.211194 | 1.00E-137 | 1 | CM3-CT0275-031199-031-a08 cDNA /gb=AW362304 |
| 179F6 | 105 | 551 | AI823649 | Hs.211535 | 0 | 1 | wi85g03.x1 3' end /clone=IMAGE:2400148 |
| 477G12 | 2439 | 4050 | NM_020993 | Hs.211563 | 0 | 4 | B-cell CLL/lymphoma 7A (BCL7A), mRNA /cds=(953 |
| 39A11 | 5178 | 5792 | L10717 | Hs.211576 | 0 | 2 | T cell-specific tyrosine kinase mRNA, complete |
| 187B9 | 5365 | 5790 | NM_005546 | Hs.211576 | 0 | 1 | IL2-inducible T-cell kinase (ITK), mRNA /cds= |
| 152C2 | 3965 | 4297 | Z22551 | Hs.211577 | 1.00E-174 | 1 | kinectin gene /cds=(69,4139) /gb=Z22551 /gi=296 |
| 120A2 | 2556 | 2917 | NM_005955 | Hs.211581 | 0 | 1 | metal-regulatory transcription factor 1 (MTF |
| 147A2 | 2915 | 4407 | M59465 | Hs.211600 | 0 | 6 | tumor necrosis factor alpha inducible protein A20 mRNA |
| 583B12 | 2404 | 3981 | NM_006290 | Hs.211600 | 0 | 11 | tumor necrosis factor, alpha-induced protein |
| 589F3 | 1905 | 2274 | AF090693 | Hs.211610 | 0 | 1 | apoptosis-related RNA binding protein (NAPOR- |
| 470G11 | 277 | 462 | AI862623 | Hs.211744 | 5.00E-99 | 1 | wh99h10.x1 cDNA, 3' end /clone=IMAGE:2388931 |
| 473F2 | 195 | 423 | BE675092 | Hs.211828 | 2.00E-95 | 1 | 7f02d07.x1 cDNA, 3' end /clone=IMAGE:3293485 |
| 517D2 | 1059 | 1366 | BC000747 | Hs.211973 | 1.00E-162 | 2 | Similar to homolog of Yeast RRP4 (ribosomal RN |
| 109D9 | 391 | 533 | AI922921 | Hs.212553 | 2.00E-68 | 1 | wn81c05.x1 cDNA, 3' end /clone=IMAGE:2452232 |
| 494H12 | 172 | 549 | AI912585 | Hs.213385 | 0 | 3 | we11d07.x1 cDNA, 3' end /clone=IMAGE:2340781 |
| 596G11 | 4740 | 5687 | AB007916 | Hs.214646 | 0 | 8 | mRNA for KIAA0447 protein, partial cds /cds=(2 |
| 104C12 | 843 | 1787 | AL031282 | Hs.215595 | 0 | 2 | DNA sequence from clone 283E3 on chromosome 1p36.21-36 |
| 124F8 | 1391 | 2913 | NM_002074 | Hs.215595 | 0 | 4 | guanine nucleotide binding protein (G protein) |
| 157E8 | 1264 | 1627 | AK001548 | Hs.215766 | 0 | 4 | FLJ10686 fis, clone NT2RP3000252, highly |
| 519G3 | 1729 | 2094 | NM_012341 | Hs.215766 | 0 | 1 | GTP-binding protein (NGB), mRNA /cds=(23,1924 |
| 473E7 | 2278 | 2472 | AB022663 | Hs.215857 | 3.00E-52 | 1 | HFB30 mRNA, complete cds /cds=(236,1660) /gb= |
| 104F7 | 4 | 1324 | D00017 | Hs.217493 | 0 | 3 | for lipocortin II, complete cds /cds=(49,1 |
| 58G2 | 11 | 1324 | NM_004039 | Hs.217493 | 0 | 7 | annexin A2 (ANXA2), mRNA /cds=(49,1068) /gb=N |
| 467D4 | 27 | 443 | AI392814 | Hs.221014 | 1.00E-180 | 1 | tg10a02.x1 cDNA, 3' end /clone=IMAGE:2108330 |
| 463B1 | 69 | 457 | AV686223 | Hs.221642 | 0 | 1 | AV686223 cDNA, 5' end /clone=GKCGXH11 /clone_ |
| 464D10 | 295 | 552 | BF058398 | Hs.221695 | 1.00E-115 | 1 | 7k30d01.x1 cDNA, 3' end /clone=IMAGE:3476785 |
| 466C12 | 1 | 427 | AI540165 | Hs.222186 | 0 | 1 | td10d05.x1 cDNA, 3' end /clone=IMAGE:2075241 |
| 125H10 | 2596 | 2917 | AB046830 | Hs.222746 | 0 | 1 | mRNA for KIAA1610 protein, partial cds /cds=(0 |
| 473C4 | 1 | 193 | BF435098 | Hs.222833 | 9.00E-72 | 1 | 7p05g01.x1 cDNA, 3' end /clone=IMAGE:3645097 |
| 37B4 | 18 | 371 | AW389509 | Hs.223747 | 1.00E-147 | 1 | CM3-ST0163-051099-019-b11 /gb=AW389509 |
| 470H7 | 106 | 357 | AI766706 | Hs.223935 | 1.00E-116 | 1 | wi02g11.x1 cDNA, 3' end /clone=IMAGE:2389124 |
| 472D12 | 1 | 370 | AL133721 | Hs.224680 | 0 | 1 | DKFZp761H09121_r1 cDNA, 5' end /clone=DKFZp76 |
| 124E4 | 53 | 208 | AI874107 | Hs.224760 | 7.00E-50 | 3 | wm49b01.x1 cDNA, 3' end /clone=IMAGE:2439241 |
| 477G3 | 146 | 412 | AI400714 | Hs.225567 | 1.00E-141 | 1 | tg93g12.x1 cDNA, 3' end /clone=IMAGE:2116390 |
| 112F12 | 2313 | 2799 | AL163279 | Hs.225674 | 0 | 1 | chromosome 21 segment HS21C079 /cds=(0,6888) |
| 118D12 | 6187 | 6775 | NM_015384 | Hs.225767 | 0 | 1 | IDN3 protein (IDN3), mRNA /cds=(706,7182) /gb |
| 109B7 | 2208 | 3315 | AF119417 | Hs.225939 | 0 | 2 | nonfunctional GM3 synthase mRNA, alternative |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|--|
| 125A8 | 2877 | 3381 | NM_006999 | Hs.225951 | 0 | 1 | topoisomerase-related function protein 4-1 |
| 129C8 | 5510 | 5893 | AF012108 | Hs.225977 | 0 | 1 | Amplified in Breast Cancer (AIB1) mRNA, comple |
| 39G12 | 4498 | 4859 | NM_014977 | Hs.227133 | 1.00E-93 | 2 | KIAA0670 protein/acinus (KIAA0670), mRNA /cd |
| 153D10 | 1 | 286 | AF000145 | Hs.227400 | 1.00E-139 | 2 | germinal center kinase related protein kinase |
| 464B12 | 901 | 1425 | AL050131 | Hs.227429 | 0 | 1 | mRNA; cDNA DKFZp5861111 (from clone DKFZp58611 |
| 459D9 | 3828 | 4314 | NM_004841 | Hs.227806 | 0 | 1 | ras GTPase activating protein-like (NGAP), mR |
| 135E9 | 135 | 773 | NM_004049 | Hs.227817 | 0 | 1 | BCL2-related protein A1 (BCL2A1), mRNA /cds=(|
| 59F10 | 123 | 808 | Y09397 | Hs.227817 | 0 | 12 | GRS protein /cds=(102,629) /gb=Y09397 / |
| 516H4 | 1901 | 2462 | NM_014287 | Hs.227823 | 0 | 1 | pM5 protein (PM5), mRNA /cds=(0,3668) /gb=NM_0 |
| 107C12 | 2776 | 3390 | Y15906 | Hs.227913 | 0 | 1 | for XAGL protein /cds=(132,1646) /gb=Y159 |
| 152C7 | 171 | 1390 | AF052155 | Hs.227949 | 0 | 2 | clone 24761 mRNA sequence /cds=UNKNOWN /gb=AF |
| 522G8 | 108 | 293 | AI917348 | Hs.228486 | 2.00E-70 | 1 | ts83d10.x1 cDNA, 3' end /clone=IMAGE:2237875 |
| 66C7 | 304 | 445 | AI094726 | Hs.228795 | 1.00E-26 | 1 | qa08f05.x1 cDNA, 3' end /clone=IMAGE:1686177 |
| 585D1 | 51 | 294 | AI199388 | Hs.228817 | 5.00E-73 | 1 | qs75e05.x1 cDNA, 3' end /clone=IMAGE:1943936 |
| 468E9 | 113 | 324 | AI523873 | Hs.228926 | 7.00E-77 | 2 | tg97c12.x1 cDNA, 3' end /clone=IMAGE:2116726 |
| 466F1 | 44 | 139 | AI380491 | Hs.229374 | 3.00E-39 | 2 | tf95b10.x1 cDNA, 3' end /clone=IMAGE:2107003 |
| 182F1 | 40 | 465 | AI354231 | Hs.229385 | 1.00E-138 | 4 | qv12c04.x1 cDNA, 3' end /clone=IMAGE:1981350 |
| 465C1 | 237 | 316 | AW812896 | Hs.229868 | 3.00E-38 | 1 | RC3-ST0186-250200-018-a11 cDNA /gb=AW812896 |
| 178H7 | 42 | 353 | AI581732 | Hs.229918 | 1.00E-68 | 5 | ar74f03.x1 cDNA, 3' end /clone=IMAGE:2128349 |
| 72H6 | 48 | 534 | AI818777 | Hs.229990 | 1.00E-85 | 3 | w11f10.x1 cDNA, 3' end /clone=IMAGE:2424619 |
| 181E9 | 52 | 279 | AI827451 | Hs.229993 | 1.00E-66 | 1 | w17d11.x1 cDNA, 3' end /clone=IMAGE:2425173 |
| 38H1 | 225 | 311 | AI579979 | Hs.230430 | 1.00E-25 | 1 | tq45a01.x1 cDNA, 3' end /clone=IMAGE:2211720 |
| 489G11 | 66 | 369 | AI818596 | Hs.230492 | 1.00E-112 | 5 | wk74d04.x1 cDNA, 3' end /clone=IMAGE:2421127 |
| 118D6 | 40 | 161 | AI025427 | Hs.230752 | 6.00E-37 | 1 | ow27g06.s1 cDNA, 3' end /clone=IMAGE:1648090 |
| 462H6 | 305 | 437 | AI087055 | Hs.230805 | 3.00E-67 | 1 | oy70c09.x1 cDNA, 3' end /clone=IMAGE:1671184 |
| 107C11 | 93 | 240 | AI796419 | Hs.230939 | 1.00E-40 | 1 | wj17f02.x1 cDNA, 3' end /clone=IMAGE:2403099 |
| 591A1 | 65 | 316 | AA767883 | Hs.231154 | 7.00E-59 | 4 | oa30h07.s1 cDNA, 3' end /clone=IMAGE:1306525 |
| 471B3 | 177 | 519 | BE407125 | Hs.231510 | 1.00E-166 | 1 | 601301818F1 cDNA, 5' end /clone=IMAGE:3636412 |
| 64G11 | 609 | 950 | AL542592 | Hs.231816 | 1.00E-166 | 1 | AL542592 cDNA /clone=CS0DE012YA05-(5-prime) |
| 108G1 | 1 | 210 | AW006867 | Hs.231987 | 1.00E-109 | 1 | ws15d07.x1 cDNA, 3' end /clone=IMAGE:2497261 |
| 115F3 | 44 | 185 | AW016002 | Hs.232000 | 7.00E-75 | 2 | UI-H-BI0p-abh-h-06-0-UI.s1 cDNA, 3' end /clo |
| 138A6 | 4771 | 5194 | D15050 | Hs.232068 | 0 | 1 | transcription factor AREB6, complete cds /cd |
| 472A6 | 311 | 497 | BF195579 | Hs.232257 | 1.00E-78 | 1 | 7n85c03.x1 cDNA, 3' end /clone=IMAGE:3571205 |
| 111A7 | 285 | 463 | AW026667 | Hs.233261 | 1.00E-41 | 1 | ww15d09.x1 cDNA, 3' end /clone=IMAGE:2529617 |
| 67G8 | 292 | 560 | BE719483 | Hs.233383 | 4.00E-94 | 3 | MR1-HT0858-020800-001-c06 /gb=BE719483 |
| 123B11 | 180 | 351 | AW006045 | Hs.233560 | 5.00E-82 | 1 | wz81b09.x1 cDNA, 3' end /clone=IMAGE:2565209 |
| 472E3 | 1 | 319 | AW027530 | Hs.233564 | 1.00E-180 | 1 | ww74c06.x1 cDNA, 3' end /clone=IMAGE:2535274 |
| 36F11 | 943 | 1896 | Z85996 | Hs.233750 | 0 | 6 | DNA sequence from PAC 431A14 on chromosome 6p21. Conta |
| 184G6 | 49 | 491 | BF694761 | Hs.233936 | 0 | 9 | 602080851F2 cDNA, 5' end /clone=IMAGE:4245133 |
| 599C7 | 12 | 540 | NM_006471 | Hs.233936 | 0 | 55 | myosin, light polypeptide, regulatory, non-s |
| 156B4 | 405 | 774 | AF054185 | Hs.233952 | 1.00E-164 | 1 | proteasome subunit HSPC complete cds /c |
| 595G5 | 85 | 315 | NM_002792 | Hs.233952 | 1.00E-126 | 1 | proteasome (prosome, macropain) subunit, alp |
| 67F5 | 108 | 556 | AK000654 | Hs.234149 | 0 | 1 | FLJ20647 fis, clone KAT02147 /cds=(90,836 |
| 591B6 | 1 | 555 | NM_017918 | Hs.234149 | 0 | 6 | hypothetical protein FLJ20647 (FLJ20647), mR |
| 111B7 | 1887 | 2217 | AK023204 | Hs.234265 | 1.00E-120 | 1 | cDNA FLJ13142 fis, clone NT2RP3003212, modera |
| 72F6 | 314 | 2581 | AL035071 | Hs.234279 | 0 | 2 | DNA sequence from clone 1085F17 on chromosome 20q11.1 |
| 514H4 | 2105 | 2523 | NM_012325 | Hs.234279 | 0 | 1 | microtubule-associated protein, RP/EB family |
| 599A10 | 1 | 1163 | NM_002300 | Hs.234489 | 0 | 30 | lactate dehydrogenase B (LDHB), mRNA /cds=(84 |
| 163A8 | 470 | 1153 | X13794 | Hs.234489 | 0 | 4 | lactate dehydrogenase B gene exon 1 and (EC 1.1.1. |
| 125E5 | 31 | 465 | NM_000978 | Hs.234518 | 1.00E-117 | 2 | ribosomal protein L23 (RPL23), mRNA /cds=(25,4 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | |
|--------|------|------|-----------|---------------------|----|---|
| 471B1 | 1499 | 2033 | L05148 | Hs.234569 0 | 1 | protein tyrosine kinase related mRNA sequence /cds=UN |
| 466D7 | 1050 | 1402 | NM_013451 | Hs.234680 0 | 1 | fer-1 (C.elegans)-like 3 (myoferlin) (FER1L3) |
| 108B11 | 407 | 742 | X14008 | Hs.234734 0 | 1 | lysozyme gene (EC 3.2.1.17) /cds=(82,474) /gb=X14008 |
| 476A12 | 3 | 440 | AI076222 | Hs.235042 0 | 2 | oy65b09.x1 cDNA, 3' end /clone=IMAGE:1670681 |
| 464H7 | 994 | 2425 | AL157426 | Hs.235390 1.00E-22 | 1 | mRNA; cDNA DKFZp761B101 (from clone DKFZp761B1 |
| 472F2 | 2203 | 2431 | AK024137 | Hs.235498 7.00E-97 | 1 | cDNA FLJ14075 fis, clone HEMBB1001905, weakly |
| 63C7 | 1159 | 1751 | AK000260 | Hs.235712 0 | 1 | FLJ20253 fis, clone COLF6895 /cds=UNKNOWN |
| 73C8 | 39 | 485 | AI379474 | Hs.235823 0 | 1 | tc57g08.x1 cDNA, 3' end /clone=IMAGE:2068766 |
| 590H8 | 182 | 449 | AA020845 | Hs.235883 1.00E-145 | 3 | ze64a07.r1 cDNA, 5' end /clone=IMAGE:363732 / |
| 182H3 | 468 | 2009 | NM_001535 | Hs.235887 1.00E-119 | 5 | HMT1 (hnRNP methyltransferase, S. cerevisiae) |
| 119B12 | 253 | 596 | NM_003075 | Hs.236030 0 | 1 | SWI/SNF related, matrix associated, actin dep |
| 461C5 | 654 | 1112 | AK026410 | Hs.236449 0 | 1 | cDNA: FLJ22757 fis, clone KAlA0803 /cds=(92,24 |
| 182G3 | 514 | 2817 | AK023223 | Hs.236494 0 | 2 | FLJ13161 fis, clone NT2RP3003589, highly |
| 469G7 | 857 | 1336 | AK026359 | Hs.236744 0 | 1 | cDNA: FLJ22706 fis, clone HSI13163 /cds=UNKNOW |
| 592A9 | 1522 | 1888 | NM_020135 | Hs.236828 0 | 1 | putative helicase RUVBL (LOC56897), mRNA /cds |
| 177A1 | 1260 | 1704 | AK001514 | Hs.236844 1.00E-170 | 1 | FLJ10652 fis, clone NT2RP2005886 /cds=(50 |
| 594G2 | 916 | 1537 | NM_018169 | Hs.236844 0 | 2 | hypothetical protein FLJ10652 (FLJ10652), mR |
| 98D10 | 1881 | 1964 | NM_006947 | Hs.237825 9.00E-36 | 1 | signal recognition particle 72kD (SRP72), mRN |
| 72C7 | 36 | 1214 | M29696 | Hs.237868 0 | 2 | interleukin-7 receptor (IL-7) mRNA, complete cds /cd |
| 591B10 | 577 | 1658 | NM_002185 | Hs.237868 0 | 9 | interleukin 7 receptor (IL7R), mRNA /cds=(22,1 |
| 109G2 | 16 | 405 | AF116682 | Hs.238205 0 | 1 | PRO2013 mRNA, complete cds /cds=(135,380) /gb |
| 41E1 | 2163 | 2733 | U60805 | Hs.238648 0 | 1 | oncostatin-M specific receptor beta subunit (OSMRB) |
| 599C11 | 508 | 1734 | AK026110 | Hs.238707 0 | 5 | cDNA: FLJ22457 fis, clone HRC09925 /cds=(56,14 |
| 143E8 | 2 | 595 | AV700542 | Hs.238730 1.00E-177 | 6 | AV700542 cDNA, 3' end /clone=GKCAFD05 /clone_ |
| 596C11 | 77 | 658 | AW955090 | Hs.238954 0 | 5 | EST367160 cDNA /gb=AW955090 /gi=8144773 /ug= |
| 169C7 | 1371 | 1634 | AY004255 | Hs.238990 1.00E-148 | 1 | cdk inhibitor p27KIP1 mRNA, complete cds /cds= |
| 173C1 | 1599 | 1859 | BC001971 | Hs.238990 1.00E-146 | 1 | Similar to cyclin-dependent kinase inhibitor |
| 458B5 | 1539 | 1809 | AL136828 | Hs.238996 1.00E-131 | 1 | mRNA; cDNA DKFZp434K0427 (from clone DKFZp434K |
| 591H9 | 6104 | 6559 | AL157902 | Hs.239114 0 | 1 | DNA sequence from clone RP4-675C20 on chromosome 1p13 |
| 512G4 | 231 | 2376 | NM_005746 | Hs.239138 0 | 61 | pre-B-cell colony-enhancing factor (PBEF), m |
| 53D11 | 935 | 2053 | U02020 | Hs.239138 0 | 15 | pre-B cell enhancing factor (PBEF) mRNA, complete cds |
| 38B7 | 2187 | 2263 | AK025021 | Hs.239189 1.00E-36 | 1 | FLJ21368 fis, clone COL03056, highly sim |
| 458E10 | 90 | 622 | NM_016533 | Hs.239208 0 | 1 | ninjurin 2 (NINJ2), mRNA /cds=(56,484) /gb=NM |
| 184G10 | 1608 | 2056 | AK026535 | Hs.239307 0 | 1 | FLJ22882 fis, clone KAT03587, highly sim |
| 194D9 | 1544 | 1683 | NM_003680 | Hs.239307 4.00E-57 | 1 | tyrosyl-tRNA synthetase (YARS), mRNA /cds=(0, |
| 110C7 | 450 | 1216 | AF246221 | Hs.239625 0 | 4 | transmembrane protein BRI mRNA, complete cds |
| 599G9 | 446 | 1205 | NM_021999 | Hs.239625 0 | 13 | integral membrane protein 2B (ITM2B), mRNA /cd |
| 515E4 | 1404 | 1671 | NM_014515 | Hs.239720 1.00E-132 | 1 | CCR4-NOT transcription complex, subunit 2 (C |
| 115H10 | 1124 | 2079 | BC000105 | Hs.239760 0 | 2 | Similar to CG14740 gene product, clone MGC:25 |
| 466E3 | 605 | 923 | NM_005301 | Hs.239891 1.00E-164 | 2 | G protein-coupled receptor 35 (GPR35), mRNA / |
| 52B5 | 993 | 1243 | AJ223075 | Hs.239894 1.00E-106 | 1 | for TRIP protein /cds=(178,2532) /gb=AJ22 |
| 171E10 | 88 | 399 | AW002624 | Hs.240077 1.00E-145 | 1 | wu60d10.x1 cDNA, 3' end /clone=IMAGE:990854 / |
| 75C5 | 325 | 1604 | AK027191 | Hs.240443 0 | 8 | FLJ23538 fis, clone LNG08010, highly sim |
| 597D3 | 1134 | 1792 | BC001255 | Hs.240770 0 | 1 | nuclear cap binding protein subunit 2, 20kD, |
| 98A11 | 596 | 6834 | NM_005385 | Hs.241493 0 | 10 | natural killer-tumor recognition sequence (N |
| 98C10 | 1580 | 2204 | AK027187 | Hs.241507 0 | 40 | cDNA: FLJ23534 fis, clone LNG06974, highly sim |
| 463E8 | 324 | 846 | AF047002 | Hs.241520 0 | 1 | transcriptional coactivator ALY mRNA, partia |
| 514G6 | 802 | 1238 | NM_012392 | Hs.241531 0 | 3 | peflin (PEF), mRNA /cds=(12,866) /gb=NM_01239 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | |
|--------|------|------|-----------|---------------------|---|---|
| 177G4 | 1375 | 1887 | AF099149 | Hs.241558 0 | 1 | TRIAD1 type I mRNA, complete cds /cds=(144,1625 |
| 110E4 | 1320 | 1937 | AK021704 | Hs.241567 0 | 1 | FLJ11642 fis, clone HEMBA1004356, highly |
| 513B12 | 700 | 1447 | NM_016839 | Hs.241567 0 | 3 | RNA binding motif, single stranded interacting |
| 500G10 | 910 | 1249 | NM_000594 | Hs.241570 0 | 1 | tumor necrosis factor (TNF superfamily, membe |
| 514B6 | 735 | 1032 | NM_018630 | Hs.241576 1.00E-155 | 1 | hypothetical protein PRO2577 (PRO2577), mRNA |
| 590H9 | 61 | 251 | NM_016200 | Hs.241578 1.00E-104 | 1 | U6 snRNA-associated Sm-like protein LSm8 (LOC |
| 50A6 | 200 | 311 | AK026704 | Hs.242868 3.00E-57 | 3 | FLJ23051 fis, clone LNG02642 /cds=UNKNOWN |
| 104C10 | 199 | 353 | AA424812 | Hs.243029 2.00E-74 | 1 | zw04b02.s1 cDNA, 3' end /clone=IMAGE:768267 / |
| 72G4 | 182 | 415 | AW081232 | Hs.243321 1.00E-99 | 4 | xc22e08.x1 cDNA, 3' end /clone=IMAGE:2585030 |
| 521D12 | 32 | 287 | AW102836 | Hs.243457 6.00E-96 | 1 | xd38h12.x1 cDNA, 3' end /clone=IMAGE:2596103 |
| 102F3 | 79 | 157 | W45562 | Hs.243720 4.00E-26 | 1 | zc26e07.s1 cDNA, 3' end /clone=IMAGE:323460 / |
| 56D6 | 193 | 454 | M97856 | Hs.243886 1.00E-122 | 1 | histone-binding protein mRNA, complete cds /c |
| 595D8 | 25 | 495 | NM_002482 | Hs.243886 0 | 1 | nuclear autoantigenic sperm protein (histone- |
| 46G5 | 2137 | 2661 | AK000745 | Hs.243901 0 | 1 | cDNA FLJ20738 fis, clone HEP08257 |
| | | | | | | /cds=UNKNOWN |
| 477D4 | 141 | 250 | AI394001 | Hs.244666 4.00E-51 | 1 | tg06d04.x1 cDNA, 3' end /clone=IMAGE:2107975 |
| 139B7 | 50 | 235 | AW078847 | Hs.244816 4.00E-32 | 2 | xb18g07.x1 cDNA, 3' end /clone=IMAGE:2576700 |
| 472C4 | 74 | 464 | AW139918 | Hs.245138 0 | 1 | UI-H-BI1-ae-d-05-0-UI.s1 cDNA, 3' end /clon |
| 459F7 | 45 | 229 | AW080951 | Hs.245616 7.00E-58 | 1 | xc28c10.x1 cDNA, 3' end /clone=IMAGE:2585586 |
| 100A6 | 41 | 1795 | L22009 | Hs.245710 1.00E-143 | 3 | hnRNP H mRNA, complete cds /cds=(72,1421) |
| | | | | | | /gb=L22009 |
| 592G8 | 41 | 1798 | NM_005520 | Hs.245710 0 | 6 | heterogeneous nuclear ribonucleoprotein H1 |
| 71G4 | 382 | 583 | AL136607 | Hs.245798 1.00E-104 | 1 | mRNA; cDNA DKFZp564I0422 (from clone DKFZp564 |
| 118B9 | 4495 | 5528 | AK024391 | Hs.246112 0 | 4 | cDNA FLJ14329 fis, clone PLACE4000259, highly |
| 471E5 | 148 | 464 | AI568725 | Hs.246299 1.00E-177 | 1 | th15a01.x1 cDNA, 3' end /clone=IMAGE:2118312 |
| 464D11 | 26 | 526 | N28843 | Hs.246358 0 | 1 | yx59d10.r1 cDNA, 5' end /clone=IMAGE:266035 / |
| 40H7 | 550 | 1108 | S57235 | Hs.246381 0 | 1 | CD68=110kda transmembrane glycoprotein [human, |
| | | | | | | promonocy |
| 471E12 | 152 | 507 | AW117189 | Hs.246494 1.00E-149 | 1 | xd83f08.x1 cDNA, 3' end /clone=IMAGE:2604231 |
| 479C1 | 47 | 345 | AV739961 | Hs.246796 1.00E-140 | 1 | AV739961 cDNA, 5' end /clone=CBFBRA10 /clone_ |
| 472C9 | 43 | 400 | BF796642 | Hs.246818 0 | 1 | 602259846F1 cDNA, 5' end /clone=IMAGE:4343171 |
| 47F11 | 2 | 227 | AB015856 | Hs.247433 1.00E-123 | 1 | for ATF6, complete cds /cds=(68,2080) /gb |
| 179H9 | 12 | 379 | AL031313 | Hs.247783 1.00E-111 | 1 | DNA sequence from clone 581F12 on chromosome |
| | | | | | | Xq21. Co |
| 167A9 | 5 | 352 | Z00013 | Hs.247792 1.00E-163 | 5 | H.sapiens germline gene for the leader peptide and |
| | | | | | | variable |
| 72B8 | 402 | 672 | L15006 | Hs.247824 1.00E-139 | 2 | Ig superfamily CTLA-4 mRNA, complete cds /cds= |
| 488H10 | 135 | 672 | NM_005214 | Hs.247824 1.00E-146 | 5 | cytotoxic T-lymphocyte-associated protein 4 |
| 188G8 | 1 | 255 | NM_002991 | Hs.247838 1.00E-135 | 1 | small inducible cytokine subfamily A (Cys-Cys |
| 153D11 | 401 | 720 | AL049545 | Hs.247877 1.00E-133 | 2 | DNA sequence from clone 263J7 on chromosome |
| | | | | | | 6q14.3-15 |
| 44D2 | 42 | 448 | AL035604 | Hs.247894 1.00E-133 | 1 | DNA sequence from clone 38C16 on chromosome |
| | | | | | | 6q22.33-2 |
| 180B7 | 10 | 271 | L21961 | Hs.247947 4.00E-72 | 1 | Ig rearranged lambda-chain mRNA, subgroup VL3, V- |
| | | | | | | J re |
| 110B11 | 311 | 803 | U08626 | Hs.247984 0 | 1 | glutamine synthetase pseudogene /cds=(0,899) /gb=U |
| 74G5 | 361 | 965 | X14798 | Hs.248109 0 | 1 | DNA for c-ets-1 proto-oncogene /cds=(278,1603) /gb= |
| 60H10 | 214 | 527 | AW150084 | Hs.248657 1.00E-99 | 3 | xg36f03.x1 cDNA, 3' end /clone=IMAGE:2629661 |
| 64E2 | 329 | 536 | BF512500 | Hs.248689 1.00E-112 | 1 | UI-H-BI3-atw-h-10-0-UI.s1 cDNA, 3' end /clon |
| 470C6 | 278 | 470 | AI832183 | Hs.249031 1.00E-103 | 1 | wh80g09.x1 cDNA, 3' end /clone=IMAGE:2387104 |
| 146A9 | 1145 | 1422 | S63912 | Hs.249247 1.00E-113 | 1 | D10S102=FBRNP [human, fetal brain, mRNA, 3043 |
| | | | | | | nt] /cds=(30, |
| 519E8 | 37 | 628 | NM_002136 | Hs.249495 0 | 1 | heterogeneous nuclear ribonucleoprotein A1 |
| 458C7 | 2232 | 2520 | NM_000964 | Hs.250505 1.00E-163 | 1 | retinoic acid receptor, alpha (RARA), mRNA /cd |
| 476A8 | 1060 | 1601 | AF308285 | Hs.250528 0 | 1 | serologically defined breast cancer antigen N |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|-------|-------|-----------|-----------|-----------|----|--|
| 123D7 | 436 | 2077 | AL157499 | Hs.250535 | 1.00E-153 | 3 | mRNA; cDNA DKFZp434N2412 (from clone DKFZp434 |
| 477A10 | 285 | 370 | AW291304 | Hs.250600 | 2.00E-34 | 1 | UI-H-BI2-agg-b-11-0-UI.s1 cDNA, 3' end /clon |
| 172G12 | 726 | 1598 | AF182420 | Hs.250619 | 0 | 6 | MDS019 (MDS019) mRNA, complete cds /cds=(231,1 |
| 167E11 | 11633 | 13714 | NM_016252 | Hs.250646 | 1.00E-180 | 2 | baculoviral IAP repeat-containing 6 (BIRC6), |
| 591E4 | 198 | 714 | NM_002823 | Hs.250655 | 4.00E-99 | 3 | prothymosin, alpha (gene sequence 28) (PTMA), |
| 40D9 | 2289 | 3010 | M95585 | Hs.250692 | 0 | 1 | hepatic leukemia factor (HLF) mRNA, complete cds /cds |
| 110D9 | 2336 | 3259 | NM_003144 | Hs.250773 | 0 | 3 | signal sequence receptor, alpha (translocon-a |
| 166A3 | 1 | 302 | AF103458 | Hs.250806 | 6.00E-93 | 2 | isolate donor N clone N168K immunoglobulin kap |
| 110C12 | 629 | 1228 | M35416 | Hs.250811 | 0 | 1 | GTP-binding protein (RALB) mRNA, complete cds /cds=(1 |
| 458D12 | 1136 | 1714 | AY007158 | Hs.250820 | 0 | 1 | clone CDABP0113 mRNA sequence /cds=UNKNOWN /g |
| 177C5 | 658 | 823 | J02621 | Hs.251064 | 3.00E-32 | 1 | non-histone chromosomal protein HMG-14 mRNA, complet |
| 126A2 | 658 | 1009 | NM_004965 | Hs.251064 | 0 | 3 | high-mobility group (nonhistone chromosomal) |
| 523G1 | 1 | 337 | AE000660 | Hs.251465 | 1.00E-178 | 2 | T-cell receptor alpha delta locus from bases 5 |
| 40G1 | 4 | 781 | X72308 | Hs.251526 | 0 | 3 | for monocyte chemotactic protein-3 (MCP- |
| 188G7 | 1 | 1030 | NM_002789 | Hs.251531 | 0 | 3 | proteasome (prosome, macropain) subunit, alp |
| 61E12 | 578 | 2275 | NM_006537 | Hs.251636 | 0 | 2 | ubiquitin specific protease 3 (USP3), mRNA /cd |
| 38B10 | 995 | 1211 | AK026594 | Hs.251653 | 1.00E-107 | 1 | FLJ22941 fis, clone KAT08078, highly sim |
| 70C3 | 2022 | 2405 | X52142 | Hs.251871 | 0 | 1 | CTP synthetase (EC 6.3.4.2) /cds=(75,1850) / |
| 177E9 | 49 | 406 | S80990 | Hs.252136 | 1.00E-125 | 2 | ficolin [human, uterus, mRNA, 1736 nt] /cds=(532,1512) /gb |
| 50F8 | 1841 | 2048 | AK026712 | Hs.252259 | 1.00E-114 | 15 | FLJ23059 fis, clone LNG03912 /cds=(41,16 |
| 585E12 | 16 | 194 | AI383340 | Hs.252300 | 1.00E-63 | 1 | tc76g05.x1 cDNA, 3' end /clone=IMAGE:2070584 |
| 181E12 | 22 | 99 | BE963374 | Hs.252338 | 4.00E-30 | 1 | 601657137R1 cDNA, 3' end /clone=IMAGE:3866193 |
| 477H4 | 290 | 451 | AI524022 | Hs.252359 | 8.00E-87 | 1 | tg99f02.x1 cDNA, 3' end /clone=IMAGE:2116923 |
| 188G11 | 95 | 700 | NM_007104 | Hs.252574 | 0 | 2 | ribosomal protein L10a (RPL10A), mRNA /cds=(1 |
| 471H9 | 1 | 285 | AV706014 | Hs.252580 | 1.00E-145 | 1 | AV706014 cDNA, 5' end /clone=ADBAOB12 /clone_ |
| 134F9 | 1358 | 1464 | AL359626 | Hs.252588 | 5.00E-50 | 1 | mRNA; cDNA DKFZp564F172 (from clone DKFZp564F1 |
| 597B10 | 13 | 279 | NM_000981 | Hs.252723 | 1.00E-149 | 28 | ribosomal protein L19 (RPL19), mRNA /cds=(28,6 |
| 120D7 | 962 | 1674 | NM_006054 | Hs.252831 | 0 | 5 | reticulon 3 (RTN3), mRNA /cds=(124,834) /gb=N |
| 593B10 | 102 | 467 | AW191929 | Hs.252989 | 7.00E-93 | 1 | xl77c10.x1 cDNA, 3' end /clone=IMAGE:2680722 |
| 482C11 | 32 | 122 | AW195119 | Hs.253151 | 3.00E-33 | 1 | xn66b07.x1 cDNA, 3' end /clone=IMAGE:2699413 |
| 472C6 | 34 | 279 | AW204029 | Hs.253384 | 1.00E-137 | 1 | UI-H-BI1-aen-d-02-0-UI.s1 cDNA, 3' end /clon |
| 472D4 | 27 | 440 | AW205624 | Hs.253502 | 0 | 1 | UI-H-BI1-afr-e-01-0-UI.s1 cDNA, 3' end /clon |
| 472D1 | 120 | 362 | BF750565 | Hs.253550 | 1.00E-133 | 1 | RC1-BN0410-261000-014-f11 cDNA /gb=BF750565 |
| 480F11 | 367 | 558 | AW237483 | Hs.253820 | 1.00E-105 | 1 | xm72e01.x1 cDNA, 3' end /clone=IMAGE:2689752 |
| 472B5 | 35 | 363 | AI432340 | Hs.254006 | 1.00E-169 | 1 | tg54e06.x1 cDNA, 3' end /clone=IMAGE:2112610 |
| 75E5 | 1 | 904 | M14328 | Hs.254105 | 0 | 5 | alpha enolase mRNA, complete cds /cds=(94,1398) /gb= |
| 592A12 | 1 | 1100 | NM_001428 | Hs.254105 | 0 | 5 | enolase 1, (alpha) (ENO1), mRNA /cds=(94,1398) |
| 472D10 | 183 | 414 | AI364936 | Hs.255100 | 1.00E-126 | 1 | qz23c12.x1 cDNA, 3' end /clone=IMAGE:2027734 |
| 479H9 | 43 | 184 | AW292772 | Hs.255119 | 2.00E-70 | 1 | UI-H-BW0-aij-d-03-0-UI.s1 cDNA, 3' end /clon |
| 480A2 | 18 | 523 | AW293267 | Hs.255178 | 0 | 1 | UI-H-BW0-aii-e-10-0-UI.s1 cDNA, 3' end /clon |
| 480B7 | 16 | 298 | AW293895 | Hs.255249 | 1.00E-116 | 1 | UI-H-BW0-ain-f-10-0-UI.s1 cDNA, 3' end /clon |
| 479H11 | 23 | 202 | AW293955 | Hs.255255 | 3.00E-79 | 1 | UI-H-BW0-aik-d-05-0-UI.s1 cDNA, 3' end /clon |
| 480A4 | 415 | 598 | AW294681 | Hs.255336 | 5.00E-66 | 1 | UI-H-BW0-ail-g-10-0-UI.s1 cDNA, 3' end /clon |
| 480A7 | 223 | 427 | AW294695 | Hs.255339 | 1.00E-103 | 1 | UI-H-BW0-aim-a-02-0-UI.s1 cDNA, 3' end /clon |
| 480A8 | 26 | 338 | BF514247 | Hs.255340 | 1.00E-167 | 1 | UI-H-BW1-ani-h-09-0-UI.s1 cDNA, 3' end /clon |
| 480C12 | 239 | 483 | AW295088 | Hs.255389 | 1.00E-124 | 1 | UI-H-BW0-ait-d-09-0-UI.s1 cDNA, 3' end /clon |
| 480F9 | 1 | 423 | BF531016 | Hs.255390 | 0 | 1 | 602072345F1 cDNA, 5' end /clone=IMAGE:4215251 |
| 480B3 | 68 | 377 | AW295610 | Hs.255446 | 1.00E-161 | 1 | UI-H-BW0-aip-c-03-0-UI.s1 cDNA, 3' end /clon |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|---|---|
| 460H5 | 44 | 427 | AA455707 | Hs.255452 | 1.00E-161 | 1 | aa22d09.r1 cDNA, 5' end /clone=IMAGE:814001 / |
| 480B12 | 132 | 212 | AW295664 | Hs.255454 | 7.00E-39 | 1 | UI-H-BW0-aip-g-12-0-UI.s1 cDNA, 3' end /clon |
| 472E7 | 163 | 489 | AI439645 | Hs.255490 | 1.00E-166 | 1 | tc91e08.x1 cDNA, 3' end /clone=IMAGE:2073542 |
| 480D12 | 84 | 258 | AW296005 | Hs.255492 | 8.00E-90 | 1 | UI-H-BW0-aiu-b-01-0-UI.s1 cDNA, 3' end /clon |
| 480F4 | 34 | 464 | AW296063 | Hs.255501 | 0 | 1 | UI-H-BW0-aiu-g-08-0-UI.s1 cDNA, 3' end /clon |
| 480D5 | 18 | 404 | AW296490 | Hs.255554 | 0 | 2 | UI-H-BW0-aiq-f-08-0-UI.s1 cDNA, 3' end /clon |
| 480E1 | 95 | 379 | AW296532 | Hs.255559 | 1.00E-101 | 1 | UI-H-BW0-aiv-b-07-0-UI.s1 cDNA, 3' end /clon |
| 480E5 | 17 | 326 | AW296545 | Hs.255560 | 1.00E-128 | 1 | UI-H-BW0-aiv-c-11-0-UI.s1 cDNA, 3' end /clon |
| 480F2 | 20 | 330 | AW296730 | Hs.255573 | 1.00E-160 | 1 | UI-H-BW0-aix-f-12-0-UI.s1 cDNA, 3' end /clon |
| 480G7 | 38 | 479 | AW296797 | Hs.255579 | 0 | 1 | UI-H-BW0-ajb-e-07-0-UI.s1 cDNA, 3' end /clon |
| 480C9 | 19 | 274 | AW297339 | Hs.255637 | 1.00E-117 | 1 | UI-H-BW0-air-c-03-0-UI.s1 cDNA, 3' end /clon |
| 480C4 | 70 | 191 | AW297400 | Hs.255647 | 1.00E-49 | 1 | UI-H-BW0-ais-a-05-0-UI.s1 cDNA, 3' end /clon |
| 480G5 | 17 | 242 | AW297522 | Hs.255661 | 2.00E-87 | 1 | UI-H-BW0-aja-e-02-0-UI.s1 cDNA, 3' end /clon |
| 480F10 | 230 | 560 | AW294654 | Hs.255687 | 0 | 1 | UI-H-BW0-ail-d-10-0-UI.s1 cDNA, 3' end /clon |
| 480G9 | 47 | 582 | AW297813 | Hs.255695 | 0 | 1 | UI-H-BW0-aiy-g-09-0-UI.s1 cDNA, 3' end /clon |
| 480G10 | 31 | 453 | AW297827 | Hs.255697 | 0 | 1 | UI-H-BW0-aiy-h-11-0-UI.s1 cDNA, 3' end /clon |
| 482G6 | 16 | 242 | AW339651 | Hs.255927 | 3.00E-78 | 1 | he15g04.x1 cDNA, 3' end /clone=IMAGE:2919126 |
| 469B11 | 4 | 221 | AW341086 | Hs.256031 | 1.00E-99 | 1 | xz92h04.x1 cDNA, 3' end /clone=IMAGE:2871703 |
| 140E7 | 2870 | 3589 | M32315 | Hs.256278 | 1.00E-84 | 2 | tumor necrosis factor receptor mRNA, complete cds /cd |
| 189H12 | 2839 | 3294 | NM_001066 | Hs.256278 | 0 | 2 | tumor necrosis factor receptor superfamily, m |
| 99H11 | 83 | 589 | NM_005620 | Hs.256290 | 0 | 4 | S100 calcium-binding protein A11 (calgizzarin |
| 58C7 | 1778 | 2264 | AJ271747 | Hs.256583 | 0 | 1 | partial mRNA for double stranded RNA binding nu |
| 482F4 | 373 | 628 | AV719442 | Hs.256959 | 1.00E-124 | 1 | AV719442 cDNA, 5' end /clone=GLCBNA01 /clone_ |
| 482F5 | 8 | 377 | AW440866 | Hs.256961 | 1.00E-179 | 1 | he05f02.x1 cDNA, 3' end /clone=IMAGE:2918139 |
| 482F8 | 191 | 315 | AW440974 | Hs.256971 | 2.00E-62 | 1 | he06e12.x1 cDNA, 3' end /clone=IMAGE:2918254 |
| 479E7 | 136 | 567 | AW444482 | Hs.256979 | 0 | 2 | UI-H-BI3-akb-e-05-0-UI.s1 cDNA, 3' end /clon |
| 471H5 | 3 | 432 | AI438957 | Hs.257066 | 0 | 1 | tc89b05.x1 cDNA, 3' end /clone=IMAGE:2073297 |
| 472G3 | 233 | 617 | AW450350 | Hs.257283 | 0 | 1 | UI-H-BI3-akn-c-01-0-UI.s1 cDNA, 3' end /clon |
| 472G11 | 112 | 338 | AI809475 | Hs.257466 | 1.00E-101 | 1 | wh76d06.x1 cDNA, 3' end /clone=IMAGE:2386667 |
| 479F7 | 22 | 421 | AW452467 | Hs.257572 | 0 | 1 | UI-H-BI3-als-e-09-0-UI.s1 cDNA, 3' end /clon |
| 479G9 | 95 | 304 | AW452513 | Hs.257579 | 1.00E-81 | 1 | UI-H-BW1-ame-b-03-0-UI.s1 cDNA, 3' end /clon |
| 479F11 | 16 | 329 | AW453021 | Hs.257640 | 1.00E-163 | 1 | UI-H-BW1-ama-c-02-0-UI.s1 cDNA, 3' end /clon |
| 479G4 | 45 | 441 | AW453044 | Hs.257646 | 0 | 1 | UI-H-BW1-ama-e-01-0-UI.s1 cDNA, 3' end /clon |
| 482F9 | 11 | 256 | AW467193 | Hs.257667 | 1.00E-108 | 1 | he07a04.x1 cDNA, 3' end /clone=IMAGE:2918286 |
| 482G2 | 9 | 271 | AW467400 | Hs.257680 | 1.00E-112 | 1 | he10f11.x1 cDNA, 3' end /clone=IMAGE:2918637 |
| 482G8 | 108 | 428 | AW467437 | Hs.257682 | 1.00E-177 | 1 | he17d05.x1 cDNA, 3' end /clone=IMAGE:2919273 |
| 482G12 | 1 | 417 | AW467501 | Hs.257687 | 0 | 1 | he19e06.x1 cDNA, 3' end /clone=IMAGE:2919490 |
| 482H4 | 39 | 143 | AW467746 | Hs.257695 | 3.00E-51 | 1 | he23d05.x1 cDNA, 3' end /clone=IMAGE:2919849 |
| 482H6 | 1 | 116 | AW467863 | Hs.257705 | 2.00E-59 | 1 | he27c04.x1 cDNA, 3' end /clone=IMAGE:2920230 |
| 482H7 | 1 | 321 | AW467864 | Hs.257706 | 1.00E-156 | 1 | he27c05.x1 cDNA, 3' end /clone=IMAGE:2920232 |
| 482H9 | 1 | 112 | AW467992 | Hs.257709 | 1.00E-47 | 1 | he30b01.x1 cDNA, 3' end /clone=IMAGE:2920489 |
| 483A2 | 20 | 429 | AW468207 | Hs.257716 | 0 | 1 | he34a12.x1 cDNA, 3' end /clone=IMAGE:2920894 |
| 483A9 | 11 | 373 | AW468431 | Hs.257727 | 0 | 1 | he37h11.x1 cDNA, 3' end /clone=IMAGE:2921253 |
| 483B2 | 2 | 241 | AW468621 | Hs.257743 | 1.00E-119 | 1 | he42e03.x1 cDNA, 3' end /clone=IMAGE:2921692 |
| 75B1 | 157 | 246 | BE531180 | Hs.258494 | 5.00E-44 | 1 | 601278313F1 cDNA, 5' end /clone=IMAGE:3610443 |
| 585F6 | 2200 | 4106 | AL136549 | Hs.258503 | 0 | 8 | mRNA; cDNA DKFZp761112121 (from clone DKFZp761 |
| 169E2 | 5186 | 5415 | U20489 | Hs.258609 | 1.00E-119 | 2 | glomerular epithelial protein 1 (GLEPP1) comple |
| 127A5 | 2142 | 2477 | AB037790 | Hs.258730 | 1.00E-177 | 1 | mRNA for KIAA1369 protein, partial cds /cds=(0 |
| 171B12 | 4202 | 4314 | Y10129 | Hs.258742 | 4.00E-45 | 2 | mybpc3 gene /cds=(33,3857) /gb=Y10129 /gi=20583 |
| 75B7 | 531 | 682 | L14542 | Hs.258850 | 3.00E-81 | 1 | lectin-like type II integral membrane protein (NKG2-E |
| 471G5 | 344 | 473 | AI144328 | Hs.259084 | 3.00E-61 | 1 | oy84g04.x1 cDNA, 3' end /clone=IMAGE:1672566 |
| 479B7 | 73 | 307 | AF161364 | Hs.259683 | 1.00E-123 | 1 | HSPC101 mRNA, partial cds /cds=(0,556) /gb=AF |
| 146B11 | 1942 | 2174 | AL136842 | Hs.260024 | 8.00E-92 | 1 | DKFZp434A0530 (from clone DKFZp434A |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|---|
| 584A1 | 1085 | 1470 | AL022398 | Hs.261373 | 1.00E-166 | 1 | DNA sequence from PAC 434O14 on chromosome 1q32 |
| 148B1 | 119 | 817 | X60656 | Hs.261802 | 0 | 2 | elongation factor 1-beta /cds=(95,772) |
| 60G3 | 203 | 3170 | NM_001634 | Hs.262476 | 0 | 15 | S-adenosylmethionine decarboxylase 1 (AMD1) |
| 462E7 | 292 | 374 | AW300868 | Hs.262789 | 8.00E-40 | 1 | xk07d09.x1 cDNA, 3' end /clone=IMAGE:2666033 |
| 56F11 | 33 | 234 | BF243724 | Hs.263414 | 4.00E-82 | 1 | 601877832F1 cDNA, 5' end /clone=IMAGE:4106359 |
| 119C5 | 2414 | 2664 | NM_002108 | Hs.263435 | 1.00E-137 | 1 | histidine ammonia-lyase (HAL), mRNA /cds=(297 |
| 105A4 | 3225 | 3775 | AK025774 | Hs.264190 | 0 | 3 | FLJ22121 fis, clone HEP18876, highly sim |
| 469H1 | 369 | 576 | AI380111 | Hs.264298 | 1.00E-103 | 1 | tf98a11.x1 cDNA, 3' end /clone=IMAGE:2107292 |
| 181A3 | 2434 | 2768 | NM_002535 | Hs.264981 | 1.00E-148 | 2 | 2'-5'oligoadenylate synthetase 2 (OAS2), tra |
| 41B7 | 3209 | 3885 | M59911 | Hs.265829 | 0 | 1 | integrin alpha-3 chain mRNA, complete cds /cds=(73,32 |
| 75F9 | 264 | 452 | AW150944 | Hs.265838 | 2.00E-96 | 1 | xg42e09.x1 cDNA, 3' end /clone=IMAGE:2630248 |
| 99C3 | 2684 | 3155 | AK000680 | Hs.266175 | 0 | 2 | cDNA FLJ20673 fis, clone KAlA4464 /cds=(104,14 |
| 598E12 | 2417 | 2894 | AK026669 | Hs.266940 | 0 | 2 | cDNA: FLJ23016 fis, clone LNG00874 /cds=UNKNOW |
| 468B6 | 863 | 1515 | NM_016569 | Hs.267182 | 0 | 1 | TBX3-iso protein (TBX3-iso), mRNA /cds=(116,1 |
| 115E11 | 1234 | 1713 | AF271994 | Hs.267288 | 0 | 1 | dopamine responsive protein DRG-1 mRNA, compl |
| 114A4 | 31 | 382 | NM_024095 | Hs.267400 | 1.00E-179 | 1 | hypothetical protein MGC5540 (MGC5540), mRNA |
| 166C7 | 1315 | 1919 | AK001749 | Hs.267604 | 0 | 2 | FLJ10887 fis, clone NT2RP4002018, weakly |
| 56A8 | 564 | 3624 | AB033054 | Hs.267690 | 0 | 3 | for KIAA1228 protein, partial cds /cds=(0 |
| 70B10 | 229 | 2138 | AK001471 | Hs.268012 | 0 | 3 | FLJ10609 fis, clone NT2RP2005276, highly |
| 178D10 | 1831 | 2796 | NM_012255 | Hs.268555 | 0 | 2 | 5'-3' exoribonuclease 2 (XRN2), mRNA /cds=(68, |
| 168B9 | 451 | 881 | AF068235 | Hs.268763 | 0 | 1 | barrier-to-autointegration factor mRNA, com |
| 465F2 | 91 | 433 | AA613224 | Hs.270264 | 0 | 1 | no19d06.s1 cDNA, 3' end /clone=IMAGE:1101131 |
| 469E2 | 302 | 422 | BE857296 | Hs.270293 | 1.00E-57 | 1 | 7g27b01.x1 cDNA, 3' end /clone=IMAGE:3307657 |
| 465D10 | 284 | 405 | AI270476 | Hs.270341 | 4.00E-51 | 1 | qu88e12.x1 cDNA, 3' end /clone=IMAGE:1979182 |
| 473F10 | 831 | 1096 | AK021517 | Hs.270557 | 1.00E-140 | 1 | cDNA FLJ11455 fis, clone HEMBA1001497 /cds=UNK |
| 193A10 | 458 | 563 | AI818951 | Hs.270614 | 5.00E-31 | 1 | wj89e12.x1 cDNA, 3' end /clone=IMAGE:2410030 |
| 458E11 | 44 | 264 | W03955 | Hs.270717 | 1.00E-118 | 1 | za62d04.r1 cDNA, 5' end /clone=IMAGE:297127 / |
| 163C12 | 280 | 954 | M30704 | Hs.270833 | 1.00E-168 | 2 | amphiregulin (AR) mRNA, complete cds, clones lambda-A |
| 196F4 | 208 | 567 | NM_001657 | Hs.270833 | 1.00E-158 | 1 | amphiregulin (schwannoma-derived growth fac |
| 464G2 | 378 | 529 | AW172850 | Hs.270999 | 4.00E-77 | 1 | xj04f02.x1 cDNA, 3' end /clone=IMAGE:2656251 |
| 464F5 | 131 | 476 | AW572930 | Hs.271264 | 0 | 1 | hf17f07.x1 cDNA, 3' end /clone=IMAGE:2932165 |
| 41G6 | 458 | 880 | Y16645 | Hs.271387 | 0 | 1 | for monocyte chemotactic protein-2 /cds= |
| 464F2 | 139 | 220 | AW975086 | Hs.271420 | 2.00E-34 | 1 | EST387192 cDNA /gb=AW975086 /gi=8166291 /ug= |
| 178E10 | 961 | 1452 | AK021715 | Hs.271541 | 0 | 1 | cDNA FLJ11653 fis, clone HEMBA1004538 /cds=UNK |
| 129E1 | 73 | 441 | NM_016049 | Hs.271614 | 1.00E-136 | 1 | CGI-112 protein (LOC51016), mRNA /cds=(158,78 |
| 40C9 | 4195 | 4949 | X17033 | Hs.271986 | 0 | 1 | integrin alpha-2 subunit /cds=(48,3593) /gb |
| 108E1 | 917 | 1331 | NM_006811 | Hs.272168 | 0 | 2 | tumor differentially expressed 1 (TDE1), mRNA |
| 155H10 | 232 | 715 | AL021395 | Hs.272279 | 1.00E-164 | 1 | DNA sequence from clone RP1-269M15 on chromosome 20q1 |
| 159D3 | 38 | 238 | AL034343 | Hs.272295 | 1.00E-106 | 4 | DNA sequence from clone RP1-108C2 on chromosome 6p12. |
| 477C3 | 744 | 1166 | AL133015 | Hs.272307 | 0 | 2 | mRNA; cDNA DKFZp434O2417 (from clone DKFZp434O |
| 173D12 | 228 | 594 | AL121934 | Hs.272340 | 1.00E-140 | 5 | DNA sequence from clone RP11-209A2 on chromosome 6. C |
| 472D9 | 27 | 418 | NM_016135 | Hs.272398 | 0 | 1 | transcription factor ets (TEL2), mRNA /cds=(7 |
| 465F9 | 1885 | 2345 | NM_013351 | Hs.272409 | 0 | 1 | T-box 21 (TBX21), mRNA /cds=(211,1818) /gb=NM |
| 41E11 | 1 | 277 | NM_004167 | Hs.272493 | 1.00E-113 | 1 | small inducible cytokine subfamily A (Cys-Cys |
| 462E11 | 8 | 526 | NM_001503 | Hs.272529 | 0 | 1 | glycosylphosphatidylinositol specific phos |
| 104C6 | 210 | 327 | AE000659 | Hs.272550 | 5.00E-61 | 1 | T-cell receptor alpha delta locus from bases 2 |
| 596A3 | 411 | 1208 | NM_013392 | Hs.272736 | 0 | 5 | nuclear receptor binding protein (NRBP), mRNA |
| 75C2 | 1892 | 2188 | AK000316 | Hs.272793 | 1.00E-165 | 1 | FLJ20309 fis, clone HEP07296 /cds=(41,127 |
| 58C6 | 1 | 956 | NM_006009 | Hs.272897 | 0 | 2 | Tubulin, alpha, brain-specific (TUBA3), mRNA |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|--|
| 190H8 | 3246 | 3771 | AK024471 | Hs.273230 | 1.00E-165 | 2 | mRNA for FLJ00064 protein, partial cds /cds=(0 |
| 590E11 | 1512 | 1860 | NM_014230 | Hs.273307 | 1.00E-168 | 4 | signal recognition particle 68kD (SRP68), mRN |
| 588H2 | 696 | 1454 | NM_000516 | Hs.273385 | 0 | 3 | guanine nucleotide binding protein (G protein) |
| 165E9 | 3186 | 3695 | NM_014871 | Hs.273397 | 0 | 1 | KIAA0710 gene product (KIAA0710), mRNA /cds=(|
| 462A6 | 394 | 496 | AA527312 | Hs.273775 | 2.00E-42 | 1 | ng36a08.s1 cDNA, 3' end /clone=IMAGE:936854 / |
| 587F1 | 1763 | 1978 | AL050353 | Hs.274170 | 1.00E-112 | 1 | mRNA; cDNA DKFZp564C0482 (from clone DKFZp564C |
| 177E5 | 1448 | 1876 | AK000765 | Hs.274248 | 0 | 1 | FLJ20758 fis, clone HEP01508 /cds=(464,13 |
| 59E7 | 1 | 301 | AF151049 | Hs.274344 | 1.00E-159 | 3 | HSPC215 mRNA, complete cds /cds=(92,451) /gb= |
| 174A6 | 931 | 1352 | NM_004301 | Hs.274350 | 0 | 1 | BAF53 (BAF53A), mRNA /cds=(136,1425) /gb=NM_0 |
| 99E2 | 718 | 1391 | NM_018477 | Hs.274369 | 0 | 4 | uncharacterized hypothalamus protein HARP11 |
| 117F6 | 3046 | 3478 | AB037844 | Hs.274396 | 0 | 2 | mRNA for KIAA1423 protein, partial cds /cds=(0 |
| 52F3 | 1724 | 2342 | NM_005346 | Hs.274402 | 1.00E-149 | 48 | heat shock 70kD protein 1 (HSPA1B), mRNA /cds=(|
| 516B1 | 719 | 1026 | NM_018975 | Hs.274428 | 1.00E-161 | 2 | TRF2-interacting telomeric RAP1 protein (RAP |
| 104A1 | 1943 | 2396 | AK002127 | Hs.274439 | 0 | 1 | FLJ11265 fis, clone PLACE1009158 /cds=(30 |
| 137D6 | 1697 | 1817 | NM_001403 | Hs.274466 | 8.00E-49 | 1 | eukaryotic translation elongation factor 1 a |
| 108D11 | 321 | 646 | X16863 | Hs.274467 | 1.00E-160 | 1 | Fc-gamma RIII-1 cDNA for Fc-gamma receptor III-1 (CD |
| 107F1 | 567 | 895 | AF283771 | Hs.274472 | 1.00E-168 | 1 | clone TCBAP0774 mRNA sequence /cds=UNKNOWN /g |
| 517B9 | 4 | 480 | NM_002128 | Hs.274472 | 0 | 3 | high-mobility group (nonhistone chromosomal) |
| 514C8 | 254 | 539 | M12888 | Hs.274474 | 1.00E-144 | 2 | T-cell receptor germline beta-chain gene C-region C- |
| 460G5 | 602 | 775 | M12679 | Hs.274485 | 3.00E-94 | 1 | Cw1 antigen mRNA, complete cds /cds=(0,617) /gb=M1267 |
| 463G7 | 163 | 744 | D90145 | Hs.274535 | 0 | 4 | LD78 beta gene /cds=(86,367) /gb=D90145 /gi=219907 / |
| 472E10 | 277 | 391 | AI393960 | Hs.274851 | 6.00E-59 | 1 | tg11d04.x1 cDNA, 3' end /clone=IMAGE:2108455 |
| 115A11 | 156 | 446 | NM_014624 | Hs.275243 | 1.00E-157 | 8 | S100 calcium-binding protein A6 (calcyclin) (|
| 102C6 | 23 | 448 | AA610514 | Hs.275611 | 1.00E-161 | 1 | np93h02.s1 /clone=IMAGE:1133907 /gb=AA6 |
| 160E3 | 24 | 304 | AA757952 | Hs.275773 | 1.00E-74 | 3 | zg49e07.s1 3' end /clone=IMAGE:396708 / |
| 500B8 | 26 | 536 | NM_022551 | Hs.275865 | 0 | 3 | ribosomal protein S18 (RPS18), mRNA /cds=(46,5 |
| 522D9 | 184 | 593 | NM_001959 | Hs.275959 | 0 | 1 | eukaryotic translation elongation factor 1 b |
| 151H4 | 1 | 196 | AA984890 | Hs.276063 | 5.00E-58 | 1 | am62e06.s1 cDNA, 3' end /clone=IMAGE:1576642 |
| 476B10 | 362 | 615 | BF510670 | Hs.276341 | 1.00E-116 | 1 | UI-H-BI4-aof-b-08-0-UI.s1 cDNA, 3' end /clon |
| 144F10 | 73 | 279 | AI318342 | Hs.276562 | 8.00E-57 | 1 | ta73c09.x1 3' end /clone=IMAGE:2049712 |
| 593G1 | 17 | 88 | BE747210 | Hs.276718 | 2.00E-26 | 1 | 601580926F1 cDNA, 5' end /clone=IMAGE:3929430 |
| 473E3 | 205 | 488 | AI380791 | Hs.276766 | 1.00E-144 | 1 | tg04b12.x1 cDNA, 3' end /clone=IMAGE:2107775 |
| 598A2 | 72 | 427 | NM_001803 | Hs.276770 | 0 | 19 | CDW52 antigen (CAMPATH-1 antigen) (CDW52), mR |
| 170H2 | 83 | 432 | X62466 | Hs.276770 | 0 | 1 | CAMPATH-1 (CDW52) antigen /cds=(33,218) |
| 464F7 | 2 | 454 | AI492640 | Hs.276903 | 0 | 2 | qz18a06.x1 cDNA, 3' end /clone=IMAGE:2021842 |
| 464E5 | 102 | 191 | AI493726 | Hs.276907 | 3.00E-44 | 2 | qz12f08.x1 cDNA, 3' end /clone=IMAGE:2021319 |
| 50B5 | 42 | 308 | AI581383 | Hs.276988 | 5.00E-77 | 1 | to71c02.x1 cDNA, 3' end /clone=IMAGE:2183714 |
| 468C6 | 40 | 279 | AI740667 | Hs.277201 | 1.00E-64 | 1 | wg07b07.x1 cDNA, 3' end /clone=IMAGE:2364373 |
| 111D12 | 1 | 562 | AI749435 | Hs.277224 | 1.00E-118 | 9 | at24b04.x1 cDNA, 3' end /clone=IMAGE:2356015 |
| 459B4 | 176 | 367 | AI811065 | Hs.277293 | 2.00E-38 | 1 | tr03f05.x1 cDNA, 3' end /clone=IMAGE:2217249 |
| 477H3 | 6227 | 6584 | NM_013449 | Hs.277401 | 1.00E-132 | 1 | bromodomain adjacent to zinc finger domain, 2A |
| 54A8 | 34 | 301 | AW050975 | Hs.277672 | 3.00E-48 | 1 | wz25f04.x1 cDNA, 3' end /clone=IMAGE:2559103 |
| 459E4 | 1532 | 2061 | NM_006389 | Hs.277704 | 0 | 1 | oxygen regulated protein (150kD) (ORP150), mR |
| 109B6 | 3281 | 3721 | U65785 | Hs.277704 | 0 | 1 | 150 kDa oxygen-regulated protein ORP150 mRNA, complet |
| 524H7 | 2979 | 3350 | NM_005899 | Hs.277721 | 0 | 1 | membrane component, chromosome 17, surface ma |
| 472F10 | 425 | 556 | AW082714 | Hs.277738 | 5.00E-69 | 1 | xb61f07.x1 cDNA, 3' end /clone=IMAGE:2580805 |
| 176D1 | 113 | 269 | AW262728 | Hs.277994 | 6.00E-32 | 1 | xq94a12.x1 cDNA, 3' end /clone=IMAGE:2758270 |
| 464H4 | 2138 | 3563 | NM_016733 | Hs.278027 | 0 | 9 | LIM domain kinase 2 (LIMK2), transcript varian |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|--|
| 145C9 | 533 | 1446 | D13316 | Hs.278238 | 0 | 3 | transcription factor, E4TF1-47, complete cds |
| 161C3 | 339 | 560 | NM_002041 | Hs.278238 | 1.00E-123 | 1 | GA-binding protein transcription factor, bet |
| 74C9 | 345 | 1048 | AK026632 | Hs.278242 | 0 | 3 | FLJ22979 fis, clone KAT11379, highly sim |
| 59E2 | 255 | 782 | L24804 | Hs.278270 | 0 | 2 | (p23) mRNA, complete cds /cds=(232,714) /gb=L24804 / |
| 521H10 | 8 | 461 | AI720536 | Hs.278302 | 1.00E-114 | 4 | as83c02.x1 cDNA, 3' end /clone=IMAGE:2335298 |
| 118C6 | 830 | 1104 | NM_001995 | Hs.278333 | 1.00E-148 | 1 | fatty-acid-Coenzyme A ligase, long-chain 1 (|
| 104E9 | 248 | 417 | AF151054 | Hs.278429 | 2.00E-78 | 1 | HSPC220 mRNA, complete cds /cds=(288,818) /gb |
| 594F10 | 379 | 1760 | NM_016520 | Hs.278429 | 0 | 4 | hepatocellular carcinoma-associated antigen |
| 126D11 | 7374 | 7716 | NM_006289 | Hs.278559 | 0 | 1 | talín (TLN), mRNA /cds=(126,7751) /gb=Nm_0062 |
| 589E6 | 3078 | 5778 | NM_003105 | Hs.278571 | 0 | 3 | sortilin-related receptor, L(DLR class) A re |
| 102C10 | 669 | 1180 | D14041 | Hs.278573 | 0 | 1 | for H-2K binding factor-2, complete cds / |
| 526H8 | 167 | 4709 | NM_015874 | Hs.278573 | 0 | 5 | H-2K binding factor-2 (LOC51580), mRNA /cds=(|
| 120A12 | 732 | 1305 | AB029031 | Hs.278586 | 0 | 1 | mRNA for KIAA1108 protein, partial cds /cds=(0 |
| 126F4 | 3138 | 3515 | AF035737 | Hs.278589 | 0 | 2 | general transcription factor 2-1 (GTF2I) mRNA |
| 40A7 | 3179 | 3864 | U24578 | Hs.278625 | 0 | 1 | RP1 and complement C4B precursor (C4B) genes, partial |
| 50C4 | 4401 | 4581 | AB002334 | Hs.278671 | 2.00E-60 | 1 | KIAA0336 gene, complete cds /cds=(253,5004) |
| 106E12 | 104 | 1222 | D50525 | Hs.278693 | 0 | 11 | TI-227H /cds=UNKNOWN /gb=D50525 /gi=1167502 |
| 467E10 | 168 | 542 | BE973840 | Hs.278704 | 1.00E-145 | 1 | 601680647F1 cDNA, 5' end /clone=IMAGE:3951154 |
| 75F2 | 1121 | 1772 | J04755 | Hs.278718 | 0 | 37 | ferritin H processed pseudogene, complete cds /cds=UN |
| 170E12 | 204 | 843 | AL121735 | Hs.278736 | 0 | 2 | Isoform of human GTP-binding protein G25K /cds=(104,679) / |
| 103F4 | 589 | 926 | NM_019597 | Hs.278857 | 0 | 1 | heterogeneous nuclear ribonucleoprotein H2 |
| 37F8 | 3 | 519 | U01923 | Hs.278857 | 0 | 1 | BTk region clone ftp-3 mRNA /cds=UNKNOWN /gb=U01923 / |
| 66B11 | 2195 | 2512 | AB029027 | Hs.279039 | 1.00E-172 | 1 | for KIAA1104 protein, complete cds /cds=(|
| 171G3 | 219 | 815 | AK027258 | Hs.279040 | 0 | 2 | FLJ23605 fis, clone LNG15982, highly sim |
| 172E12 | 18 | 95 | NM_014065 | Hs.279040 | 4.00E-27 | 2 | HT001 protein (HT001), mRNA /cds=(241,1203) / |
| 596A12 | 1 | 225 | BE220869 | Hs.279231 | 2.00E-78 | 1 | hu01g02.x1 cDNA, 3' end /clone=IMAGE:3165362 |
| 61H2 | 20 | 220 | BE279328 | Hs.279429 | 2.00E-32 | 3 | 601157666F1 cDNA, 5' end /clone=IMAGE:3504328 |
| 458E12 | 1835 | 2473 | NM_014160 | Hs.279474 | 0 | 1 | HSPC070 protein (HSPC070), mRNA /cds=(331,158 |
| 110F3 | 983 | 1614 | NM_016160 | Hs.279518 | 0 | 1 | amyloid precursor protein homolog HSD-2 (LOC5 |
| 37E5 | 39 | 732 | AK001403 | Hs.279521 | 0 | 1 | FLJ10541 fis, clone NT2RP2001381 /cds=(3 |
| 66D6 | 6 | 463 | BE502919 | Hs.279522 | 0 | 1 | hz81b08.x1 cDNA, 3' end /clone=IMAGE:3214359 |
| 123A11 | 411 | 903 | NM_013237 | Hs.279529 | 0 | 2 | px19-like protein (PX19), mRNA /cds=(176,835) |
| 185A10 | 809 | 1324 | NM_002817 | Hs.279554 | 0 | 1 | proteasome (prosome, macropain) 26S subunit, |
| 472H9 | 88 | 543 | AL582047 | Hs.279555 | 0 | 1 | AL582047 cDNA /clone=CS0DL003YD01-(3-prime) |
| 41A2 | 1 | 326 | AK000575 | Hs.279581 | 1.00E-162 | 1 | FLJ20568 fis, clone REC00775 /cds=(6,422) |
| 135F4 | 648 | 935 | NM_016283 | Hs.279586 | 1.00E-110 | 1 | adrenal gland protein AD-004 (LOC51578), mRNA |
| 69D9 | 841 | 935 | D16217 | Hs.279607 | 9.00E-40 | 1 | calpastatin, complete cds /cds=(162,2288) / |
| 116B6 | 938 | 1562 | NM_001750 | Hs.279607 | 0 | 1 | calpastatin (CAST), mRNA /cds=(66,1358) /gb= |
| 473F4 | 6847 | 7401 | NM_007329 | Hs.279611 | 0 | 1 | deleted in malignant brain tumors 1 (DMBT1), tr |
| 123C7 | 2488 | 2684 | NM_021644 | Hs.279681 | 1.00E-105 | 1 | heterogeneous nuclear ribonucleoprotein H3 |
| 586E2 | 357 | 633 | NM_014169 | Hs.279761 | 3.00E-97 | 1 | HSPC134 protein (HSPC134), mRNA /cds=(45,716) |
| 464D6 | 383 | 524 | NM_016154 | Hs.279771 | 1.00E-33 | 1 | ras-related GTP-binding protein 4b (RAB4B), m |
| 99G9 | 1375 | 1835 | NM_013388 | Hs.279784 | 0 | 1 | prolactin regulatory element binding (PREB), |
| 590F4 | 1045 | 1540 | NM_003883 | Hs.279789 | 0 | 2 | histone deacetylase 3 (HDAC3), mRNA /cds=(55,1 |
| 163E1 | 59 | 564 | NM_015932 | Hs.279813 | 0 | 3 | hypothetical protein (HSPC014), mRNA /cds=(8 |
| 525G5 | 3914 | 4160 | NM_014819 | Hs.279849 | 1.00E-138 | 1 | KIAA0438 gene product (KIAA0438), mRNA /cds=(|
| 598A10 | 9 | 821 | NM_003295 | Hs.279860 | 0 | 19 | tumor protein, translationally-controlled 1 |
| 526C8 | 734 | 1166 | NM_016007 | Hs.279867 | 0 | 1 | CGI-59 protein (LOC51625), mRNA /cds=(2,1153) |
| 183G12 | 758 | 1093 | NM_017774 | Hs.279893 | 0 | 1 | hypothetical protein FLJ20342 (FLJ20342), mR |
| 36B3 | 247 | 611 | AK025623 | Hs.279901 | 0 | 1 | FLJ21970 fis, clone HEP05733, highly sim |
| 592G3 | 479 | 1052 | NM_016146 | Hs.279901 | 0 | 4 | PTD009 protein (PTD009), mRNA /cds=(257,916) |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | |
|--------|------|------|-----------|---------------------|----|---|
| 38F5 | 811 | 1256 | AF151875 | Hs.279918 0 | 4 | CGI-117 protein mRNA, complete cds /cds=(456,9 |
| 161E3 | 542 | 862 | NM_016391 | Hs.279918 1.00E-151 | 1 | hypothetical protein (HSPC111), mRNA /cds=(6 |
| 584F11 | 10 | 212 | NM_014248 | Hs.279919 1.00E-112 | 2 | ring-box 1 (RBX1), mRNA /cds=(6,332) /gb=NM_0 |
| 588H7 | 400 | 1155 | NM_003404 | Hs.279920 0 | 12 | tyrosine 3-monooxygenase/tryptophan 5-monoo |
| 169C8 | 400 | 1155 | X57346 | Hs.279920 1.00E-131 | 2 | HS1 protein /cds=(372,1112) /gb=X57346 |
| 147A1 | 209 | 1978 | AK025927 | Hs.279921 0 | 8 | FLJ22274 fis, clone HRC03616, highly sim |
| 591H11 | 48 | 1810 | NM_016127 | Hs.279921 1.00E-176 | 33 | HSPC035 protein (LOC51669), mRNA /cds=(16,103 |
| 69D1 | 727 | 1776 | NM_014366 | Hs.279923 0 | 3 | putative nucleotide binding protein, estradio |
| 52C6 | 303 | 1151 | V00522 | Hs.279930 0 | 2 | encoding major histocompatibility complex gene |
| 158C11 | 2483 | 2785 | D84224 | Hs.279946 1.00E-166 | 2 | methionyl tRNA synthetase, complete c |
| 194E7 | 1525 | 1767 | NM_004990 | Hs.279946 1.00E-125 | 1 | methionine-tRNA synthetase (MARS), mRNA /cds |
| 62E5 | 215 | 701 | U93243 | Hs.279948 0 | 1 | Ubc6p homolog mRNA, complete cds /cds=(27,983) |
| 145G3 | 1 | 1882 | AK024090 | Hs.281434 1.00E-147 | 5 | FLJ14028 fis, clone HEMBA1003838 /cds=UN |
| 473A6 | 1 | 310 | BE552131 | Hs.282091 1.00E-158 | 1 | hw29b05.x1 cDNA, 3' end /clone=IMAGE:3184305 |
| 52C12 | 1 | 455 | R67739 | Hs.282401 0 | 1 | yi28c06.r1 cDNA, 5' end /clone=IMAGE:140554 / |
| 112A3 | 5072 | 5274 | NM_006165 | Hs.282441 3.00E-83 | 1 | nuclear factor related to kappa B binding prote |
| 61H3 | 443 | 577 | AV648638 | Hs.282867 2.00E-68 | 4 | AV648638 cDNA, 3' end /clone=GLCBL12 /clone_ |
| 37D3 | 38 | 766 | AF287008 | Hs.283022 0 | 5 | triggering receptor expressed on monocytes 1 |
| 125C5 | 32 | 748 | NM_018643 | Hs.283022 0 | 13 | triggering receptor expressed on myeloid cell |
| 41B1 | 597 | 1084 | NM_018636 | Hs.283106 0 | 2 | hypothetical protein PRO2987 (PRO2987), mRNA |
| 111E9 | 1111 | 1405 | AB037802 | Hs.283109 1.00E-152 | 1 | mRNA for KIAA1381 protein, partial cds /cds=(0 |
| 169D7 | 5 | 175 | BE672733 | Hs.283216 2.00E-37 | 1 | 7b75g07.x1 3' end /clone=IMAGE:3234108 |
| 74G11 | 47 | 384 | BE676472 | Hs.283267 1.00E-151 | 1 | 7f30c05.x1 cDNA, 3' end /clone=IMAGE:3296168 |
| 191A5 | 256 | 890 | NM_018507 | Hs.283330 0 | 3 | hypothetical protein PRO1843 (PRO1843), mRNA |
| 465B7 | 114 | 638 | AW979262 | Hs.283410 0 | 2 | EST391372 cDNA /gb=AW979262 /gi=8170550 /ug= |
| 143E1 | 1970 | 2258 | NM_020217 | Hs.283611 1.00E-110 | 1 | hypothetical protein DKFZp5471014 (DKFZp5471 |
| 54E9 | 385 | 739 | AF116620 | Hs.283630 0 | 3 | PRO1068 mRNA, complete cds /cds=UNKNOWN |
| 462D10 | 63 | 279 | NM_007220 | Hs.283646 1.00E-119 | 1 | /gb=A |
| 518B11 | 359 | 690 | NM_016056 | Hs.283670 1.00E-167 | 2 | carbonic anhydrase VB, mitochondrial (CA5B), |
| 36H5 | 1 | 226 | BE778549 | Hs.283674 8.00E-85 | 1 | CGI-119 protein (LOC51643), mRNA /cds=(0,776) |
| 126H10 | 907 | 1431 | NM_017801 | Hs.283685 0 | 1 | 601466063F1 cDNA, 5' end /clone=IMAGE:3869391 |
| 69B1 | 2288 | 3232 | AF103803 | Hs.283690 0 | 6 | hypothetical protein FLJ20396 (FLJ20396), mR |
| 98B1 | 162 | 489 | NM_018476 | Hs.283719 1.00E-110 | 1 | clone H41 unknown mRNA /cds=(323,1099) /gb=AF |
| 39C3 | 997 | 3088 | NM_020151 | Hs.283722 0 | 2 | uncharacterized hypothalamus protein HBEX2 |
| 592E4 | 13 | 2219 | NM_020357 | Hs.283728 0 | 2 | GTT1 protein (GTT1), mRNA /cds=(553,1440) /gb |
| 142F11 | 138 | 371 | AF173296 | Hs.283740 1.00E-130 | 1 | PEST-containing nuclear protein (pcnp), mRNA |
| 592F3 | 480 | 858 | NM_013234 | Hs.283781 0 | 2 | e(y)2 homolog mRNA, complete cds /cds=(216,521 |
| 159E5 | 3 | 281 | AL121916 | Hs.283838 1.00E-113 | 6 | muscle specific gene (M9), mRNA /cds=(171,827) |
| 142H10 | 517 | 892 | AL121585 | Hs.283864 9.00E-70 | 2 | DNA sequence from clone RP1-189G13 on |
| 166D3 | 1 | 227 | X72475 | Hs.283972 6.00E-70 | 1 | chromosome 20. |
| 134E8 | 980 | 1302 | NM_014110 | Hs.284136 0 | 47 | DNA sequence from clone RP11-504H3 on |
| 596C5 | 30 | 705 | NM_006134 | Hs.284142 0 | 2 | chromosome 20 C |
| 74A4 | 1944 | 2157 | AL359585 | Hs.284158 1.00E-110 | 3 | for rearranged Ig kappa light chain variable |
| 159A4 | 159 | 1414 | AF165521 | Hs.284162 0 | 4 | PRO2047 protein (PRO2047), mRNA /cds=(798,968 |
| 597F9 | 836 | 1000 | NM_016304 | Hs.284162 1.00E-88 | 1 | chromosome 21 open reading frame 4 (C21ORF4), m |
| 462D2 | 655 | 1306 | NM_016301 | Hs.284164 0 | 1 | cDNA DKFZp762B195 (from clone DKFZp762B1 |
| 458C6 | 720 | 910 | AP001753 | Hs.284189 1.00E-102 | 1 | ribosomal protein L30 isolog (L30) mRNA, compl |
| 165D5 | 1482 | 2302 | AB040120 | Hs.284205 0 | 2 | 60S ribosomal protein L30 isolog (LOC51187), m |
| | | | | | | protein x 0004 (LOC51184), mRNA /cds=(31,885) |
| | | | | | | genomic DNA, chromosome 21q, section 97/105 / |
| | | | | | | mRNA for BCG induced integral membrane protein |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|-----|--|
| 180C12 | 309 | 602 | BF381953 | Hs.284235 | 1.00E-148 | 2 | 601816251F1 cDNA, 5' end /clone=IMAGE:4050061 |
| 67D9 | 27 | 2026 | AK024969 | Hs.284249 | 0 | 10 | FLJ21316 fis, clone COL02253, highly sim |
| 39D1 | 307 | 2899 | U90552 | Hs.284283 | 0 | 5 | butyrophilin (BTF5) mRNA, complete cds /cds=(359,190) |
| 147C8 | 391 | 556 | AF161451 | Hs.284295 | 2.00E-58 | 1 | HSPC333 mRNA, partial cds /cds=(0,443) /gb=AF |
| 192C12 | 333 | 484 | AV700210 | Hs.284605 | 5.00E-57 | 1 | AV700210 cDNA, 3' end /clone=GKBALC03 /clone_ |
| 49G11 | 380 | 523 | AV700636 | Hs.284674 | 4.00E-33 | 1 | AV700636 cDNA, 3' end /clone=GKBAGH12 /clone_ |
| 115C11 | 375 | 1001 | AK023291 | Hs.285017 | 0 | 1 | cDNA FLJ13229 fis, clone OVARC1000106 /cds=(15 |
| 458H8 | 1544 | 2233 | AK023459 | Hs.285107 | 0 | 1 | cDNA FLJ13397 fis, clone PLACE1001351 /cds=(22 |
| 70F4 | 11 | 605 | AV700298 | Hs.285173 | 0 | 4 | AV700298 cDNA, 3' end /clone=GKCBVGO5 /clone_ |
| 66C6 | 684 | 1415 | NM_001300 | Hs.285313 | 0 | 5 | core promoter element binding protein (COPEB), |
| 169F2 | 4 | 460 | BF684382 | Hs.285555 | 0 | 2 | 602141836F1 5' end /clone=IMAGE:4302776 |
| 171F12 | 646 | 839 | X58529 | Hs.285823 | 6.00E-99 | 2 | rearranged immunoglobulin mRNA for mu heavy chain enh |
| 142F10 | 1438 | 1728 | AK025788 | Hs.285833 | 1.00E-152 | 1 | FLJ22135 fis, clone HEP20858 /cds=UNKNOWN |
| 171H2 | 1 | 2500 | AL050376 | Hs.285853 | 5.00E-21 | 1 | mRNA; cDNA DKFZp586J101 (from clone DKFZp586J1 |
| 40C5 | 786 | 1163 | AK026603 | Hs.286124 | 0 | 2 | FLJ22950 fis, clone KAT09618, highly sim |
| 458D9 | 55 | 684 | NM_016041 | Hs.286131 | 0 | 1 | CGI-101 protein (LOC51009), mRNA /cds=(6,635) |
| 458D1 | 1 | 310 | AK025886 | Hs.286194 | 1.00E-151 | 1 | cDNA: FLJ22233 fis, clone HRC02016 /cds=(35,12 |
| 515C10 | 817 | 1136 | AK021791 | Hs.286212 | 1.00E-138 | 1 | cDNA FLJ11729 fis, clone HEMBA1005394, modera |
| 71C7 | 285 | 2441 | AK026933 | Hs.286236 | 0 | 7 | cDNA: FLJ23280 fis, clone HEP07194 /cds=(468,1 |
| 184B9 | 372 | 612 | BE965319 | Hs.286754 | 3.00E-66 | 2 | 601659229R1 cDNA, 3' end /clone=IMAGE:3895783 |
| 586C12 | 18 | 381 | NM_000996 | Hs.287361 | 0 | 3 | ribosomal protein L35a (RPL35A), mRNA /cds=(6 |
| 36C6 | 152 | 685 | AJ277247 | Hs.287369 | 0 | 37 | for interleukin 21 (IL-21 gene) /cds=(71, |
| 513H8 | 17 | 690 | NM_020525 | Hs.287369 | 0 | 510 | interleukin 22 (IL22), mRNA /cds=(71,610) /gb |
| 586G2 | 3978 | 4107 | NM_021621 | Hs.287387 | 3.00E-68 | 1 | caspase recruitment domain protein 7 (CARD7), |
| 99D12 | 2330 | 2851 | NM_015906 | Hs.287414 | 0 | 1 | transcriptional intermediary factor 1 gamma (|
| 182A2 | 284 | 576 | AK024331 | Hs.287631 | 1.00E-156 | 1 | cDNA FLJ14269 fis, clone PLACE1003864 /cds=UN |
| 465A11 | 2226 | 2321 | AK024372 | Hs.287634 | 1.00E-42 | 1 | cDNA FLJ14310 fis, clone PLACE3000271 /cds=(40 |
| 190A11 | 679 | 1126 | AK026769 | Hs.287725 | 0 | 1 | cDNA: FLJ23116 fis, clone LNG07945, highly sim |
| 75E2 | 479 | 837 | AL390738 | Hs.287788 | 1.00E-146 | 3 | DNA sequence from clone RP11-438F9 on chromosome 13 C |
| 59B7 | 488 | 1071 | AK022537 | Hs.287863 | 0 | 1 | FLJ12475 fis, clone NT2RM1000962 /cds=(16 |
| 460E8 | 1611 | 1979 | AK024092 | Hs.287864 | 0 | 1 | cDNA FLJ14030 fis, clone HEMBA1004086 /cds=UNK |
| 465F11 | 5714 | 6271 | NM_006312 | Hs.287994 | 0 | 1 | nuclear receptor co-repressor 2 (NCOR2), mRNA |
| 150E12 | 2041 | 2720 | AK026834 | Hs.287995 | 0 | 3 | FLJ23181 fis, clone LNG11094 /cds=UNKNOWN |
| 52D9 | 703 | 1482 | AB016247 | Hs.288031 | 0 | 1 | for sterol-C5-desaturase, complete cds |
| 37F4 | 1091 | 1655 | AK025375 | Hs.288061 | 1.00E-141 | 20 | FLJ21722 fis, clone COLF0522, highly sim |
| 188G5 | 1081 | 1753 | NM_001101 | Hs.288061 | 0 | 69 | actin, beta (ACTB), mRNA /cds=(73,1200) /gb=N |
| 171C12 | 2103 | 2426 | AB046857 | Hs.288140 | 1.00E-158 | 1 | KIAA1637 protein, partial cds /cds=(0 |
| 104E8 | 1354 | 1790 | AK023078 | Hs.288141 | 0 | 1 | FLJ13016 fis, clone NT2RP3000624, modera |
| 181A4 | 1890 | 2507 | AK022030 | Hs.288178 | 0 | 2 | cDNA FLJ11968 fis, clone HEMBB1001133 /cds=UNK |
| 129A1 | 3522 | 3748 | J04144 | Hs.288204 | 1.00E-125 | 1 | angiotensin I-converting enzyme mRNA, complete cds / |
| 598D12 | 1464 | 1947 | AK025643 | Hs.288224 | 0 | 3 | cDNA: FLJ21990 fis, clone HEP06386 /cds=(22,49 |
| 52E6 | 920 | 1388 | AK023402 | Hs.288416 | 0 | 2 | FLJ13340 fis, clone OVARC1001942, weakly |
| 165E3 | 303 | 640 | NM_020666 | Hs.288417 | 0 | 1 | protein serine threonine kinase Clk4 (CLK4), |
| 53D3 | 1 | 153 | AK022280 | Hs.288435 | 6.00E-76 | 1 | FLJ12218 fis, clone MAMMA1001075, modera |
| 586C2 | 223 | 448 | BF110312 | Hs.288443 | 1.00E-63 | 3 | 7n36d08.x1 cDNA, 3' end /clone=IMAGE:3566654 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|--|
| 521F12 | 1922 | 2248 | AK026923 | Hs.288455 | 0 | 1 | cDNA: FLJ23270 fis, clone COL10309, highly sim |
| 120A11 | 825 | 1855 | AK026078 | Hs.288555 | 0 | 2 | cDNA: FLJ22425 fis, clone HRC08686 /cds=UNKNOWN |
| 129D11 | 1723 | 1984 | AK023470 | Hs.288673 | 1.00E-143 | 2 | FLJ13408 fis, clone PLACE1001672, weakly |
| 109B12 | 1686 | 2086 | AK025215 | Hs.288708 | 1.00E-121 | 8 | FLJ21562 fis, clone COL06420 /cds=(238,2 |
| 178F11 | 387 | 558 | NM_005402 | Hs.288757 | 3.00E-93 | 1 | v-ral simian leukemia viral oncogene homolog |
| 58F8 | 1262 | 1604 | AK022735 | Hs.288836 | 0 | 1 | cDNA FLJ12673 fis, clone NT2RM4002344 /cds=(2, |
| 163E11 | 360 | 1687 | AK024094 | Hs.288856 | 1.00E-25 | 2 | FLJ14032 fis, clone HEMBA1004353, highly |
| 105B4 | 741 | 1243 | AK025092 | Hs.288872 | 0 | 1 | FLJ21439 fis, clone COL04352 /cds=(206,1 |
| 106D10 | 1598 | 2291 | AB014515 | Hs.288891 | 0 | 3 | for KIAA0615 protein, complete cds /cds={ |
| 460F8 | 154 | 2487 | NM_021818 | Hs.288906 | 1.00E-150 | 2 | VW Domain-Containing Gene (VW45), mRNA /cds=(|
| 48A6 | 560 | 1258 | NM_017644 | Hs.288922 | 0 | 1 | hypothetical protein FLJ20059 (FLJ20059), mR |
| 168B10 | 1271 | 1747 | AK023320 | Hs.288929 | 0 | 1 | FLJ13258 fis, clone OVARC1000862, modera |
| 114E2 | 2395 | 2849 | AK023256 | Hs.288932 | 0 | 1 | cDNA FLJ13194 fis, clone NT2RP3004378, weakly |
| 586F9 | 368 | 730 | AK026363 | Hs.288936 | 1.00E-162 | 4 | cDNA: FLJ22710 fis, clone HSI13340 /cds=UNKNOWN |
| 180B4 | 831 | 959 | NM_000344 | Hs.288986 | 1.00E-32 | 1 | survival of motor neuron 1, telomeric (SMN1), |
| 149A12 | 10 | 1958 | AK025467 | Hs.289008 | 0 | 5 | FLJ21814 fis, clone HEP01068 /cds=UNKNOWN |
| 117B5 | 5160 | 5611 | NM_012231 | Hs.289024 | 1.00E-141 | 1 | PR domain containing 2, with ZNF domain (PRDM2) |
| 469A5 | 3132 | 3365 | AK024456 | Hs.289034 | 1.00E-106 | 1 | mRNA for FLJ00048 protein, partial cds /cds=(2 |
| 461F6 | 396 | 473 | AK024197 | Hs.289037 | 7.00E-37 | 1 | cDNA FLJ14135 fis, clone MAMMA1002728 /cds=UN |
| 176G11 | 1049 | 1811 | AK024669 | Hs.289069 | 0 | 4 | cDNA: FLJ21016 fis, clone CAE05735 /cds=(90,11 |
| 473A5 | 1343 | 1937 | NM_013326 | Hs.289080 | 0 | 1 | colon cancer-associated protein Mic1 (MIC1), |
| 591G2 | 14 | 2259 | NM_005348 | Hs.289088 | 0 | 14 | heat shock 90kD protein 1, alpha (HSPCA), mRNA |
| 70D3 | 21 | 2912 | X15183 | Hs.289088 | 0 | 17 | 90-kDa heat-shock protein /cds=(60,2258) /g |
| 37E8 | 780 | 1509 | AK026033 | Hs.289092 | 0 | 5 | FLJ22380 fis, clone HRC07453, highly sim |
| 74B10 | 408 | 791 | X00453 | Hs.289095 | 1.00E-153 | 2 | gene fragment for DX alpha-chain signal peptide, |
| 518B5 | 870 | 1128 | NM_005313 | Hs.289101 | 1.00E-119 | 1 | glucose regulated protein, 58kD (GRP58), mRNA |
| 472A3 | 116 | 304 | X83300 | Hs.289103 | 4.00E-84 | 1 | H.sapiens SMA4 mRNA /cds=(66,488) /gb=X83300 /gi=603028 / |
| 112G6 | 1703 | 2550 | NM_001166 | Hs.289107 | 0 | 5 | baculoviral IAP repeat-containing 2 (BIRC2), |
| 37F11 | 1996 | 2580 | U37547 | Hs.289107 | 0 | 2 | IAP homolog B (MIHB) mRNA, complete cds /cds=(1159,301 |
| 169A12 | 371 | 588 | X57812 | Hs.289110 | 2.00E-84 | 1 | rearranged immunoglobulin lambda light chain /c |
| 472D6 | 2102 | 2424 | AF294900 | Hs.289118 | 1.00E-121 | 1 | beta, beta-carotene 15,15'- dioxygenase (BCD |
| 151D1 | 2214 | 2294 | AK025846 | Hs.289721 | 1.00E-38 | 2 | FLJ22193 fis, clone HRC01108 /cds=UNKNOWN |
| 40A8 | 160 | 346 | AI761924 | Hs.289834 | 2.00E-94 | 1 | wg68h03.x1 cDNA, 3' end /clone=IMAGE:2370293 |
| 468D5 | 42 | 105 | AA719103 | Hs.290535 | 5.00E-29 | 1 | zh33d10.s1 cDNA, 3' end /clone=IMAGE:413875 / |
| 515B6 | 7 | 249 | AA837754 | Hs.291129 | 2.00E-61 | 1 | oe10d02.s1 cDNA /clone=IMAGE:1385475 /gb=AA |
| 594C9 | 16 | 319 | NM_005745 | Hs.291904 | 1.00E-150 | 1 | accessory proteins BAP31/BAP29 (DXS1357E), m |
| 476C10 | 180 | 311 | AI184710 | Hs.292276 | 8.00E-62 | 1 | qd64a01.x1 cDNA, 3' end /clone=IMAGE:1734216 |
| 466G5 | 65 | 431 | AA461604 | Hs.292451 | 0 | 1 | zx51d08.r1 cDNA, 5' end /clone=IMAGE:795759 / |
| 331F12 | 142 | 314 | BF310166 | Hs.292457 | 3.00E-85 | 1 | 601894826F1 cDNA, 5' end /clone=IMAGE:4124119 |
| 590D6 | 1 | 406 | BG339050 | Hs.292457 | 0 | 2 | 602436875F1 cDNA, 5' end /clone=IMAGE:4554643 |
| 150G5 | 160 | 431 | AI440234 | Hs.292490 | 6.00E-66 | 1 | ti99h12.x1 cDNA, 3' end /clone=IMAGE:2140199 |
| 594F8 | 319 | 447 | AA761571 | Hs.292519 | 1.00E-57 | 1 | nz23d06.s1 cDNA, 3' end /clone=IMAGE:1288619 |
| 122E2 | 91 | 307 | AI582954 | Hs.292553 | 4.00E-47 | 1 | tr98e07.x1 cDNA, 3' end /clone=IMAGE:2227140 |
| 41E5 | 363 | 463 | D59502 | Hs.292590 | 3.00E-48 | 1 | HUM041H11A cDNA, 3' end /clone=GEN-041H11 /cl |
| 99B8 | 215 | 378 | AI672433 | Hs.292615 | 6.00E-62 | 4 | wa03b05.x1 cDNA, 3' end /clone=IMAGE:2296977 |
| 72C6 | 198 | 484 | AA719537 | Hs.292877 | 1.00E-112 | 3 | zh40g12.s1 cDNA, 3' end /clone=IMAGE:414598 / |
| 157H5 | 49 | 447 | AI962127 | Hs.292901 | 1.00E-126 | 1 | wx77f07.x1 3' end /clone=IMAGE:2549701 |
| 115C2 | 2052 | 2613 | NM_006310 | Hs.293007 | 0 | 1 | aminopeptidase puromycin sensitive (NPEPPS), |
| 463F3 | 14 | 445 | AW629485 | Hs.293352 | 0 | 2 | hi59b07.x1 cDNA, 3' end /clone=IMAGE:2976565 |
| 193H8 | 94 | 333 | AI263141 | Hs.293444 | 7.00E-58 | 1 | qw90c01.x1 cDNA, 3' end /clone=IMAGE:1998336 |
| 170G9 | 46 | 713 | AI452611 | Hs.293473 | 9.00E-21 | 1 | tj27g07.x1 cDNA, 3' end /clone=IMAGE:2142780 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|---|
| 100F9 | 554 | 666 | BE905040 | Hs.293515 | 2.00E-43 | 1 | 601496859F1 cDNA, 5' end /clone=IMAGE:3898767 |
| 588G9 | 153 | 507 | BF794089 | Hs.293658 | 1.00E-143 | 1 | 602255649F1 cDNA, 5' end /clone=IMAGE:4338732 |
| 142G8 | 2 | 231 | AV701332 | Hs.293689 | 1.00E-79 | 1 | AV701332 cDNA, 5' end /clone=ADAABD03 /clone_ |
| 137A4 | 1 | 557 | BF029654 | Hs.293777 | 0 | 1 | 601765621F1 cDNA, 5' end /clone=IMAGE:3997900 |
| 478C6 | 442 | 622 | BE748123 | Hs.293842 | 3.00E-63 | 1 | 601571679F1 cDNA, 5' end /clone=IMAGE:3838675 |
| 100E7 | 198 | 488 | BE748663 | Hs.293842 | 1.00E-145 | 1 | 601571679T1 cDNA, 3' end /clone=IMAGE:3838675 |
| 110B4 | 246 | 469 | NM_016398 | Hs.293905 | 1.00E-122 | 1 | hypothetical protein (HSPC131), mRNA /cds=(1 |
| 466D2 | 198 | 543 | AW972477 | Hs.294083 | 1.00E-180 | 1 | EST384568 cDNA /gb=AW972477 /gi=8162323 /ug= |
| 100C10 | 1 | 398 | AW963235 | Hs.294092 | 0 | 2 | EST375308 /gb=AW963235 /gi=8153071 /ug= |
| 118F10 | 418 | 552 | BF245076 | Hs.294110 | 1.00E-48 | 1 | 601863910F1 cDNA, 5' end /clone=IMAGE:4082235 |
| 596H2 | 1150 | 2308 | BC002450 | Hs.294135 | 0 | 20 | ribosomal protein L4, clone MGC:776, mRNA, co |
| 596B4 | 139 | 414 | BE621121 | Hs.294309 | 7.00E-73 | 3 | 601493943F1 cDNA, 5' end /clone=IMAGE:3896051 |
| 114D4 | 600 | 738 | BE961923 | Hs.294348 | 8.00E-33 | 1 | 601655335R1 cDNA, 3' end /clone=IMAGE:3845768 |
| 66D11 | 185 | 625 | BE963811 | Hs.294578 | 1.00E-127 | 6 | 601657462R1 cDNA, 3' end /clone=IMAGE:3875846 |
| 53E11 | 433 | 701 | BE964149 | Hs.294612 | 5.00E-81 | 1 | 601657833R1 cDNA, 3' end /clone=IMAGE:3875984 |
| 179A11 | 442 | 776 | BF313856 | Hs.294754 | 9.00E-79 | 1 | 601902261F1 5' end /clone=IMAGE:4134998 |
| 102B9 | 146 | 347 | H71236 | Hs.295055 | 7.00E-90 | 2 | ys12f10.s1 cDNA, 3' end /clone=IMAGE:214603 / |
| 110F4 | 136 | 358 | H80108 | Hs.295107 | 1.00E-118 | 1 | yu09f02.s1 cDNA, 3' end /clone=IMAGE:233307 / |
| 593F2 | 78 | 381 | AF212224 | Hs.295231 | 1.00E-172 | 3 | CLK4 mRNA, complete cds /cds=(153,1514) /gb=A |
| 50G9 | 355 | 415 | AI052431 | Hs.295451 | 1.00E-26 | 2 | oz07e08.x1 cDNA, 3' end /clone=IMAGE:1674662 |
| 102E4 | 99 | 413 | AI560651 | Hs.295682 | 1.00E-146 | 8 | tq60f01.x1 cDNA, 3' end /clone=IMAGE:2213209 |
| 486F7 | 263 | 489 | BF572855 | Hs.295806 | 1.00E-100 | 1 | 602079424F2 cDNA, 5' end /clone=IMAGE:4254172 |
| 39C1 | 2054 | 2315 | AL050141 | Hs.295833 | 1.00E-144 | 6 | cDNA DKFZp586O031 (from clone DKFZp586O0 |
| 192D3 | 48 | 551 | AW081320 | Hs.295945 | 1.00E-158 | 4 | xc30f12.x1 cDNA, 3' end /clone=IMAGE:2585807 |
| 102B7 | 753 | 850 | AL117536 | Hs.295969 | 5.00E-39 | 1 | cDNA DKFZp434G012 (from clone DKFZp434G0 |
| 168D1 | 73 | 1193 | AL360190 | Hs.295978 | 1.00E-134 | 3 | mRNA full length insert cDNA clone EUROIMAGE 74 |
| 47D6 | 103 | 331 | AW150085 | Hs.295997 | 3.00E-79 | 8 | xg36f04.x1 cDNA, 3' end /clone=IMAGE:2629663 |
| 151H9 | 197 | 507 | AW264291 | Hs.296057 | 1.00E-113 | 1 | xq97g08.x1 cDNA, 3' end /clone=IMAGE:2758622 |
| 56A1 | 1034 | 1220 | AJ012504 | Hs.296151 | 3.00E-74 | 1 | activated in tumor suppression, clone TSA |
| 525D12 | 42 | 545 | AI922889 | Hs.296159 | 1.00E-148 | 42 | wn64g11.x1 cDNA, 3' end /clone=IMAGE:2450276 |
| 72C12 | 280 | 545 | AW166001 | Hs.296159 | 1.00E-84 | 10 | xf43e11.x1 cDNA, 3' end /clone=IMAGE:2620844 |
| 99B1 | 21 | 286 | BE259480 | Hs.296183 | 4.00E-81 | 3 | 601106571F1 cDNA, 5' end /clone=IMAGE:3342929 |
| 143F5 | 18 | 178 | BE962588 | Hs.296183 | 1.00E-55 | 1 | 601655929R1 cDNA, 3' end /clone=IMAGE:3855823 |
| 110A10 | 2115 | 2237 | AL096752 | Hs.296243 | 1.00E-61 | 1 | cDNA DKFZp434A012 (from clone DKFZp434A0 |
| 170G1 | 16 | 304 | BE964134 | Hs.296246 | 4.00E-96 | 1 | 601657818R1 cDNA, 3' end /clone=IMAGE:3876028 |
| 597G5 | 168 | 1564 | NM_014456 | Hs.296251 | 0 | 18 | programmed cell death 4 (PDCD4), mRNA /cds=(84 |
| 184A12 | 686 | 1564 | U96628 | Hs.296251 | 0 | 2 | nuclear antigen H731-like protein mRNA, compl |
| 479H10 | 247 | 540 | NM_002072 | Hs.296261 | 1.00E-117 | 1 | guanine nucleotide binding protein (G protein |
| 179H11 | 48 | 250 | BF315059 | Hs.296266 | 3.00E-56 | 1 | 601899090F1 5' end /clone=IMAGE:4128334 |
| 182E9 | 1576 | 2251 | AK023460 | Hs.296275 | 0 | 2 | FLJ13398 fis, clone PLACE1001377, highly |
| 459B11 | 305 | 545 | BF340402 | Hs.296317 | 1.00E-79 | 1 | 602036746F1 cDNA, 5' end /clone=IMAGE:4184602 |
| 459B12 | 349 | 721 | AK001838 | Hs.296323 | 0 | 1 | cDNA FLJ10976 fis, clone PLACE1001399 /cds=UN |
| 179F8 | 1 | 756 | BF342246 | Hs.296333 | 0 | 2 | 602013019F1 5' end /clone=IMAGE:4148741 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|-------|-------|-----------|-----------|-----------|----|--|
| 171D1 | 12 | 330 | AV693913 | Hs.296339 | 1.00E-100 | 1 | AV693913 cDNA, 5' end /clone=GKCDVG04 /clone_ |
| 39B9 | 1 | 297 | AB046771 | Hs.296350 | 1.00E-167 | 1 | for KIAA1551 protein, partial cds /cds=(0 |
| 36H12 | 547 | 1089 | M96995 | Hs.296381 | 0 | 2 | epidermal growth factor receptor-binding pro |
| 459F1 | 867 | 1020 | NM_014499 | Hs.296433 | 4.00E-76 | 1 | putative purinergic receptor (P2Y10), mRNA /c |
| 584A11 | 615 | 1287 | NM_006392 | Hs.296585 | 0 | 4 | nucleolar protein (KKE/D repeat) (NOP56), mRN |
| 593F7 | 209 | 752 | NM_005678 | Hs.296948 | 0 | 2 | SNRPN upstream reading frame (SNURF), transcr |
| 174F7 | 493 | 681 | BE253125 | Hs.297095 | 2.00E-60 | 5 | 601116648F1 cDNA, 5' end /clone=IMAGE:3357178 |
| 123H9 | 132 | 413 | BE965554 | Hs.297190 | 9.00E-88 | 1 | 601659486R1 cDNA, 3' end /clone=IMAGE:3896204 |
| 123D6 | 1105 | 1595 | AF113676 | Hs.297681 | 0 | 1 | clone FLB2803 PRO0684 mRNA, complete cds /cds= |
| 71C6 | 1076 | 1630 | NM_003380 | Hs.297753 | 0 | 2 | vimentin (VIM), mRNA /cds=(122,1522) /gb=NM_0 |
| 586G5 | 1179 | 1452 | NM_001908 | Hs.297939 | 1.00E-142 | 1 | cathepsin B (CTSB), mRNA /cds=(177,1196) /gb= |
| 521E7 | 1 | 220 | NM_001022 | Hs.298262 | 1.00E-119 | 4 | ribosomal protein S19 (RPS19), mRNA /cds=(22,4 |
| 466H7 | 9 | 339 | AW614181 | Hs.298654 | 1.00E-153 | 1 | hg77d03.x1 cDNA, 3' end /clone=IMAGE:2951621 |
| 464A4 | 675 | 1232 | BC001077 | Hs.299214 | 0 | 1 | clone IMAGE:2822295, mRNA, partial cds /cds= |
| 466F3 | 49 | 337 | AA132448 | Hs.299416 | 1.00E-141 | 1 | zo20a03.s1 cDNA, 3' end /clone=IMAGE:587404 / |
| 589B10 | 123 | 339 | AW073707 | Hs.299581 | 1.00E-55 | 30 | xb01h03.x1 cDNA, 3' end /clone=IMAGE:2575061 |
| 521H4 | 3 | 371 | NM_001000 | Hs.300141 | 1.00E-125 | 4 | ribosomal protein L39 (RPL39), mRNA /cds=(37,1 |
| 599F12 | 36 | 328 | AW243795 | Hs.300220 | 2.00E-67 | 1 | xc56f02.x1 cDNA, 3' end /clone=IMAGE:2707995 |
| 479A6 | 173 | 356 | AW262077 | Hs.300229 | 3.00E-64 | 1 | xq61e07.x1 cDNA, 3' end /clone=IMAGE:2755140 |
| 111C8 | 806 | 1350 | NM_018579 | Hs.300496 | 1.00E-147 | 6 | mitochondrial solute carrier (LOC51312), mRN |
| 459D8 | 1 | 679 | NM_014478 | Hs.300684 | 0 | 1 | calcitonin gene-related peptide-receptor co |
| 522C5 | 98 | 1360 | NM_001154 | Hs.300711 | 0 | 10 | annexin A5 (ANXA5), mRNA /cds=(192,1154) /gb= |
| 596B7 | 407 | 750 | NM_003130 | Hs.300741 | 2.00E-83 | 1 | sorcin (SRI), mRNA /cds=(12,608) /gb=NM_00313 |
| 191A3 | 210 | 440 | AA788623 | Hs.301104 | 4.00E-34 | 9 | ah29f09.s1 cDNA, 3' end /clone=1240265 /clone |
| 123E1 | 15 | 267 | BE963194 | Hs.301110 | 1.00E-60 | 11 | 601656811R1 cDNA, 3' end /clone=IMAGE:3865731 |
| 116F11 | 346 | 650 | NM_014029 | Hs.301175 | 2.00E-71 | 2 | HSPC022 protein (HSPC022), mRNA /cds=(18,623) |
| 58D4 | 489 | 611 | AW863111 | Hs.301183 | 8.00E-50 | 1 | MR3-SN0009-010400-101-f02 cDNA /gb=AW863111 |
| 122D8 | 3644 | 4034 | AB037808 | Hs.301434 | 0 | 1 | mRNA for KIAA1387 protein, partial cds /cds=(0 |
| 520F11 | 276 | 553 | BE886472 | Hs.301486 | 1.00E-111 | 1 | 601509688F1 cDNA, 5' end /clone=IMAGE:3911301 |
| 512E5 | 71 | 687 | NM_001011 | Hs.301547 | 0 | 8 | ribosomal protein S7 (RPS7), mRNA /cds=(81,665 |
| 463F9 | 168 | 689 | AV702152 | Hs.301570 | 0 | 1 | AV702152 cDNA, 5' end /clone=ADBBFH05 /clone_ |
| 117A12 | 2239 | 2395 | NM_007167 | Hs.301637 | 5.00E-78 | 1 | zinc finger protein 258 (ZNF258), mRNA /cds=(9 |
| 190A6 | 12942 | 13156 | AF155238 | Hs.301698 | 1.00E-114 | 1 | BAC 180i23 chromosome 8 map 8q24.3 beta-galacto |
| 594F12 | 1409 | 1841 | NM_005442 | Hs.301704 | 0 | 1 | eomesodermin (Xenopus laevis) homolog (EOMES) |
| 116G12 | 5477 | 5571 | AB033081 | Hs.301721 | 6.00E-47 | 1 | mRNA for KIAA1255 protein, partial cds /cds=(0 |
| 123C4 | 23 | 579 | BE260041 | Hs.301809 | 1.00E-129 | 4 | 601150579F1 cDNA, 5' end /clone=IMAGE:3503419 |
| 192E12 | 1458 | 1854 | NM_007145 | Hs.301819 | 0 | 1 | zinc finger protein 146 (ZNF146), mRNA /cds=(8 |
| 590G8 | 1100 | 1307 | AF132197 | Hs.301824 | 3.00E-57 | 1 | PRO1331 mRNA, complete cds /cds=(422,616) /gb |
| 482E5 | 1764 | 2139 | NM_001295 | Hs.301921 | 0 | 1 | chemokine (C-C motif) receptor 1 (CCR1), mRNA |
| 583C5 | 4283 | 4684 | NM_014415 | Hs.301956 | 0 | 1 | zinc finger protein (ZNF-U69274), mRNA /cds=(|
| 173G11 | 645 | 839 | X58529 | Hs.302063 | 1.00E-104 | 4 | rearranged immunoglobulin mRNA for mu heavy chain |
| 597D11 | 30 | 369 | AL137162 | Hs.302114 | 1.00E-150 | 5 | enh DNA sequence from clone RP5-843L14 on |
| 191G9 | 182 | 353 | AC004079 | Hs.302183 | 9.00E-60 | 1 | chromosome 20. PAC clone RP1-167F23 from 7p15 /cds=(0,559) /g |
| 473D2 | 102 | 333 | BF477640 | Hs.302447 | 1.00E-126 | 1 | 7r01c05.x1 cDNA /clone=IMAGE /gb=BF477640 /g |
| 479A9 | 18 | 267 | BE964028 | Hs.302585 | 7.00E-79 | 1 | 601657601R1 cDNA, 3' end /clone=IMAGE:3875617 |
| 180A5 | 894 | 1325 | NM_018295 | Hs.302981 | 0 | 2 | hypothetical protein FLJ11000 (FLJ11000), mR |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|---|
| 593H6 | 950 | 1151 | X00437 | Hs.303157 | 1.00E-104 | 1 | mRNA for T-cell specific protein /cds=(37,975) /gb=X0 |
| 51G12 | 274 | 533 | BG054649 | Hs.303214 | 1.00E-138 | 4 | 7o45b01.x1 cDNA, 3' end /clone=IMAGE:3576912 |
| 189B10 | 785 | 1024 | NM_002138 | Hs.303627 | 1.00E-133 | 2 | heterogeneous nuclear ribonucleoprotein D (|
| 99B11 | 1 | 529 | NM_002982 | Hs.303649 | 0 | 51 | small inducible cytokine A2 (monocyte chemota |
| 461E1 | 397 | 496 | AI472078 | Hs.303662 | 2.00E-28 | 1 | tj85h03.x1 cDNA, 3' end /clone=IMAGE:2148341 |
| 103A1 | 359 | 687 | AF130085 | Hs.304177 | 1.00E-151 | 1 | clone FLB8503 PRO2286 mRNA, complete cds /cds |
| 180B11 | 52 | 240 | AI824522 | Hs.304477 | 4.00E-57 | 1 | tx71d03.x1 cDNA, 3' end /clone=IMAGE:2275013 |
| 519A10 | 1 | 104 | AI880542 | Hs.304620 | 3.00E-26 | 1 | at80h05.x1 cDNA, 3' end /clone=IMAGE:2378361 |
| 479F6 | 331 | 582 | AA873734 | Hs.304886 | 1.00E-131 | 1 | oh55h07.s1 cDNA, 3' end /clone=IMAGE:1470589 |
| 176G3 | 61 | 324 | AI904802 | Hs.304919 | 2.00E-74 | 1 | IL-BT067-190199-037 cDNA /gb=AI904802 /gi=6 |
| 471G6 | 169 | 397 | AW592876 | Hs.304925 | 1.00E-122 | 1 | hg04d05.x1 cDNA, 3' end /clone=IMAGE:2944617 |
| 119D11 | 3 | 348 | AL049282 | Hs.306030 | 1.00E-179 | 1 | mRNA; cDNA DKFZp564M113 (from clone DKFZp564M1 |
| 112F7 | 2398 | 3008 | U80743 | Hs.306094 | 0 | 1 | CAGH32 mRNA, partial cds /cds=(0,1671) /gb=U80 |
| 460C1 | 243 | 533 | NM_001353 | Hs.306098 | 5.00E-71 | 1 | aldo-keto reductase family 1, member C1 (dihy |
| 126A4 | 469 | 543 | L08048 | Hs.306192 | 2.00E-28 | 1 | non-histone chromosomal protein (HMG-1) retropseudo |
| 119F3 | 2113 | 2237 | AL096752 | Hs.306327 | 3.00E-60 | 1 | mRNA; cDNA DKFZp434A012 (from clone DKFZp434A0 |
| 467F8 | 1860 | 2406 | AL390039 | Hs.307106 | 0 | 1 | DNA sequence from clone RP13-383K5 on chromosome Xq22 |
| 192B12 | 1 | 454 | X72475 | Hs.307183 | 0 | 6 | H.sapiens mRNA for rearranged Ig kappa light chain variable |
| 116H11 | 60 | 402 | AF067519 | Hs.307357 | 1.00E-160 | 1 | PITSLRE protein kinase beta SV1 isoform (CDC2L |
| 472D3 | 150 | 478 | AW975895 | Hs.307486 | 1.00E-124 | 1 | EST388004 cDNA /gb=AW975895 /gi=8167117 /ug= |
| 458B4 | 87 | 354 | AW206977 | Hs.307542 | 1.00E-143 | 1 | UI-H-BI1-afs-h-11-0-UI.s1 cDNA, 3' end /clon |
| 463A11 | 181 | 397 | AI057025 | Hs.307879 | 1.00E-69 | 1 | oy75a12.x1 cDNA, 3' end /clone=IMAGE:1671646 |
| 479C6 | 138 | 403 | BE264564 | Hs.308154 | 1.00E-144 | 1 | 601192330F1 cDNA, 5' end /clone=IMAGE:3536383 |
| 468G10 | 118 | 446 | AI361642 | Hs.309028 | 0 | 1 | qy86d04.x1 cDNA, 3' end /clone=IMAGE:2018887 |
| 461G12 | 64 | 466 | AI379735 | Hs.309117 | 7.00E-25 | 1 | tc41c11.x1 cDNA, 3' end /clone=IMAGE:2067188 |
| 466H8 | 15 | 487 | AI380278 | Hs.309120 | 0 | 1 | tf99f08.x1 cDNA, 3' end /clone=IMAGE:2107431 |
| 477C8 | 28 | 187 | AI380449 | Hs.309122 | 7.00E-84 | 1 | tg02f12.x1 cDNA, 3' end /clone=IMAGE:2107631 |
| 477C9 | 47 | 537 | AI380687 | Hs.309127 | 0 | 1 | tg03e04.x1 cDNA, 3' end /clone=IMAGE:2107710 |
| 465F4 | 68 | 631 | AI440337 | Hs.309279 | 0 | 1 | tc88b03.x1 cDNA, 3' end /clone=IMAGE:2073197 |
| 465G6 | 313 | 404 | AI475653 | Hs.309347 | 9.00E-31 | 1 | tc93b04.x1 cDNA, 3' end /clone=IMAGE:2073679 |
| 465E7 | 1 | 340 | AI475827 | Hs.309349 | 1.00E-171 | 2 | tc87a05.x1 cDNA, 3' end /clone=IMAGE:2073104 |
| 517G11 | 62 | 516 | AI707809 | Hs.309433 | 1.00E-115 | 2 | as28g09.x1 cDNA, 3' end /clone=IMAGE:2318560 |
| 468D11 | 290 | 497 | AI523766 | Hs.309484 | 1.00E-103 | 1 | tg94f07.x1 cDNA, 3' end /clone=IMAGE:2116453 |
| 186F5 | 77 | 418 | AI569898 | Hs.309629 | 1.00E-81 | 1 | tr57c12.x1 cDNA, 3' end /clone=IMAGE:2222422 |
| 116A12 | 8 | 158 | AI735206 | Hs.310333 | 2.00E-43 | 1 | at07f03.x1 cDNA, 3' end /clone=IMAGE:2354429 |
| 126G12 | 35 | 170 | AI866194 | Hs.310948 | 1.00E-54 | 1 | wl27a03.x1 cDNA, 3' end /clone=IMAGE:2426092 |
| 172G8 | 86 | 227 | AI926251 | Hs.311137 | 3.00E-44 | 1 | wo41h05.x1 cDNA, 3' end /clone=IMAGE:2457945 |
| 477D8 | 1 | 115 | AI968387 | Hs.311448 | 4.00E-42 | 2 | wu02e08.x1 cDNA, 3' end /clone=IMAGE:2515814 |
| 462F10 | 13 | 220 | AW043857 | Hs.311783 | 1.00E-107 | 1 | wy81g04.x1 cDNA, 3' end /clone=IMAGE:2554998 |
| 185A9 | 46 | 423 | AW130007 | Hs.312182 | 1.00E-130 | 2 | xf26f10.x1 cDNA, 3' end /clone=IMAGE:2619211 |
| 515F6 | 34 | 181 | AW148618 | Hs.312412 | 3.00E-58 | 2 | xe99f02.x1 cDNA, 3' end /clone=IMAGE:2616699 |
| 583E12 | 5945 | 6393 | AL133572 | Hs.312840 | 0 | 1 | mRNA; cDNA DKFZp434I0535 (from clone DKFZp434I |
| 471D5 | 306 | 411 | AW298430 | Hs.313413 | 1.00E-46 | 1 | UI-H-BW0-ajl-c-09-0-UI.s1 cDNA, 3' end /clon |
| 482F7 | 1 | 449 | AW440965 | Hs.313578 | 0 | 1 | he06d07.x1 cDNA, 3' end /clone=IMAGE:2918221 |
| 473B3 | 179 | 463 | BG150461 | Hs.313610 | 1.00E-135 | 1 | 7k01d08.x1 cDNA, 3' end /clone=IMAGE:3443006 |
| 479E9 | 138 | 434 | AW450835 | Hs.313715 | 1.00E-127 | 1 | UI-H-BI3-alf-f-06-0-UI.s1 cDNA, 3' end /clon |
| 71B9 | 344 | 577 | AI733018 | Hs.313929 | 1.00E-115 | 1 | oh60h01.x5 cDNA, 3' end /clone=IMAGE:1471441 |
| 479B6 | 217 | 443 | AW629176 | Hs.314085 | 2.00E-70 | 1 | hi52a04.x1 cDNA, 3' end /clone=IMAGE:2975886 |
| 191F11 | 55 | 123 | BE255377 | Hs.314898 | 1.00E-26 | 1 | 601115405F1 cDNA, 5' end /clone=IMAGE:3355872 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|----|---|
| 522F11 | 14 | 204 | BE962883 | Hs.314941 | 9.00E-83 | 3 | 601656423R1 cDNA, 3' end /clone=IMAGE:3856325 |
| 195F12 | 120 | 363 | BE351010 | Hs.315050 | 2.00E-77 | 1 | ht22g04.x1 cDNA, 3' end /clone=IMAGE:3147510 |
| 173A5 | 429 | 824 | BE410105 | Hs.315263 | 1.00E-133 | 1 | 601302278F1 cDNA, 5' end /clone=IMAGE:3637002 |
| 481B2 | 1063 | 1283 | NM_006255 | Hs.315366 | 3.00E-72 | 1 | protein kinase C, eta (PRKCH), mRNA /cds=(166,2 |
| 459G1 | 1428 | 1700 | NM_006850 | Hs.315463 | 1.00E-124 | 1 | suppression of tumorigenicity 16 (melanoma di |
| 113H4 | 22 | 359 | BE901218 | Hs.315633 | 1.00E-127 | 2 | 601676034F1 cDNA, 5' end /clone=IMAGE:3958617 |
| 583B7 | 510 | 754 | BE963666 | Hs.316047 | 2.00E-55 | 2 | 601656685R1 cDNA, 3' end /clone=IMAGE:3865820 |
| 466E10 | 488 | 644 | AV729160 | Hs.316771 | 1.00E-54 | 1 | AV729160 cDNA, 5' end /clone=HTCCAB04 /clone_ |
| 597A6 | 50 | 249 | AV710763 | Hs.316785 | 4.00E-31 | 2 | AV710763 cDNA, 5' end /clone=CuAAJH09 /clone_ |
| 123C3 | 41 | 529 | BF183507 | Hs.318215 | 1.00E-158 | 1 | 601809991R1 cDNA, 3' end /clone=IMAGE:4040470 |
| 193E12 | 15 | 2274 | NM_006074 | Hs.318501 | 0 | 7 | stimulated trans-acting factor (50 kDa) (STAF |
| 165D8 | 727 | 1344 | BC002867 | Hs.318693 | 0 | 1 | clone IMAGE:3940519, mRNA, partial cds /cds= |
| 49F8 | 520 | 1094 | M16942 | Hs.318720 | 0 | 1 | MHC class II HLA-DRw53-associated glycoprotein beta- |
| 172E10 | 310 | 944 | NM_016018 | Hs.318725 | 0 | 1 | CGI-72 protein (LOC51105), mRNA /cds=(69,1400 |
| 585B1 | 51 | 296 | BF696330 | Hs.318782 | 6.00E-90 | 4 | 602125273F1 cDNA, 5' end /clone=IMAGE:4281906 |
| 45E12 | 208 | 737 | NM_000636 | Hs.318885 | 0 | 7 | superoxide dismutase 2, mitochondrial (SOD2) |
| 460G2 | 409 | 663 | BG106948 | Hs.318893 | 5.00E-96 | 1 | 602291361F1 cDNA, 5' end /clone=IMAGE:4386159 |
| 480C1 | 155 | 325 | BF889206 | Hs.319926 | 4.00E-74 | 1 | RC6-TN0073-041200-013-H02 cDNA /gb=BF889206 |
| 178F1 | 1 | 387 | BG112503 | Hs.320972 | 1.00E-133 | 3 | 602282105F1 cDNA, 5' end /clone=IMAGE:4369633 |
| 176G4 | 1092 | 1339 | AL110236 | Hs.321022 | 1.00E-136 | 1 | mRNA; cDNA DKFZp566P1124 (from clone DKFZp566P |
| 461H6 | 1701 | 2239 | NM_024101 | Hs.321130 | 0 | 1 | hypothetical protein MGC2771 (MGC2771), mRNA |
| 513F2 | 605 | 1614 | AK001111 | Hs.321245 | 0 | 2 | cDNA FLJ10249 fis, clone HEMBB1000725, highly |
| 525B4 | 9 | 251 | BE871962 | Hs.321262 | 6.00E-98 | 15 | 601448005F1 cDNA, 5' end /clone=IMAGE:3852001 |
| 467A4 | 1974 | 2223 | AK026270 | Hs.321454 | 6.00E-87 | 1 | cDNA: FLJ22617 fis, clone HSI05379, highly sim |
| 589F10 | 39 | 276 | BF970928 | Hs.321477 | 5.00E-77 | 1 | 602270204F1 cDNA, 5' end /clone=IMAGE:4358425 |
| 125A7 | 1102 | 1584 | BC000627 | Hs.321677 | 0 | 1 | Signal transducer and activator of transcript |
| 597H3 | 2786 | 2920 | AL136542 | Hs.322456 | 4.00E-46 | 2 | mRNA; cDNA DKFZp761D0211 (from clone DKFZp761D |
| 465E2 | 40 | 107 | BE747224 | Hs.322643 | 7.00E-22 | 1 | 601580941F1 cDNA, 5' end /clone=IMAGE:3929386 |
| 515A12 | 1 | 698 | AL050376 | Hs.322645 | 0 | 2 | mRNA; cDNA DKFZp586J101 (from clone DKFZp586J1 |
| 589H11 | 26 | 265 | BG283132 | Hs.322653 | 4.00E-79 | 6 | 602406784F1 cDNA, 5' end /clone=IMAGE:4518957 |
| 586E5 | 1939 | 2162 | AK025200 | Hs.322680 | 1.00E-120 | 3 | cDNA: FLJ21547 fis, clone COL06206 /cds=UNKNOW |
| 595A2 | 1 | 306 | BG311130 | Hs.322804 | 2.00E-70 | 2 | ia55a08.y1 cDNA, 5' end /clone_end=5' /gb=BG3 |
| 459H11 | 742 | 951 | BC002746 | Hs.322824 | 1.00E-111 | 1 | Similar to dodecenoyl-Coenzyme A delta isome |
| 64C3 | 655 | 887 | NM_020368 | Hs.322901 | 1.00E-112 | 1 | disrupter of silencing 10 (SAS10), mRNA /cds=(|
| 591B8 | 3626 | 4574 | D80006 | Hs.322903 | 0 | 3 | mRNA for KIAA0184 gene, partial cds /cds=(0,2591) /gb |
| 458C3 | 5106 | 5198 | NM_003035 | Hs.323032 | 3.00E-43 | 1 | TAL1 (SCL) interrupting locus (SIL), mRNA /cds |
| 526B7 | 2132 | 2750 | NM_024334 | Hs.323193 | 0 | 2 | hypothetical protein MGC3222 (MGC3222), mRNA |
| 167F4 | 467 | 731 | NM_014953 | Hs.323346 | 1.00E-136 | 2 | KIAA1008 protein (KIAA1008), mRNA /cds=(93,28 |
| 194B8 | 1913 | 3596 | AB051480 | Hs.323463 | 0 | 9 | mRNA for KIAA1693 protein, partial cds /cds=(0 |
| 478H9 | 75 | 564 | BF700502 | Hs.323662 | 0 | 1 | 602128860F1 cDNA, 5' end /clone=IMAGE:4285502 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|-----------|-----------|---|--|
| 119B1 | 1598 | 2284 | NM_014664 | Hs.323712 | 0 | 2 | KIAA0615 gene product (KIAA0615), mRNA /cds=(|
| 167H2 | 1410 | 3683 | AB046771 | Hs.323822 | 0 | 4 | mRNA for KIAA1551 protein, partial cds /cds=(0 |
| 595C12 | 1 | 528 | NM_021998 | Hs.323950 | 0 | 6 | zinc finger protein 6 (CMPX1) (ZNF6), mRNA /cd |
| 462F1 | 1 | 356 | AK026836 | Hs.324060 | 1.00E-176 | 1 | cDNA: FLJ23183 fis, clone LNG11477 /cds=(226,7 |
| 122D10 | 217 | 424 | AK026091 | Hs.324187 | 2.00E-83 | 1 | cDNA: FLJ22438 fis, clone HRC09232, highly sim |
| 525B2 | 1028 | 3282 | AL136739 | Hs.324275 | 0 | 2 | mRNA; cDNA DKFZp434D2111 (from clone |
| 459B6 | 3 | 482 | BF668584 | Hs.324342 | 0 | 1 | DKFZp434D |
| 583D10 | 232 | 466 | NM_021104 | Hs.324406 | 1.00E-130 | 2 | 602123634F1 cDNA, 5' end /clone=IMAGE:4280408 |
| 118F8 | 2262 | 2819 | NM_016824 | Hs.324470 | 0 | 1 | ribosomal protein L41 (RPL41), mRNA /cds=(83,1 |
| 461A5 | 46 | 391 | AW968541 | Hs.324481 | 1.00E-111 | 1 | adducin 3 (gamma) (ADD3), transcript variant 1 |
| 467F11 | 927 | 1189 | NM_000817 | Hs.324784 | 1.00E-147 | 1 | EST380617 cDNA /gb=AW968541 /gi=8158382 /ug= |
| 103E12 | 1686 | 1771 | AK024863 | Hs.325093 | 9.00E-42 | 1 | glutamate decarboxylase 1 (brain, 67kD) (GAD1 |
| 521E11 | 4276 | 4689 | AB028990 | Hs.325530 | 0 | 1 | cDNA: FLJ21210 fis, clone COL00479 /cds=UNKNOWN |
| 480A9 | 112 | 333 | AA760848 | Hs.325874 | 1.00E-108 | 1 | mRNA for KIAA1067 protein, partial cds /cds=(0 |
| 71G8 | 2619 | 2868 | NM_001964 | Hs.326035 | 1.00E-116 | 1 | nz14f06.s1 cDNA, 3' end /clone=IMAGE:1287779 |
| 593D6 | 742 | 3372 | NM_004735 | Hs.326159 | 0 | 4 | early growth response 1 (EGR1), mRNA /cds=(270, |
| 463G9 | 42 | 608 | AW975482 | Hs.326165 | 0 | 1 | leucine rich repeat (in FLII) interacting prot |
| 526B12 | 2380 | 2639 | U83857 | Hs.326247 | 1.00E-143 | 2 | EST387591 cDNA /gb=AW975482 /gi=8166696 /ug= |
| 36A1 | 63 | 338 | AA010282 | NA | 1.00E-116 | 1 | Aac11 (aac11) mRNA, complete cds /cds=(77,1663) |
| 459D10 | 67 | 164 | AA044450 | NA | 3.00E-47 | 1 | /gb= |
| 469E6 | 1 | 216 | AA069335 | NA | 1.00E-104 | 1 | zi08h07.r1 Soares_fetal_liver_spleen_1NFLS_S1 |
| 463B2 | 4 | 205 | AA077131 | NA | 4.00E-88 | 1 | cDNA |
| 68H9 | 17 | 383 | AA101212 | NA | 0 | 1 | zk55a02.r1 Soares_pregnant_uterus_NbHPU cDNA |
| 458F3 | 120 | 498 | AA115345 | NA | 0 | 1 | clone |
| 459E6 | 36 | 532 | AA122297 | NA | 0 | 1 | zf74e10.r1 Soares_pineal_gland_N3HPG cDNA clone |
| 462C5 | 1 | 122 | AA136584 | NA | 2.00E-59 | 1 | Brain cDNA Library cDNA clone 7B08E10 |
| 594A1 | 60 | 412 | AA149078 | NA | 0 | 1 | endothelial cell 937223 cDNA clone IMAGE:549605 3' |
| 515A9 | 329 | 449 | AA182528 | NA | 2.00E-46 | 1 | zi09f11.r1 Soares_pregnant_uterus_NbHPU cDNA |
| 75H4 | 7 | 371 | AA187234 | NA | 1.00E-119 | 1 | clone |
| 73F10 | 1 | 544 | AA210786 | NA | 0 | 1 | zk97a11.r1 Soares_pregnant_uterus_NbHPU cDNA |
| 525D8 | 1 | 119 | AA214691 | NA | 6.00E-60 | 1 | clone |
| 37H4 | 250 | 401 | AA243144 | NA | 3.00E-48 | 1 | zk97a11.r1 Soares_pregnant_uterus_NbHPU cDNA |
| 463B10 | 145 | 408 | AA250809 | NA | 1.00E-123 | 1 | clone |
| 464E10 | 1 | 303 | AA251184 | NA | 1.00E-119 | 1 | clone |
| 477H8 | 1 | 123 | AA252909 | NA | 4.00E-58 | 3 | clone |
| 465C3 | 1 | 279 | AA258979 | NA | 1.00E-129 | 1 | clone |
| 588G6 | 275 | 529 | AA280051 | NA | 2.00E-94 | 1 | clone |
| 465E9 | 74 | 429 | AA282774 | NA | 0 | 1 | clone |
| 459E7 | 49 | 466 | AA283061 | NA | 0 | 1 | clone |
| 164B4 | 41 | 329 | AA284232 | NA | 1.00E-148 | 2 | clone |
| 461G8 | 289 | 532 | AA290921 | NA | 1.00E-123 | 1 | clone |
| 470G7 | 29 | 441 | AA290993 | NA | 0 | 1 | clone |
| 500A12 | 1 | 519 | AA307854 | NA | 1.00E-174 | 1 | clone |
| 471F4 | 9 | 326 | AA309188 | NA | 1.00E-153 | 1 | (HCC) cell line cDNA 5' end similar to |
| 194B6 | 134 | 467 | AA312681 | NA | 1.00E-163 | 1 | cDNA |
| | | | | | | | cDNA 5' end |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|----------|----|-----------|----|--|
| 69F3 | 5 | 321 | AA314369 | NA | 1.00E-176 | 1 | (HCC) cell line II cDNA 5' end similar |
| 67G10 | 1 | 171 | AA319163 | NA | 3.00E-64 | 2 | cDNA 5' end |
| 99A5 | 1 | 287 | AA322158 | NA | 1.00E-136 | 1 | cDNA 5' end similar to similar to tropomyosin |
| 171B1 | 13 | 310 | AA332553 | NA | 1.00E-135 | 1 | cDNA 5' end |
| 485D11 | 46 | 210 | AA360634 | NA | 2.00E-75 | 1 | cDNA 5' end |
| 462G2 | 1 | 183 | AA377352 | NA | 4.00E-89 | 2 | cDNA 5' end |
| 523A8 | 1 | 407 | AA397592 | NA | 0 | 1 | cDNA clone IMAGE:728546 5' |
| 171G10 | 1 | 409 | AA401648 | NA | 0 | 2 | cDNA clone IMAGE:726936 5' |
| 100F5 | 42 | 172 | AA402069 | NA | 4.00E-60 | 1 | cDNA clone IMAGE:727161 5' |
| 459H7 | 48 | 375 | AA412436 | NA | 1.00E-163 | 1 | cDNA clone IMAGE:731446 5' |
| 102A8 | 25 | 120 | AA418765 | NA | 1.00E-46 | 1 | cDNA clone IMAGE:767795 5' |
| 73A3 | 1 | 424 | AA426506 | NA | 0 | 1 | cDNA clone IMAGE:768117 5' |
| 72E10 | 1 | 442 | AA427653 | NA | 0 | 11 | tumor NbHOT cDNA clone IMAGE:770045 5' |
| 72A1 | 1 | 261 | AA429783 | NA | 1.00E-142 | 1 | zw57b01.r1 Soares_total_fetus_Nb2HF8_9w cDNA clone |
| 460D12 | 126 | 388 | AA431959 | NA | 1.00E-93 | 1 | cDNA clone IMAGE:782188 3' |
| 460B11 | 1 | 437 | AA454987 | NA | 0 | 1 | cDNA clone IMAGE:811916 5' |
| 518A8 | 1 | 329 | AA457757 | NA | 1.00E-177 | 1 | fetal retina 937202 cDNA clone IMAGE:838756 5' |
| 460F7 | 47 | 490 | AA460876 | NA | 0 | 1 | zx69d04.r1 Soares_total_fetus_Nb2HF8_9w cDNA clone |
| 118H12 | 1 | 304 | AA476568 | NA | 1.00E-163 | 1 | zx02f11.r1 Soares_total_fetus_Nb2HF8_9w cDNA clone |
| 40F11 | 1 | 533 | AA479163 | NA | 0 | 1 | cDNA clone IMAGE:754246 5' similar to gb:X15606 |
| 470F3 | 76 | 356 | AA482019 | NA | 1.00E-142 | 1 | cDNA clone IMAGE:746046 3' |
| 466C2 | 1 | 354 | AA490796 | NA | 1.00E-148 | 1 | cDNA clone IMAGE:824101 5' |
| 464A9 | 228 | 364 | AA496483 | NA | 7.00E-71 | 1 | tumor NbHOT cDNA clone IMAGE:755690 5' similar to |
| 123D11 | 99 | 297 | AA501725 | NA | 1.00E-103 | 1 | cDNA clone IMAGE:929806 similar to contains Alu |
| 119G10 | 128 | 374 | AA501934 | NA | 1.00E-134 | 1 | cDNA clone IMAGE:956346 |
| 166A11 | 19 | 140 | AA516406 | NA | 1.00E-48 | 1 | cDNA clone IMAGE:923858 3' |
| 36G1 | 5 | 480 | AA524720 | NA | 0 | 1 | cDNA clone IMAGE:937468 3' |
| 109H9 | 37 | 286 | AA573427 | NA | 1.00E-130 | 2 | cDNA clone IMAGE:1028913 3' |
| 477B2 | 8 | 273 | AA579400 | NA | 1.00E-143 | 1 | cDNA clone IMAGE:915561 similar to contains Alu |
| 178C10 | 1 | 354 | AA588755 | NA | 1.00E-177 | 1 | cDNA clone IMAGE:1084243 3' |
| 486G7 | 35 | 99 | AA613460 | NA | 6.00E-28 | 1 | cDNA clone IMAGE:1144571 similar to contains |
| 472E9 | 27 | 389 | AA628833 | NA | 1.00E-119 | 1 | af37g04.s1 Soares_total_fetus_Nb2HF8_9w cDNA clone |
| 100C3 | 122 | 505 | AA639796 | NA | 0 | 1 | cDNA clone IMAGE:1159029 3' |
| 518A7 | 39 | 226 | AA665359 | NA | 4.00E-83 | 1 | cDNA clone IMAGE:1205697 similar to |
| 473D9 | 377 | 446 | AA683244 | NA | 1.00E-30 | 1 | schizo brain S11 cDNA clone IMAGE:971252 3' |
| 523D7 | 80 | 502 | AA701667 | NA | 1.00E-158 | 1 | zi43g09.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA |
| 472B1 | 37 | 130 | AA744774 | NA | 1.00E-35 | 1 | cDNA clone IMAGE:1283731 3' |
| 98C9 | 10 | 254 | AA748714 | NA | 1.00E-111 | 1 | cDNA clone IMAGE:1270595 3' |
| 196D7 | 3 | 442 | AA806222 | NA | 0 | 1 | cDNA clone IMAGE:1409989 3' |
| 118A8 | 10 | 381 | AA806766 | NA | 0 | 1 | cDNA clone IMAGE:1338727 3' |
| 98B3 | 56 | 159 | AA826572 | NA | 7.00E-47 | 1 | cDNA clone IMAGE:1416447 3' |
| 154D9 | 38 | 405 | AA846378 | NA | 1.00E-164 | 1 | cDNA clone IMAGE:1394232 3' |
| 459C2 | 1 | 491 | AA909983 | NA | 0 | 2 | Soares_NFL_T_GBC_S1 cDNA clone IMAGE:1523142 3' |
| 486A7 | 1 | 176 | AA916990 | NA | 1.00E-72 | 1 | Soares_NFL_T_GBC_S1 cDNA clone IMAGE:1527333 3' |
| 460D2 | 78 | 537 | AA923567 | NA | 0 | 1 | cDNA clone IMAGE:1536231 3' |
| 105F4 | 86 | 390 | AA974839 | NA | 4.00E-94 | 1 | cDNA clone IMAGE:1567639 3' |
| 461H7 | 295 | 383 | AA974991 | NA | 2.00E-30 | 1 | Soares_NFL_T_GBC_S1 cDNA clone IMAGE:1560953 3' |
| 162B1 | 398 | 470 | AA976045 | NA | 9.00E-28 | 1 | cDNA clone IMAGE:1558392 3' |
| 53D8 | 1 | 422 | AA984245 | NA | 1.00E-162 | 1 | schizo brain S11 cDNA clone IMAGE:1629672 3' |
| 524A5 | 3568 | 4037 | AB020681 | NA | 0 | 1 | mRNA for KIAA0874 protein, partial cds Length = 4440 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|----------|----|-----------|-----|--|
| 174H3 | 81 | 271 | AB021288 | NA | 1.00E-101 | 1 | mRNA for beta 2-microglobulin, complete cds Length = 925 |
| 115A2 | 1920 | 2309 | AB034747 | NA | 0 | 4 | SIMPLE mRNA for small integral membrane protein of lysosome/late endos |
| 39G7 | 1578 | 1920 | AB040875 | NA | 1.00E-135 | 3 | hxCT mRNA for cystine/glutamate exchanger, complete cds Length = 2000 |
| 149H2 | 430 | 713 | AB044971 | NA | 1.00E-158 | 1 | mRNA for nucleolar phosphoprotein Nopp34, complete cds Length = 1005 |
| 458F6 | 780 | 1235 | AB045118 | NA | 0 | 1 | FRAT2 mRNA, complete cds Length = 2164 |
| 459D12 | 2694 | 3564 | AB045278 | NA | 0 | 2 | beta3GnT5 mRNA for beta1,3-N-acetylglucosaminyltransferase 5, complete |
| 103H7 | 1294 | 1933 | AB049881 | NA | 1.00E-139 | 1 | similar to Macaca fascicularis brain cDNA, clone:QnpA-18828 Length = 2517 |
| 102E11 | 1142 | 1772 | AB050511 | NA | 0 | 1 | similar to Macaca fascicularis brain cDNA, clone:QnpA-18828 Length = 2518 |
| 460C3 | 798 | 930 | AB050514 | NA | 9.00E-54 | 1 | similar to Macaca fascicularis brain cDNA, clone:QnpA-18828 Length = 2519 |
| 480A10 | 4649 | 5183 | AB058677 | NA | 0 | 1 | mRNA for MEGF11 protein (KIAA1781), complete cds Length = 5702 |
| 142G10 | 2251 | 2430 | AB060884 | NA | 6.00E-44 | 1 | similar to Macaca fascicularis brain cDNA clone:QtrA-13024, full insert sequence |
| 494G5 | 1585 | 1998 | AF005213 | NA | 0 | 1 | ankyrin 1 (ANK1) mRNA, complete cds Length = 2651 |
| 154C6 | 520 | 826 | AF005775 | NA | 1.00E-150 | 3 | caspase-like apoptosis regulatory protein 2 (clarp) mRNA, alternative |
| 186B6 | 772 | 1248 | AF039575 | NA | 0 | 1 | heterogeneous nuclear ribonucleoprotein D0B mRNA, partial cds |
| 471A4 | 395 | 611 | AF061944 | NA | 6.00E-84 | 1 | kinase deficient protein KDP mRNA, partial cds Length = 2653 |
| 37G5 | 277 | 525 | AF067529 | NA | 1.00E-129 | 1 | PITSLRE protein kinase beta SV18 isoform (CDC2L2) mRNA, partial cds |
| 479D1 | 1270 | 1570 | AF070635 | NA | 1.00E-144 | 1 | clone 24818 mRNA sequence Length = 1643 |
| 491E2 | 38 | 226 | AF086214 | NA | 9.00E-74 | 1 | full length insert cDNA clone ZC64D04 Length = 691 |
| 517C2 | 230 | 465 | AF086431 | NA | 1.00E-113 | 1 | full length insert cDNA clone ZD79H10 Length = 530 |
| 593C6 | 1 | 359 | AF113210 | NA | 0 | 5 | MSTP030 mRNA, complete cds Length = 1024 |
| 191A8 | 135 | 1169 | AF113213 | NA | 0 | 3 | MSTP033 mRNA, complete cds Length = 1281 |
| 144E9 | 799 | 943 | AF116679 | NA | 9.00E-29 | 1 | PRO2003 mRNA, complete cds Length = 1222 |
| 106E3 | 583 | 1187 | AF116702 | NA | 0 | 2 | PRO2446 mRNA, complete cds Length = 1356 |
| 72F8 | 878 | 1205 | AF130094 | NA | 1.00E-175 | 1 | clone FLC0165 mRNA sequence Length = 1548 |
| 458G9 | 730 | 1463 | AF157116 | NA | 0 | 1 | clone 274512, mRNA sequence Length = 2172 |
| 139F11 | 18 | 229 | AF161430 | NA | 1.00E-115 | 1 | HSPC312 mRNA, partial cds Length = 360 |
| 149H10 | 406 | 621 | AF161455 | NA | 3.00E-95 | 2 | HSPC337 mRNA, partial cds Length = 1033 |
| 68A9 | 19 | 243 | AF173954 | NA | 2.00E-27 | 1 | Cloning vector pGEM-URA3, complete sequence Length = 4350 |
| 165B7 | 65 | 418 | AF202092 | NA | 0 | 1 | PC3-96 mRNA, complete cds Length = 1068 |
| 52H1 | 361 | 594 | AF212226 | NA | 1.00E-34 | 1 | RPL24 mRNA, complete cds Length = 1474 |
| 162H8 | 52 | 404 | AF212233 | NA | 1.00E-179 | 1 | microsomal signal peptidase subunit mRNA, complete cds Length = 794 |
| 54E10 | 680 | 1316 | AF212241 | NA | 0 | 3 | CDA02 mRNA, complete cds Length = 2179 |
| 117D8 | 2052 | 2482 | AF248648 | NA | 0 | 3 | RNA-binding protein BRUNOL2 mRNA, complete cds Length = 2615 |
| 75E3 | 326 | 662 | AF249845 | NA | 0 | 2 | isolate Siddi 10 hypervariable region I, mitochondrial sequence |
| 459G12 | 791 | 1267 | AF260237 | NA | 0 | 1 | hairly/enhancer of split 6 (HES6) mRNA, complete cds Length = 1286 |
| 177F6 | 1968 | 2423 | AF267856 | NA | 0 | 1 | HT033 mRNA, complete cds Length = 2972 |
| 115G8 | 996 | 1399 | AF267863 | NA | 0 | 1 | DC43 mRNA, complete cds Length = 2493 |
| 501H3 | 426 | 1152 | AF279437 | NA | 0 | 107 | interleukin 22 (IL22) mRNA, complete cds Length = 1167 |
| 174B4 | 900 | 1332 | AF283771 | NA | 0 | 2 | clone TCBAPO774 mRNA sequence Length = 1814 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|----------|----|-----------|---|--|
| 126C7 | 454 | 843 | AF332864 | NA | 1.00E-116 | 2 | similar to Mus Ras association domain family 3 protein (Rassf3) mRNA |
| 105A9 | 232 | 624 | AF333025 | NA | 1.00E-140 | 1 | prokineticin 2 precursor (PROK2) mRNA, complete cds Length = 1406 |
| 186F1 | 4543 | 5058 | AF347010 | NA | 0 | 3 | mitochondrion, complete genome Length = 16570 |
| 590B12 | 4684 | 5053 | AF347013 | NA | 0 | 1 | mitochondrion, complete genome Length = 16566 |
| 517H7 | 4669 | 5058 | AF347015 | NA | 0 | 1 | mitochondrion, complete genome Length = 16571 |
| 596E9 | 220 | 295 | AI027844 | NA | 3.00E-34 | 1 | cDNA clone IMAGE:1671612 3' |
| 599B3 | 608 | 609 | AI039890 | NA | 1.00E-45 | 1 | ox97d11.x1 Soares_senescent_fibroblasts_NbHSF cDNA |
| 189H9 | 22 | 524 | AI041828 | NA | 0 | 1 | oy34b08.x1 Soares_parathyroid_tumor_NbHPA cDNA clone |
| 471F6 | 63 | 526 | AI084224 | NA | 0 | 1 | cDNA clone IMAGE:1671418 3' |
| 142E9 | 6 | 372 | AI091533 | NA | 1.00E-179 | 1 | oo23d05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone |
| 72D2 | 65 | 529 | AI131018 | NA | 0 | 6 | qb82e07.x1 Soares_fetal_heart_NbHH19W cDNA clone |
| 468F6 | 9 | 428 | AI223400 | NA | 0 | 1 | cDNA clone IMAGE:1838447 3' similar to TR:O15383 |
| 185H1 | 94 | 199 | AI267714 | NA | 5.00E-50 | 1 | SB pool 1 cDNA clone IMAGE:2038526 |
| 166A9 | 1 | 480 | AI275205 | NA | 0 | 1 | cDNA clone IMAGE:1990616 3' |
| 499F2 | 4 | 395 | AI281442 | NA | 0 | 2 | cDNA clone IMAGE:1967452 3' |
| 517H5 | 155 | 457 | AI298509 | NA | 1.00E-158 | 1 | cDNA clone IMAGE:1896546 3' |
| 144F7 | 24 | 364 | AI299573 | NA | 0 | 1 | cDNA clone IMAGE:1900105 3' |
| 519E9 | 52 | 408 | AI352690 | NA | 1.00E-180 | 1 | cDNA clone IMAGE:1946884 3' |
| 466F9 | 172 | 440 | AI361839 | NA | 1.00E-109 | 1 | cDNA clone IMAGE:2022012 3' |
| 144C9 | 118 | 373 | AI362793 | NA | 7.00E-63 | 1 | cDNA clone IMAGE:2018948 3' similar to gb:M60854 |
| 464B11 | 19 | 455 | AI363001 | NA | 0 | 1 | cDNA clone IMAGE:2018452 3' similar to contains |
| 127B6 | 40 | 257 | AI370412 | NA | 6.00E-96 | 1 | cDNA clone IMAGE:1987587 3' |
| 166C4 | 58 | 271 | AI371227 | NA | 1.00E-62 | 1 | cDNA clone IMAGE:1987633 3' similar to |
| 467G7 | 1 | 450 | AI380016 | NA | 0 | 1 | cDNA clone IMAGE:2109169 3' similar to |
| 466C5 | 316 | 497 | AI380390 | NA | 8.00E-44 | 1 | cDNA clone IMAGE:2107088 3' |
| 466B5 | 200 | 477 | AI381586 | NA | 1.00E-126 | 1 | cDNA clone IMAGE:2074796 3' |
| 458G10 | 347 | 444 | AI384128 | NA | 2.00E-40 | 1 | cDNA clone IMAGE:2088819 3' similar to contains |
| 467A8 | 415 | 522 | AI391500 | NA | 1.00E-41 | 1 | cDNA clone IMAGE:2107686 3' |
| 477D1 | 14 | 269 | AI392705 | NA | 1.00E-137 | 2 | cDNA clone IMAGE:2109581 3' |
| 467B11 | 1 | 293 | AI393970 | NA | 1.00E-122 | 1 | cDNA clone IMAGE:2107950 3' |
| 522D3 | 250 | 526 | AI419082 | NA | 1.00E-127 | 1 | cDNA clone IMAGE:2103029 3' |
| 149A11 | 25 | 313 | AI440491 | NA | 1.00E-132 | 1 | cDNA clone IMAGE:2073277 3' |
| 471C1 | 77 | 215 | AI458739 | NA | 1.00E-50 | 1 | cDNA clone IMAGE:2149471 3' similar to gb:S85655 |
| 116E10 | 162 | 503 | AI469584 | NA | 1.00E-171 | 1 | cDNA clone IMAGE:2156522 3' |
| 472C8 | 1 | 369 | AI498316 | NA | 0 | 1 | cDNA clone IMAGE:2160886 3' similar to TR:Q62717 |
| 468E8 | 2 | 451 | AI523854 | NA | 3.00E-92 | 1 | cDNA clone IMAGE:2116683 3' |
| 477B5 | 23 | 295 | AI524624 | NA | 2.00E-86 | 1 | cDNA clone IMAGE:2075323 3' |
| 193H3 | 368 | 489 | AI525644 | NA | 4.00E-34 | 1 | cDNA 5' |
| 66F1 | 277 | 436 | AI571519 | NA | 7.00E-84 | 2 | cDNA clone IMAGE:2225079 3' similar to gb:J03909 |
| 171A11 | 225 | 429 | AI581199 | NA | 1.00E-101 | 3 | cDNA clone IMAGE:2154787 3' similar to |
| 116F2 | 337 | 429 | AI597917 | NA | 4.00E-42 | 1 | cDNA clone IMAGE:2258495 3' similar to contains |
| 461G10 | 9 | 398 | AI627495 | NA | 1.00E-179 | 1 | cDNA clone IMAGE:2285386 3' |
| 594D11 | 206 | 434 | AI628930 | NA | 1.00E-110 | 1 | cDNA clone IMAGE:2281541 3' similar to |
| 489H9 | 1 | 507 | AI633798 | NA | 0 | 4 | cDNA clone IMAGE:2242115 3' |
| 171G7 | 212 | 431 | AI634972 | NA | 1.00E-103 | 1 | cDNA clone IMAGE:2284157 3' |
| 165C12 | 270 | 581 | AI651212 | NA | 1.00E-175 | 1 | cDNA clone IMAGE:2304186 3' |
| 64B3 | 1 | 529 | AI678099 | NA | 0 | 1 | Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2330166 3' |
| 134H3 | 186 | 289 | AI684022 | NA | 1.00E-34 | 1 | cDNA clone IMAGE:2267411 3' |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|----------|----|-----------|---|---|
| 110B8 | 169 | 496 | AI688560 | NA | 1.00E-132 | 1 | Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2330535 3' |
| 459F2 | 160 | 542 | AI697756 | NA | 0 | 1 | cDNA clone IMAGE:2341330 3' |
| 481F11 | 21 | 340 | AI700738 | NA | 1.00E-167 | 1 | cDNA clone IMAGE:2343628 3' |
| 488C5 | 37 | 533 | AI701165 | NA | 0 | 4 | cDNA clone IMAGE:2340734 3' |
| 104D9 | 116 | 241 | AI709236 | NA | 4.00E-60 | 1 | HPLRB6 cDNA clone IMAGE:2353865 3' similar to wg47a05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 |
| 112E1 | 18 | 576 | AI742850 | NA | 0 | 1 | cDNA clone |
| 113H12 | 5 | 140 | AI748827 | NA | 1.00E-63 | 1 | HPLRB6 cDNA clone IMAGE:2356401 3' |
| 458B8 | 150 | 474 | AI760353 | NA | 0 | 1 | cDNA clone IMAGE:2387703 3' |
| 461H11 | 334 | 578 | AI762870 | NA | 1.00E-111 | 1 | cDNA clone IMAGE:2397996 3' |
| 458D10 | 1 | 465 | AI765153 | NA | 0 | 1 | cDNA clone IMAGE:2393531 3' |
| 38B5 | 2 | 295 | AI766963 | NA | 1.00E-140 | 1 | cDNA clone IMAGE:2400693 3' |
| 471A2 | 320 | 394 | AI796317 | NA | 2.00E-31 | 1 | cDNA clone IMAGE:2384100 3' |
| 74D10 | 15 | 377 | AI802547 | NA | 1.00E-124 | 2 | cDNA clone IMAGE:2186739 3' similar to TR:O15510 |
| 482C9 | 117 | 409 | AI803065 | NA | 1.00E-164 | 1 | tj47a07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone |
| 480C5 | 177 | 517 | AI807278 | NA | 0 | 1 | Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2357909 3' |
| 175B12 | 228 | 513 | AI817153 | NA | 1.00E-132 | 1 | cDNA clone IMAGE:2413005 3' |
| 66E10 | 14 | 268 | AI858771 | NA | 1.00E-119 | 1 | cDNA clone IMAGE:2429769 3' |
| 470H6 | 65 | 500 | AI880607 | NA | 0 | 1 | HPLRB6 cDNA clone IMAGE:2355013 3' |
| 181D12 | 7 | 512 | AI884548 | NA | 0 | 1 | cDNA clone IMAGE:2437818 3' similar to gb:L06797 |
| 468H6 | 52 | 528 | AI884671 | NA | 0 | 1 | cDNA clone IMAGE:2431488 3' |
| 597C9 | 284 | 383 | AI904071 | NA | 1.00E-48 | 1 | cDNA |
| 467C2 | 206 | 351 | AI917642 | NA | 2.00E-59 | 1 | cDNA clone IMAGE:2392330 3' |
| 459D1 | 25 | 575 | AI948513 | NA | 0 | 1 | cDNA clone IMAGE:2470532 3' |
| 166E11 | 152 | 280 | AI954499 | NA | 4.00E-54 | 1 | cDNA clone IMAGE:2550263 3' |
| 493D7 | 2032 | 2171 | AJ001235 | NA | 4.00E-29 | 1 | similar to Papio hamadryas ERV-9 like LTR insertion Length = 2240 |
| 116B1 | 1169 | 1744 | AJ009771 | NA | 0 | 1 | mRNA for putative RING finger protein, partial Length = 3038 |
| 137B9 | 296 | 407 | AJ271637 | NA | 4.00E-32 | 1 | similar to Elaeis guineensis microsatellite DNA, clone mEgCIR0219 |
| 483E6 | 4250 | 4492 | AJ278191 | NA | 1.00E-95 | 1 | similar to Mus musculus mRNA for putative mc7 protein (mc7 gene) |
| 144A8 | 988 | 1152 | AK001163 | NA | 1.00E-75 | 1 | cDNA FLJ10301 fis, clone NT2RM2000032 Length = 1298 |
| 525C11 | 49 | 496 | AK001451 | NA | 0 | 1 | cDNA FLJ10589 fis, clone NT2RP2004389 |
| 177D9 | 707 | 980 | AK004265 | NA | 7.00E-76 | 1 | similar to Mus 18 days embryo cDNA, RIKEN full- length enriched library, |
| 111E10 | 777 | 1121 | AK004400 | NA | 1.00E-112 | 1 | similar to Mus 18 days embryo cDNA, RIKEN full- length enriched library, |
| 458G4 | 650 | 1259 | AK008020 | NA | 8.00E-86 | 1 | similar to Mus adult male small intestine cDNA, RIKEN full-length enrich |
| 47G7 | 31 | 328 | AK009988 | NA | 1.00E-111 | 1 | similar to Mus adult male tongue cDNA, RIKEN full- length enriched librar |
| 69G7 | 1801 | 1987 | AK012426 | NA | 5.00E-68 | 3 | similar to Mus 11 days embryo cDNA, RIKEN full- length enriched library, |
| 62C10 | 1092 | 1267 | AK013164 | NA | 6.00E-46 | 2 | similar to Mus 10, 11 days embryo cDNA, RIKEN full- length enriched libra |
| 46D9 | 3243 | 3564 | AK014408 | NA | 1.00E-104 | 1 | similar to Mus 12 days embryo embryonic body below diaphragm region |
| 178C11 | 2069 | 2326 | AK016683 | NA | 9.00E-83 | 1 | similar to Mus adult male testis cDNA, RIKEN full- length enriched librar |
| 102C12 | 698 | 1339 | AK018758 | NA | 0 | 1 | similar to Mus adult male liver cDNA, RIKEN full- length enriched library |
| 585B3 | 1278 | 1873 | AK021925 | NA | 0 | 1 | cDNA FLJ11863 fis, clone HEMBA1006926 Length = 2029 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|----------|----|-----------|---|--|
| 46F3 | 1377 | 2006 | AK022057 | NA | 0 | 1 | cDNA FLJ11995 fis, clone HEMBB1001443, highly similar to Rattus norveg |
| 73E7 | 344 | 1112 | AK023512 | NA | 0 | 9 | cDNA FLJ13450 fis, clone PLACE1003027, highly similar to Homo sapiens |
| 465B12 | 681 | 1338 | AK024202 | NA | 0 | 1 | cDNA FLJ14140 fis, clone MAMMA1002858, highly similar to Rat cMG1 |
| 142D12 | 254 | 358 | AK024740 | NA | 9.00E-27 | 1 | cDNA: FLJ21087 fis, clone CAS03323 Length = 826 |
| 472F7 | 1330 | 1623 | AK024764 | NA | 1.00E-164 | 1 | cDNA: FLJ21111 fis, clone CAS05384, highly similar to AF144700 Homo sa |
| 521A3 | 26 | 195 | AK024976 | NA | 2.00E-90 | 1 | cDNA: FLJ21323 fis, clone COL02374 Length = 1348 |
| 465D1 | 2091 | 2255 | AK025769 | NA | 1.00E-74 | 1 | cDNA: FLJ22116 fis, clone HEP18520 Length = 2271 |
| 595E9 | 16 | 546 | AK026264 | NA | 0 | 1 | cDNA: FLJ22611 fis, clone HSI04961 Length = 1426 |
| 103E1 | 1353 | 1866 | AK026334 | NA | 1.00E-126 | 1 | cDNA: FLJ22681 fis, clone HSI10693 Length = 1903 |
| 524F3 | 1635 | 1742 | AK026443 | NA | 9.00E-51 | 2 | cDNA: FLJ22790 fis, clone KAIA2176, highly similar to HUMPMCA |
| 196H10 | 938 | 1286 | AK026819 | NA | 6.00E-82 | 1 | cDNA: FLJ23166 fis, clone LNG09880 Length = 1941 |
| 172F7 | 349 | 738 | AK027258 | NA | 0 | 1 | cDNA: FLJ23605 fis, clone LNG15982, highly similar to AF113539 Homo sa |
| 187B10 | 1583 | 2142 | AK027260 | NA | 1.00E-129 | 1 | cDNA: FLJ23607 fis, clone LNG16050 Length = 2560 |
| 190F11 | 76 | 636 | AL042081 | NA | 0 | 1 | (synonym: htes3) cDNA clone DKFZp434P171 3' |
| 525A9 | 1 | 653 | AL042370 | NA | 0 | 1 | (synonym: htes3) cDNA clone DKFZp434A1821 5' |
| 464G8 | 59 | 686 | AL042376 | NA | 0 | 1 | (synonym: htes3) cDNA clone DKFZp434A2421 5' |
| 172B12 | 380 | 624 | AL047171 | NA | 1.00E-131 | 1 | (synonym: hute1) cDNA clone DKFZp586F2018 5' |
| 193F3 | 915 | 1309 | AL049305 | NA | 1.00E-133 | 1 | mRNA; cDNA DKFZp564A186 (from clone DKFZp564A186) Length = 1669 |
| 111H8 | 102 | 660 | AL049356 | NA | 1.00E-146 | 1 | mRNA; cDNA DKFZp566E233 (from clone DKFZp566E233) Length = 808 |
| 526E6 | 118 | 551 | AL049932 | NA | 1.00E-147 | 2 | mRNA; cDNA DKFZp564H2416 (from clone DKFZp564H2416) Length = 1865 |
| 37C8 | 707 | 996 | AL050218 | NA | 1.00E-156 | 1 | mRNA; cDNA DKFZp586I0923 (from clone DKFZp586I0923) Length = 1282 |
| 72A9 | 1235 | 1391 | AL110164 | NA | 2.00E-70 | 1 | mRNA; cDNA DKFZp586I0324 (from clone DKFZp586I0324) Length = 1705 |
| 107C8 | 1042 | 1398 | AL117644 | NA | 0 | 2 | mRNA; cDNA DKFZp434M095 (from clone DKFZp434M095) Length = 1455 |
| 62E7 | 1 | 475 | AL120453 | NA | 1.00E-117 | 1 | (synonym: hamy2) cDNA clone DKFZp761I208 5' |
| 492A7 | 77 | 390 | AL121406 | NA | 1.00E-101 | 1 | (synonym: hmel2) cDNA clone DKFZp762G117 5' |
| 598B1 | 443 | 812 | AL133879 | NA | 1.00E-172 | 1 | (synonym: hamy2) cDNA clone DKFZp761J0114 5' |
| 458C10 | 47 | 351 | AL133913 | NA | 5.00E-76 | 1 | (synonym: hamy2) cDNA clone DKFZp761M2014 5' |
| 98E7 | 922 | 2284 | AL136558 | NA | 0 | 6 | mRNA; cDNA DKFZp761B1514 (from clone DKFZp761B1514) Length = 3453 |
| 157F6 | 3511 | 3847 | AL136797 | NA | 0 | 1 | mRNA; cDNA DKFZp434N031 (from clone DKFZp434N031); complete cds |
| 68B4 | 1009 | 1595 | AL136932 | NA | 0 | 1 | mRNA; cDNA DKFZp586H1322 (from clone DKFZp586H1322); complete cds |
| 458B6 | 278 | 955 | AL137601 | NA | 0 | 1 | mRNA; cDNA DKFZp434E0811 (from clone DKFZp434E0811); partial cds |
| 172C9 | 1866 | 2423 | AL137608 | NA | 0 | 1 | mRNA; cDNA DKFZp434J1111 (from clone DKFZp434J1111); partial cds |
| 72G1 | 194 | 474 | AL138429 | NA | 1.00E-151 | 1 | (synonym: htes3) cDNA clone DKFZp434E0629 3' |
| 463H12 | 12 | 356 | AL513780 | NA | 1.00E-124 | 1 | cDNA clone CL0BA003ZF07 5 prime |
| 181B6 | 43 | 638 | AL520535 | NA | 0 | 1 | cDNA clone CS0DB006YD20 3 prime |
| 69B6 | 352 | 858 | AL520892 | NA | 0 | 1 | cDNA clone CS0DB002YG16 5 prime |
| 182A5 | 119 | 617 | AL521097 | NA | 0 | 1 | cDNA clone CS0DB001YA13 3 prime |
| 458E9 | 3 | 865 | AL528020 | NA | 0 | 2 | cDNA clone CS0DC028YO09 3 prime |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|-----|-----|----------|----|-----------|---|------------------------------------|
| 485C11 | 1 | 431 | AL532303 | NA | 0 | 1 | cDNA clone CS0DM014YJ04 5 prime |
| 196G3 | 78 | 698 | AL532406 | NA | 0 | 1 | cDNA clone CS0DM014YL03 5 prime |
| 105H4 | 154 | 486 | AL533737 | NA | 1.00E-156 | 1 | cDNA clone CS0DF002YH09 5 prime |
| 594G1 | 337 | 756 | AL534564 | NA | 0 | 1 | cDNA clone CS0DF004YI09 5 prime |
| 524A9 | 403 | 906 | AL540260 | NA | 0 | 1 | cDNA clone CS0DF032YF03 3 prime |
| 118H5 | 433 | 532 | AL540399 | NA | 4.00E-39 | 1 | cDNA clone CS0DE001YM08 5 prime |
| 124C2 | 270 | 815 | AL543900 | NA | 0 | 1 | cDNA clone CS0DI005YK13 3 prime |
| 471D3 | 216 | 403 | AL550229 | NA | 9.00E-49 | 1 | cDNA clone CS0DI039YD11 5 prime |
| 191F2 | 324 | 844 | AL554506 | NA | 0 | 1 | cDNA clone CS0DI083YJ17 5 prime |
| 166F6 | 64 | 576 | AL556016 | NA | 0 | 1 | cDNA clone CS0DK010YH04 5 prime |
| 467G9 | 61 | 401 | AL556919 | NA | 1.00E-138 | 1 | cDNA clone CS0DK012YI02 5 prime |
| 37D7 | 149 | 685 | AL559029 | NA | 0 | 1 | cDNA clone CS0DJ010YJ11 5 prime |
| 590B3 | 76 | 287 | AL559422 | NA | 1.00E-111 | 2 | cDNA clone CS0DJ013YN07 5 prime |
| 181H2 | 168 | 780 | AL559555 | NA | 0 | 1 | cDNA clone CS0DJ013YP21 5 prime |
| 589E3 | 28 | 447 | AL561074 | NA | 0 | 1 | cDNA clone CS0DL001YN01 5 prime |
| 487F9 | 326 | 739 | AL561892 | NA | 1.00E-149 | 1 | cDNA clone CS0DB006YL04 3 prime |
| 68F10 | 12 | 658 | AL562895 | NA | 0 | 1 | cDNA clone CS0DC021YO20 3 prime |
| 157D7 | 2 | 108 | AL565736 | NA | 1.00E-28 | 1 | cDNA clone CS0DF007YC06 3 prime |
| 177B1 | 231 | 505 | AL567986 | NA | 1.00E-128 | 1 | cDNA clone CS0DF036YI04 3 prime |
| 512E3 | 627 | 815 | AL575666 | NA | 1.00E-94 | 1 | cDNA clone CS0DI069YD02 3 prime |
| 112E10 | 193 | 623 | AL575755 | NA | 0 | 1 | cDNA clone CS0DI070YG17 3 prime |
| 70H7 | 197 | 757 | AL576149 | NA | 0 | 1 | cDNA clone CS0DI072YK21 3 prime |
| 37F1 | 275 | 411 | AL577970 | NA | 1.00E-43 | 1 | cDNA clone CS0DK008YK22 3 prime |
| 65D4 | 278 | 828 | AL578975 | NA | 0 | 1 | cDNA clone CS0DK012YN01 3 prime |
| 182G2 | 70 | 684 | AL579745 | NA | 0 | 1 | cDNA clone CS0DJ003YG20 5 prime |
| 194F9 | 450 | 669 | AL582354 | NA | 3.00E-94 | 1 | cDNA clone CS0DL006YH05 3 prime |
| 184F2 | 27 | 501 | AL583322 | NA | 2.00E-37 | 1 | cDNA clone CS0DL012YI10 5 prime |
| 40A3 | 432 | 638 | AL583391 | NA | 4.00E-83 | 1 | cDNA clone CS0DL012YA12 3 prime |
| 53G7 | 6 | 462 | AU117298 | NA | 0 | 1 | sapiens cDNA clone HEMBA1001091 5' |
| 37G7 | 218 | 706 | AU118159 | NA | 0 | 1 | sapiens cDNA clone HEMBA1002998 5' |
| 180F9 | 174 | 698 | AU120731 | NA | 0 | 1 | sapiens cDNA clone HEMBB1001298 5' |
| 191F1 | 298 | 608 | AU135154 | NA | 1.00E-137 | 1 | sapiens cDNA clone PLACE1001348 5' |
| 466G7 | 11 | 125 | AU158636 | NA | 1.00E-53 | 1 | sapiens cDNA clone PLACE4000063 3' |
| 67F9 | 1 | 453 | AV648670 | NA | 0 | 2 | cDNA clone GLCBLH08 3' |
| 155D6 | 97 | 337 | AV650434 | NA | 1.00E-104 | 1 | cDNA clone GLCCEG06 3' |
| 596H6 | 1 | 397 | AV651615 | NA | 0 | 1 | cDNA clone GLCCRF09 3' |
| 99D5 | 41 | 232 | AV653169 | NA | 6.00E-78 | 1 | cDNA clone GLCDIB01 3' |
| 331C10 | 33 | 365 | AV654188 | NA | 1.00E-103 | 6 | cDNA clone GLCDTC01 3' |
| 121A12 | 70 | 188 | AV659358 | NA | 3.00E-47 | 1 | cDNA clone GLCFWC05 3' |
| 460G9 | 69 | 476 | AV687530 | NA | 0 | 1 | cDNA clone GK CATH08 5' |
| 470F5 | 1 | 174 | AV689330 | NA | 2.00E-50 | 1 | cDNA clone GKCDJE03 5' |
| 109E8 | 71 | 471 | AV705900 | NA | 0 | 1 | cDNA clone ADBBFE11 5' |
| 166C9 | 121 | 226 | AV709955 | NA | 2.00E-26 | 1 | cDNA clone ADCABF08 5' |
| 117F1 | 69 | 582 | AV710415 | NA | 0 | 1 | cDNA clone CuAAND10 5' |
| 523C9 | 41 | 536 | AV716565 | NA | 0 | 6 | cDNA clone DCBCAF01 5' |
| 103D7 | 1 | 164 | AV716644 | NA | 3.00E-77 | 2 | cDNA clone DCBAUG10 5' |
| 195F11 | 232 | 459 | AV716791 | NA | 1.00E-113 | 2 | cDNA clone DCBAZC04 5' |
| 63C4 | 208 | 421 | AV719659 | NA | 1.00E-101 | 1 | cDNA clone GLCGRA09 5' |
| 496C4 | 156 | 563 | AV719938 | NA | 0 | 1 | cDNA clone GLCFUC08 5' |
| 479A1 | 120 | 469 | AV720984 | NA | 1.00E-162 | 1 | cDNA clone HTBBIC02 5' |
| 499D6 | 70 | 406 | AV721008 | NA | 1.00E-112 | 4 | cDNA clone HTBBHG03 5' |
| 461C8 | 182 | 676 | AV723437 | NA | 0 | 1 | cDNA clone HTBBUE10 5' |
| 585G1 | 173 | 552 | AV724531 | NA | 0 | 1 | cDNA clone HTBARD04 5' |
| 113B8 | 1 | 149 | AV724559 | NA | 3.00E-40 | 1 | cDNA clone HTBCFB08 5' |
| 111H4 | 497 | 498 | AV724665 | NA | 0 | 1 | cDNA clone HTBAYG03 5' |
| 458F5 | 1 | 534 | AV730135 | NA | 0 | 1 | cDNA clone HTFAHA06 5' |
| 589F6 | 21 | 226 | AV735258 | NA | 6.00E-70 | 1 | cDNA clone cdAAIF03 5' |
| 172C8 | 209 | 426 | AV738173 | NA | 9.00E-98 | 1 | cDNA clone CBMAHC04 5' |
| 464G3 | 43 | 498 | AV743635 | NA | 0 | 1 | cDNA clone CBLBAC03 5' |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|-----|-----|----------|----|-----------|---|---|
| 72D4 | 43 | 384 | AV745692 | NA | 1.00E-178 | 2 | cDNA clone NPAACB06 5' |
| 592G12 | 175 | 571 | AV749844 | NA | 1.00E-176 | 1 | cDNA clone NPCBVG08 5' |
| 169F6 | 110 | 250 | AV755117 | NA | 3.00E-28 | 1 | cDNA clone TPAABA12 5' |
| 99H3 | 200 | 513 | AV755367 | NA | 1.00E-131 | 2 | cDNA clone BMFAIB02 5' |
| 595G9 | 399 | 549 | AV756188 | NA | 2.00E-31 | 1 | cDNA clone BMFABD08 5' |
| 595A12 | 8 | 572 | AW002985 | NA | 0 | 2 | cDNA clone IMAGE:2475831 3' |
| 586B7 | 184 | 330 | AW004905 | NA | 8.00E-50 | 1 | cDNA clone IMAGE:2565317 3' similar to |
| 591D6 | 15 | 436 | AW021037 | NA | 0 | 1 | Cochlea cDNA clone IMAGE:2483601 5' |
| 188F1 | 135 | 476 | AW021551 | NA | 0 | 1 | Cochlea cDNA clone IMAGE:2484414 5' |
| 467E8 | 73 | 474 | AW027160 | NA | 1.00E-162 | 1 | Soares_thymus_NHFT cDNA clone IMAGE:2512983 3' similar to |
| 472G2 | 11 | 110 | AW064187 | NA | 9.00E-38 | 1 | CD4 intrathymic T-cell cDNA library cDNA 3' |
| 598F3 | 43 | 453 | AW071894 | NA | 0 | 1 | cDNA clone IMAGE:2501169 3' |
| 181C7 | 10 | 96 | AW131768 | NA | 8.00E-41 | 1 | cDNA clone IMAGE:2619947 3' |
| 181D1 | 69 | 216 | AW134512 | NA | 2.00E-77 | 1 | UI-H-BI1-abv-e-05-0-UI.s1 NCI_CGAP_Sub3 cDNA clone IMAGE:2713065 3' |
| 472B10 | 339 | 458 | AW136717 | NA | 4.00E-54 | 1 | UI-H-BI1-adm-a-03-0-UI.s1 NCI_CGAP_Sub3 cDNA clone IMAGE:2717092 3' |
| 166B9 | 240 | 408 | AW137104 | NA | 6.00E-88 | 1 | UI-H-BI1-acp-e-02-0-UI.s1 NCI_CGAP_Sub3 cDNA clone IMAGE:2714979 3' |
| 188C1 | 323 | 461 | AW137149 | NA | 2.00E-72 | 1 | UI-H-BI1-acq-a-05-0-UI.s1 NCI_CGAP_Sub3 cDNA clone IMAGE:2715152 3' |
| 65B2 | 106 | 298 | AW148765 | NA | 7.00E-75 | 1 | cDNA clone IMAGE:2616915 3' |
| 524C3 | 234 | 429 | AW151854 | NA | 1.00E-76 | 2 | cDNA clone IMAGE:2623546 3' similar to |
| 479A8 | 6 | 327 | AW161820 | NA | 1.00E-151 | 1 | brain 00004 cDNA clone IMAGE:2781653 3' |
| 585E10 | 7 | 391 | AW166442 | NA | 0 | 1 | Soares_NHCE_cervix cDNA clone IMAGE:2697403 3' |
| 482C6 | 9 | 329 | AW188398 | NA | 1.00E-133 | 1 | cDNA clone IMAGE:2665252 3' |
| 522G11 | 39 | 516 | AW248322 | NA | 0 | 1 | cDNA clone IMAGE:2820662 5' |
| 473D5 | 283 | 416 | AW274156 | NA | 4.00E-69 | 1 | Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2814367 3' |
| 71C12 | 20 | 530 | AW293159 | NA | 0 | 2 | UI-H-BW0-aib-b-08-0-UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2729414 3' |
| 472H11 | 205 | 501 | AW293424 | NA | 1.00E-151 | 1 | UI-H-BI2-ahm-a-12-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2727094 3' |
| 465H11 | 17 | 124 | AW293426 | NA | 1.00E-48 | 1 | UI-H-BI2-ahm-b-02-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2727122 3' |
| 461H8 | 19 | 452 | AW295965 | NA | 0 | 1 | UI-H-BI2-ahh-f-07-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2726917 3' |
| 464B7 | 250 | 551 | AW300500 | NA | 3.00E-95 | 1 | cDNA clone IMAGE:2774602 3' |
| 465C7 | 1 | 322 | AW338115 | NA | 0 | 1 | cDNA clone IMAGE:2833029 3' |
| 466H5 | 10 | 523 | AW341449 | NA | 0 | 1 | Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2909026 3' similar to |
| 461D9 | 12 | 325 | AW379049 | NA | 1.00E-134 | 1 | HT0230 cDNA |
| 186E8 | 51 | 277 | AW380881 | NA | 1.00E-103 | 1 | HT0283 cDNA |
| 180D4 | 260 | 348 | AW384988 | NA | 2.00E-30 | 1 | HT0427 cDNA |
| 472C1 | 13 | 404 | AW390233 | NA | 1.00E-122 | 1 | ST0181 cDNA |
| 462G12 | 236 | 321 | AW402007 | NA | 3.00E-40 | 1 | UI-HF-BK0-aao-g-02-0-UI.r1 NIH_MGC_36 cDNA clone IMAGE:3054530 5' |
| 177H2 | 18 | 338 | AW405863 | NA | 9.00E-52 | 1 | UI-HF-BL0-acf-e-06-0-UI.r1 NIH_MGC_37 cDNA clone IMAGE:3059026 5' |
| 140G10 | 6 | 308 | AW440517 | NA | 1.00E-152 | 1 | cDNA clone IMAGE:2890615 3' |
| 482A10 | 1 | 231 | AW440869 | NA | 1.00E-114 | 1 | cDNA clone IMAGE:2918151 3' similar to contains |
| 40B2 | 18 | 353 | AW444632 | NA | 4.00E-45 | 1 | UI-H-BI3-ajw-b-11-0-UI.s1 NCI_CGAP_Sub5 cDNA clone IMAGE:2733260 3' |
| 61C2 | 21 | 392 | AW444812 | NA | 0 | 1 | UI-H-BI3-ajy-d-11-0-UI.s1 NCI_CGAP_Sub5 cDNA clone IMAGE:2733380 3' |
| 461H10 | 151 | 248 | AW449610 | NA | 8.00E-48 | 1 | UI-H-BI3-aku-g-11-0-UI.s1 NCI_CGAP_Sub5 cDNA clone IMAGE:2735804 3' |
| 479E10 | 9 | 425 | AW451293 | NA | 0 | 1 | UI-H-BI3-alh-f-06-0-UI.s1 NCI_CGAP_Sub5 cDNA clone IMAGE:2736899 3' |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|-----|-----|----------|----|-----------|---|---|
| 489G6 | 16 | 303 | AW452023 | NA | 1.00E-125 | 1 | UI-H-BI3-alm-f-06-0-UI.s1 NCI_CGAP_Sub5 cDNA clone IMAGE:2737306 3' |
| 463H8 | 99 | 289 | AW452096 | NA | 1.00E-103 | 1 | UI-H-BI3-alo-d-02-0-UI.s1 NCI_CGAP_Sub5 cDNA clone IMAGE:3068186 3' |
| 459B8 | 71 | 535 | AW499658 | NA | 0 | 1 | UI-HF-BR0p-ajj-c-07-0-UI.r1 NIH_MGC_52 cDNA clone IMAGE:3074677 5' |
| 37A2 | 128 | 395 | AW499828 | NA | 1.00E-110 | 1 | UI-HF-BN0-ake-c-06-0-UI.r1 NIH_MGC_50 cDNA clone IMAGE:3076619 5' |
| 112E5 | 88 | 557 | AW499829 | NA | 0 | 1 | UI-HF-BN0-ake-c-07-0-UI.r1 NIH_MGC_50 cDNA clone IMAGE:3076621 5' |
| 523F5 | 435 | 517 | AW500534 | NA | 4.00E-36 | 1 | UI-HF-BN0-akj-d-04-0-UI.r1 NIH_MGC_50 cDNA clone IMAGE:3077406 5' |
| 476E10 | 152 | 450 | AW501528 | NA | 1.00E-129 | 1 | UI-HF-BP0p-ajf-c-02-0-UI.r1 NIH_MGC_51 cDNA clone IMAGE:3073923 5' |
| 67D10 | 36 | 413 | AW504212 | NA | 0 | 1 | UI-HF-BN0-alp-a-11-0-UI.r1 NIH_MGC_50 cDNA clone IMAGE:3080348 5' |
| 100E10 | 29 | 364 | AW504293 | NA | 1.00E-159 | 1 | UI-HF-BN0-alg-b-10-0-UI.r1 NIH_MGC_50 cDNA clone IMAGE:3079267 5' |
| 484D12 | 35 | 353 | AW510795 | NA | 1.00E-167 | 1 | Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2911933 3' similar to |
| 480B2 | 109 | 446 | AW572538 | NA | 1.00E-162 | 1 | cDNA clone IMAGE:2832030 3' |
| 465D2 | 272 | 464 | AW573211 | NA | 2.00E-49 | 1 | Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2933767 3' similar to |
| 47G6 | 125 | 126 | AW614193 | NA | 1.00E-51 | 1 | cDNA clone IMAGE:2951662 3' |
| 499D7 | 1 | 341 | AW630825 | NA | 0 | 2 | cDNA clone IMAGE:2969854 5' |
| 62H5 | 10 | 423 | AW651682 | NA | 0 | 2 | cDNA clone IMAGE:2901099 5' |
| 104A7 | 3 | 461 | AW778854 | NA | 0 | 1 | cDNA clone IMAGE:3037337 3' |
| 484H1 | 9 | 453 | AW780057 | NA | 0 | 1 | cDNA clone IMAGE:3036046 3' |
| 491E8 | 18 | 348 | AW792856 | NA | 1.00E-164 | 2 | UM0001 cDNA |
| 65D11 | 64 | 648 | AW810442 | NA | 0 | 3 | ST0125 cDNA |
| 596F6 | 49 | 623 | AW813133 | NA | 0 | 1 | ST0189 cDNA |
| 518H1 | 131 | 386 | AW819894 | NA | 1.00E-133 | 1 | ST0294 cDNA |
| 115A7 | 1 | 315 | AW836389 | NA | 1.00E-169 | 3 | LT0030 cDNA |
| 486D9 | 32 | 237 | AW837717 | NA | 1.00E-65 | 1 | LT0042 cDNA |
| 477B12 | 84 | 253 | AW837808 | NA | 4.00E-67 | 1 | LT0042 cDNA |
| 121A11 | 253 | 444 | AW842489 | NA | 1.00E-98 | 1 | CN0032 cDNA |
| 472E6 | 132 | 447 | AW846856 | NA | 1.00E-149 | 1 | CT0195 cDNA |
| 164F9 | 1 | 462 | AW856490 | NA | 0 | 1 | CT0290 cDNA |
| 103C4 | 23 | 366 | AW859565 | NA | 0 | 1 | CT0355 cDNA |
| 129D3 | 81 | 295 | AW866426 | NA | 1.00E-108 | 1 | SN0024 cDNA |
| 501F9 | 88 | 421 | AW873028 | NA | 1.00E-170 | 3 | cDNA clone IMAGE:3120038 3' |
| 98G4 | 1 | 294 | AW873326 | NA | 1.00E-107 | 1 | cDNA clone IMAGE:3009400 3' |
| 72D5 | 55 | 648 | AW886511 | NA | 0 | 1 | OT0083 cDNA |
| 460A5 | 101 | 294 | AW891344 | NA | 1.00E-102 | 1 | NT0079 cDNA |
| 459E9 | 196 | 260 | AW945538 | NA | 8.00E-28 | 1 | EN0024 cDNA |
| 479H5 | 17 | 224 | AW948395 | NA | 1.00E-102 | 1 | FN0040 cDNA |
| 165E7 | 2 | 599 | AW949461 | NA | 0 | 1 | MAGA cDNA |
| 123G9 | 104 | 715 | AW954112 | NA | 0 | 2 | MAGC cDNA |
| 183F3 | 84 | 503 | AW954476 | NA | 1.00E-159 | 1 | MAGC cDNA |
| 196C6 | 8 | 189 | AW954580 | NA | 5.00E-98 | 1 | MAGC cDNA |
| 515H10 | 1 | 512 | AW955265 | NA | 0 | 1 | MAGC cDNA |
| 41E8 | 16 | 671 | AW957139 | NA | 1.00E-145 | 2 | MAGD cDNA |
| 66A7 | 335 | 503 | AW958538 | NA | 4.00E-85 | 1 | MAGE cDNA |
| 465G8 | 169 | 615 | AW960484 | NA | 0 | 1 | MAGF cDNA |
| 519E6 | 44 | 290 | AW960593 | NA | 1.00E-134 | 1 | MAGF cDNA |
| 594F4 | 306 | 571 | AW963171 | NA | 1.00E-112 | 1 | MAGH cDNA |
| 155B2 | 30 | 673 | AW964218 | NA | 0 | 3 | MAGH cDNA |
| 173B5 | 1 | 553 | AW965078 | NA | 0 | 1 | MAGI cDNA |
| 176A6 | 7 | 312 | AW965490 | NA | 1.00E-136 | 1 | MAGI cDNA |
| 498H9 | 1 | 456 | AW965987 | NA | 0 | 2 | MAGI cDNA |
| 517D11 | 105 | 484 | AW966098 | NA | 0 | 2 | MAGI cDNA |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|----------|----|-----------|---|--|
| 166H7 | 63 | 559 | AW967388 | NA | 0 | 1 | MAGJ cDNA |
| 462C8 | 69 | 212 | AW967948 | NA | 2.00E-72 | 1 | MAGJ cDNA |
| 189C5 | 8 | 566 | AW968561 | NA | 0 | 1 | MAGJ cDNA |
| 459C3 | 129 | 587 | AW969359 | NA | 0 | 2 | MAGK cDNA |
| 174C1 | 155 | 527 | AW969546 | NA | 1.00E-170 | 1 | MAGK cDNA |
| 191F6 | 158 | 543 | AW973953 | NA | 1.00E-152 | 2 | MAGM cDNA |
| 461G9 | 311 | 437 | AW974749 | NA | 7.00E-47 | 1 | MAGN cDNA |
| 104D1 | 182 | 594 | AW993791 | NA | 0 | 1 | BN0034 cDNA |
| 188F5 | 734 | 1292 | AY007110 | NA | 0 | 4 | clone TCCCTA00084 mRNA sequence Length = 1656 |
| 48D7 | 692 | 1169 | AY029066 | NA | 1.00E-76 | 4 | Humanin (HN1) mRNA, complete cds Length = 1567 |
| 55B8 | 1802 | 2045 | BC000141 | NA | 3.00E-96 | 1 | Similar to myelocytomatosis oncogene, clone MGC:5183, mRNA |
| 37A8 | 34 | 301 | BC000374 | NA | 1.00E-101 | 1 | ribosomal protein L18, clone MGC:8373, mRNA, complete cds |
| 178E5 | 20 | 551 | BC000408 | NA | 5.00E-53 | 1 | acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase |
| 596G2 | 27 | 263 | BC000449 | NA | 3.00E-43 | 2 | Similar to ubiquitin C, clone MGC:8448, mRNA, complete cds |
| 179A3 | 693 | 1002 | BC000514 | NA | 1.00E-160 | 3 | ribosomal protein L13a, clone MGC:8547, mRNA, complete cds |
| 158F10 | 169 | 522 | BC000523 | NA | 1.00E-157 | 1 | Similar to ribosomal protein S24, clone MGC:8595, mRNA, complete cds |
| 515G5 | 34 | 270 | BC000530 | NA | 7.00E-38 | 1 | ribosomal protein L19, clone MGC:8653, mRNA, complete cds |
| 39B6 | 286 | 1073 | BC000590 | NA | 0 | 9 | actin related protein 2/3 complex, subunit 2 (34 kD), clone MGC:1416, |
| 169A4 | 929 | 1314 | BC000672 | NA | 0 | 1 | guanine nucleotide binding protein (G protein), beta polypeptide 2-like |
| 166H4 | 1350 | 1745 | BC000771 | NA | 1.00E-169 | 8 | Similar to tropomyosin 4, clone MGC:3261, mRNA, complete cds |
| 331F9 | 482 | 949 | BC000967 | NA | 0 | 1 | clone IMAGE:3449287, mRNA, partial cds Length = 2156 |
| 526C6 | 633 | 829 | BC001169 | NA | 1.00E-100 | 1 | Similar to esterase 10, clone MGC:1873, mRNA, complete cds |
| 135G12 | 1598 | 1766 | BC001303 | NA | 6.00E-42 | 1 | Similar to splicing factor, arginine/serine-rich 2 (SC-35), clone MGC: |
| 491C6 | 613 | 714 | BC001385 | NA | 3.00E-34 | 1 | Similar to leucine rich repeat (in FLII) interacting protein 1, clone |
| 108D10 | 234 | 641 | BC001399 | NA | 2.00E-79 | 1 | ferritin, heavy polypeptide 1, clone MGC:1749, mRNA, complete cds |
| 196H5 | 1387 | 1899 | BC001412 | NA | 6.00E-55 | 4 | eukaryotic translation elongation factor 1 alpha 1, clone MGC:1332, mR |
| 460F5 | 973 | 1350 | BC001413 | NA | 0 | 1 | clone IMAGE:3140866, mRNA Length = 1634 |
| 520C5 | 348 | 472 | BC001632 | NA | 5.00E-34 | 1 | Similar to NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD), clon |
| 520D10 | 1729 | 2205 | BC001637 | NA | 0 | 2 | ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit |
| 524A1 | 564 | 922 | BC001660 | NA | 1.00E-94 | 2 | ribonuclease 6 precursor, clone MGC:1360, mRNA, complete cds |
| 121E7 | 275 | 381 | BC001697 | NA | 2.00E-26 | 1 | Similar to ribosomal protein S15a, clone MGC:2466, mRNA, complete cds |
| 109D1 | 2441 | 2835 | BC001798 | NA | 1.00E-123 | 1 | clone MGC:3157, mRNA, complete cds Length = 3041 |
| 180D9 | 741 | 921 | BC001819 | NA | 5.00E-85 | 2 | ribonuclease 6 precursor, clone MGC:3554, mRNA, complete cds |
| 72H5 | 1264 | 2808 | BC001854 | NA | 0 | 8 | methionine adenosyltransferase II, alpha, clone MGC:4537, mRNA, comple |
| 167H8 | 1099 | 1436 | BC002409 | NA | 1.00E-49 | 1 | actin, beta, clone MGC:8647, mRNA, complete cds Length = 1858 |
| 53H1 | 2398 | 2513 | BC002538 | NA | 3.00E-41 | 1 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|----------|----|-----------|----|--|
| 125B3 | 246 | 585 | BC002711 | NA | 1.00E-40 | 1 | cell division cycle 42 (GTP-binding protein, 25kD), clone MGC:3497, mR |
| 331H8 | 201 | 557 | BC002837 | NA | 0 | 1 | clone MGC:4175, mRNA, complete cds Length = 1092 |
| 150C4 | 1699 | 2040 | BC002845 | NA | 8.00E-29 | 1 | eukaryotic translation elongation factor 1 alpha 1, clone MGC:3711, mR |
| 70D7 | 345 | 850 | BC002900 | NA | 0 | 1 | Similar to proteasome (prosome, macropain) subunit, alpha type, 2, clo |
| 476B5 | 1431 | 1761 | BC002929 | NA | 1.00E-141 | 1 | clone IMAGE:3954899, mRNA, partial cds Length = 2467 |
| 38D7 | 200 | 688 | BC002971 | NA | 0 | 2 | clone IMAGE:3543711, mRNA, partial cds Length = 1934 |
| 74A11 | 652 | 1724 | BC003063 | NA | 0 | 5 | Similar to likely ortholog of yeast ARV1, clone IMAGE:3506392, mRNA |
| 105H12 | 1148 | 1370 | BC003090 | NA | 1.00E-105 | 1 | COP9 homolog, clone MGC:1297, mRNA, complete cds Length = 1637 |
| 50F4 | 8 | 301 | BC003137 | NA | 1.00E-115 | 1 | ribosomal protein S3, clone MGC:3657, mRNA, complete cds |
| 175G9 | 93 | 216 | BC003352 | NA | 1.00E-33 | 1 | tumor protein, translationally-controlled 1, clone MGC:5308, mRNA, com |
| 587E9 | 72 | 554 | BC003358 | NA | 4.00E-60 | 2 | ribosomal protein L10, clone MGC:5189, mRNA, complete cds |
| 71F8 | 491 | 911 | BC003406 | NA | 0 | 1 | cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acet |
| 512E11 | 308 | 372 | BC003563 | NA | 2.00E-27 | 1 | guanine nucleotide binding protein (G protein), gamma 5, clone MGC:196 |
| 118B11 | 76 | 343 | BC003577 | NA | 1.00E-111 | 1 | clone IMAGE:3544292, mRNA, partial cds Length = 826 |
| 107E3 | 9 | 634 | BC003697 | NA | 0 | 1 | clone MGC:5564, mRNA, complete cds Length = 2145 |
| 128D4 | 1408 | 1550 | BC004186 | NA | 1.00E-34 | 1 | guanine nucleotide binding protein, beta 1, clone MGC:2819, mRNA, comp |
| 58H6 | 554 | 859 | BC004245 | NA | 1.00E-171 | 2 | ferritin, light polypeptide, clone MGC:10465, mRNA, complete cds |
| 481D8 | 134 | 460 | BC004258 | NA | 6.00E-73 | 1 | hypothetical protein PRO1741, clone MGC:10753, mRNA, complete cds |
| 520F6 | 160 | 1400 | BC004317 | NA | 0 | 3 | clone MGC:10924, mRNA, complete cds Length = 1837 |
| 489G7 | 511 | 787 | BC004458 | NA | 2.00E-60 | 1 | enolase 1, (alpha), clone MGC:4315, mRNA, complete cds |
| 115B8 | 1162 | 1640 | BC004521 | NA | 0 | 2 | ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit |
| 118A2 | 1126 | 1369 | BC004805 | NA | 4.00E-38 | 1 | similar to Mus musculus, clone IMAGE:3584831, mRNA Length = 1910 |
| 73D2 | 1174 | 1751 | BC004872 | NA | 0 | 1 | clone MGC:11034, mRNA, complete cds Length = 2471 |
| 522E3 | 681 | 993 | BC004900 | NA | 1.00E-175 | 10 | ribosomal protein L13a, clone IMAGE:3545758, mRNA, partial cds |
| 55G12 | 1 | 232 | BC004928 | NA | 3.00E-68 | 1 | clone MGC:10493, mRNA, complete cds Length = 2567 |
| 520C2 | 3 | 139 | BC004994 | NA | 1.00E-31 | 1 | myosin regulatory light chain, clone MGC:4405, mRNA, complete cds |
| 460H4 | 1577 | 1923 | BC005101 | NA | 0 | 1 | clone IMAGE:3618561, mRNA Length = 2113 |
| 154F12 | 122 | 283 | BC005128 | NA | 2.00E-46 | 1 | ribosomal protein L7a, clone MGC:10607, mRNA, complete cds |
| 592C8 | 647 | 925 | BC005187 | NA | 2.00E-32 | 1 | Similar to hypothetical protein, clone MGC:12182, mRNA, complete cds |
| 591D1 | 726 | 837 | BC005361 | NA | 5.00E-31 | 1 | proteasome (prosome, macropain) subunit, alpha type, 4, clone MGC:1246 |
| 458A7 | 1307 | 1568 | BC005816 | NA | 4.00E-98 | 1 | Similar to deltex (Drosophila) homolog 1, clone IMAGE:3688330, mRNA, p |
| 122C6 | 263 | 378 | BC005928 | NA | 1.00E-29 | 1 | S100 calcium-binding protein A8 (calgranulin A), clone MGC:14536, mRNA |
| 47H11 | 273 | 854 | BC006008 | NA | 0 | 1 | clone IMAGE:4285740, mRNA Length = 1040 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|----------|----|-----------|---|--|
| 598E1 | 850 | 1226 | BC006176 | NA | 0 | 2 | clone IMAGE:4054156, mRNA, partial cds Length = 1423 |
| 175A1 | 570 | 887 | BC006282 | NA | 1.00E-161 | 1 | Similar to RIKEN cDNA 1110020N13 gene, clone MGC:10540 |
| 150H12 | 543 | 1098 | BC006464 | NA | 0 | 1 | calmodulin 2 (phosphorylase kinase, delta), clone MGC:2168 |
| 583E5 | 980 | 1246 | BC006849 | NA | 1.00E-127 | 1 | Similar to RIKEN cDNA 2410044K02 gene, clone MGC:5469 |
| 41H7 | 619 | 1308 | BC007004 | NA | 0 | 2 | Similar to oxysterol-binding protein-related protein 1, clone IMAGE:40 |
| 56C12 | 13 | 187 | BC007063 | NA | 6.00E-27 | 1 | peroxiredoxin 1, clone MGC:12514, mRNA, complete cds Length = 973 |
| 183C11 | 2986 | 3328 | BC007203 | NA | 1.00E-169 | 1 | hypothetical protein MGC10823, clone MGC:12957, mRNA, complete cds |
| 109H10 | 1343 | 1627 | BC007277 | NA | 1.00E-156 | 1 | Similar to RIKEN cDNA 0610039P13 gene, clone MGC:15619, mRNA |
| 588E11 | 423 | 1324 | BC007299 | NA | 0 | 3 | Similar to ATP synthase, H ⁺ transporting, mitochondrial F1 complex, al |
| 164F12 | 72 | 336 | BE002854 | NA | 1.00E-147 | 1 | BN0090 cDNA |
| 106A12 | 22 | 608 | BE005703 | NA | 0 | 1 | BN0120 cDNA |
| 472E11 | 168 | 297 | BE044364 | NA | 1.00E-66 | 1 | Soares_NFL_T_GBC_S1 cDNA clone IMAGE:3040218 3' |
| 458H11 | 2 | 510 | BE049439 | NA | 0 | 1 | cDNA clone IMAGE:2834924 3' |
| 46F7 | 18 | 527 | BE061115 | NA | 0 | 1 | BT0041 cDNA |
| 105A8 | 1 | 166 | BE085539 | NA | 3.00E-74 | 1 | BT0669 cDNA |
| 467F5 | 27 | 247 | BE086076 | NA | 1.00E-115 | 1 | BT0672 cDNA |
| 469B6 | 5 | 188 | BE091932 | NA | 6.00E-87 | 1 | BT0733 cDNA |
| 66D7 | 18 | 568 | BE160822 | NA | 0 | 1 | HT0422 cDNA |
| 593F8 | 110 | 451 | BE163106 | NA | 1.00E-165 | 1 | HT0457 cDNA |
| 468B10 | 1 | 461 | BE168334 | NA | 0 | 1 | HT0514 cDNA |
| 192E1 | 1 | 602 | BE176373 | NA | 0 | 1 | HT0585 cDNA |
| 109A9 | 100 | 377 | BE177661 | NA | 1.00E-129 | 1 | HT0598 cDNA |
| 468B9 | 27 | 145 | BE178880 | NA | 3.00E-31 | 1 | HT0609 cDNA |
| 526E11 | 6 | 222 | BE217848 | NA | 1.00E-118 | 3 | cDNA clone IMAGE:3174941 3' |
| 115H2 | 226 | 227 | BE218938 | NA | 2.00E-97 | 1 | cDNA clone IMAGE:3176478 3' |
| 126B3 | 1 | 509 | BE222301 | NA | 1.00E-151 | 1 | cDNA clone IMAGE:3166180 3' |
| 195F2 | 123 | 470 | BE222392 | NA | 4.00E-91 | 1 | cDNA clone IMAGE:3166335 3' |
| 170F7 | 1 | 375 | BE242649 | NA | 0 | 1 | acute myelogenous leukemia cell (FAB M1) Baylor-HGSC |
| 459F10 | 35 | 432 | BE247056 | NA | 5.00E-84 | 1 | cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA |
| 491G11 | 269 | 516 | BE253336 | NA | 1.00E-116 | 1 | cDNA clone IMAGE:3357826 5' |
| 471H10 | 140 | 202 | BE254064 | NA | 2.00E-26 | 1 | cDNA clone IMAGE:3354554 5' |
| 521H9 | 22 | 605 | BE292793 | NA | 0 | 2 | cDNA clone IMAGE:2987838 5' |
| 472A9 | 33 | 436 | BE297329 | NA | 0 | 1 | cDNA clone IMAGE:3532809 5' |
| 99E10 | 59 | 423 | BE328818 | NA | 0 | 1 | cDNA clone IMAGE:3181355 3' |
| 192C3 | 4 | 335 | BE348809 | NA | 0 | 1 | cDNA clone IMAGE:3152438 3' |
| 140G6 | 206 | 405 | BE348955 | NA | 3.00E-85 | 1 | cDNA clone IMAGE:3144625 3' |
| 483D12 | 1 | 534 | BE349148 | NA | 1.00E-160 | 1 | cDNA clone IMAGE:3150275 3' |
| 491H12 | 1 | 526 | BE379820 | NA | 0 | 1 | cDNA clone IMAGE:3510960 5' |
| 481D5 | 212 | 333 | BE464239 | NA | 3.00E-45 | 1 | cDNA clone IMAGE:3194693 3' |
| 469H8 | 31 | 179 | BE466500 | NA | 2.00E-71 | 1 | cDNA clone IMAGE:3195395 3' |
| 56D11 | 72 | 353 | BE467470 | NA | 1.00E-113 | 1 | cDNA clone IMAGE:3212950 3' |
| 471D10 | 1 | 249 | BE502246 | NA | 1.00E-119 | 2 | cDNA clone IMAGE:3197344 3' |
| 471C2 | 255 | 486 | BE502992 | NA | 1.00E-128 | 1 | cDNA clone IMAGE:3214462 3' |
| 56A2 | 291 | 669 | BE538333 | NA | 1.00E-164 | 1 | cDNA clone IMAGE:3454710 5' |
| 191F12 | 488 | 587 | BE547584 | NA | 9.00E-28 | 1 | cDNA clone IMAGE:3461312 5' |
| 525F3 | 5 | 236 | BE550944 | NA | 1.00E-125 | 1 | cDNA clone IMAGE:3233200 3' |
| 473B7 | 46 | 228 | BE551867 | NA | 4.00E-86 | 1 | cDNA clone IMAGE:3195555 3' |
| 467C6 | 48 | 404 | BE569141 | NA | 1.00E-162 | 1 | cDNA clone IMAGE:3681180 5' |
| 110D3 | 193 | 473 | BE613237 | NA | 1.00E-157 | 2 | cDNA clone IMAGE:3856357 3' |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|-----|-----|----------|----|-----------|---|--|
| 140F9 | 20 | 344 | BE614297 | NA | 1.00E-84 | 1 | cDNA clone IMAGE:3906037 3' |
| 473B12 | 63 | 216 | BE645630 | NA | 3.00E-51 | 1 | cDNA clone IMAGE:3288143 3' similar to contains |
| 460C2 | 156 | 594 | BE646470 | NA | 0 | 1 | cDNA clone IMAGE:3292133 3' |
| 172E5 | 329 | 491 | BE670804 | NA | 7.00E-72 | 8 | cDNA clone IMAGE:3285031 3' similar to gb:J04130 |
| 469D4 | 50 | 553 | BE674685 | NA | 0 | 1 | cDNA clone IMAGE:3292800 3' similar to TR:O60688 |
| 171F2 | 10 | 280 | BE676054 | NA | 1.00E-96 | 1 | cDNA clone IMAGE:3295273 3' |
| 102E12 | 102 | 357 | BE737348 | NA | 2.00E-93 | 1 | cDNA clone IMAGE:3640772 5' |
| 121C11 | 198 | 488 | BE748663 | NA | 1.00E-150 | 1 | cDNA clone IMAGE:3838675 3' |
| 126D1 | 208 | 449 | BE763412 | NA | 1.00E-122 | 1 | NT0036 cDNA |
| 172H5 | 52 | 581 | BE768647 | NA | 0 | 1 | FT0010 cDNA |
| 176F12 | 178 | 646 | BE792125 | NA | 0 | 1 | cDNA clone IMAGE:3936215 5' |
| 71A6 | 16 | 437 | BE825187 | NA | 0 | 1 | CN0028 cDNA |
| 115F11 | 14 | 132 | BE858152 | NA | 4.00E-60 | 1 | cDNA clone IMAGE:3306735 3' |
| 61A11 | 1 | 448 | BE872245 | NA | 0 | 1 | cDNA clone IMAGE:3850435 5' |
| 171B8 | 155 | 377 | BE875145 | NA | 8.00E-88 | 1 | cDNA clone IMAGE:3891244 5' |
| 108A6 | 370 | 539 | BE876375 | NA | 7.00E-72 | 2 | cDNA clone IMAGE:3889033 5' |
| 166B1 | 1 | 472 | BE877115 | NA | 1.00E-153 | 1 | cDNA clone IMAGE:3887598 5' |
| 63D11 | 208 | 496 | BE878973 | NA | 1.00E-141 | 1 | cDNA clone IMAGE:3895002 5' |
| 525C3 | 208 | 400 | BE879482 | NA | 7.00E-88 | 1 | cDNA clone IMAGE:3894277 5' |
| 526F7 | 335 | 603 | BE881113 | NA | 1.00E-126 | 1 | cDNA clone IMAGE:3894306 5' |
| 152G12 | 122 | 659 | BE881351 | NA | 0 | 2 | cDNA clone IMAGE:3892808 5' |
| 589H4 | 118 | 510 | BE882335 | NA | 0 | 2 | cDNA clone IMAGE:3907044 5' |
| 51B12 | 199 | 631 | BE884898 | NA | 3.00E-56 | 1 | cDNA clone IMAGE:3908551 5' |
| 114C1 | 286 | 530 | BE887646 | NA | 1.00E-121 | 1 | cDNA clone IMAGE:3913468 5' |
| 120H2 | 282 | 706 | BE888744 | NA | 0 | 1 | cDNA clone IMAGE:3915133 5' |
| 107D11 | 172 | 497 | BE891242 | NA | 0 | 1 | cDNA clone IMAGE:3917201 5' |
| 513G4 | 263 | 662 | BE891269 | NA | 0 | 1 | cDNA clone IMAGE:3917064 5' |
| 166B8 | 7 | 453 | BE891928 | NA | 0 | 1 | cDNA clone IMAGE:3920185 5' |
| 185G9 | 23 | 390 | BE894437 | NA | 1.00E-145 | 1 | cDNA clone IMAGE:3918224 5' |
| 189A8 | 211 | 485 | BE896691 | NA | 1.00E-82 | 1 | cDNA clone IMAGE:3925062 5' |
| 598A7 | 78 | 301 | BE897669 | NA | 1.00E-83 | 1 | cDNA clone IMAGE:3923346 5' |
| 191D9 | 189 | 575 | BE899595 | NA | 0 | 3 | cDNA clone IMAGE:3952215 5' |
| 331F2 | 109 | 287 | BF001438 | NA | 3.00E-96 | 2 | cDNA clone IMAGE:3313517 3' |
| 192C9 | 57 | 419 | BF033741 | NA | 0 | 1 | cDNA clone IMAGE:3857635 5' |
| 117H4 | 73 | 454 | BF056055 | NA | 0 | 1 | cDNA clone IMAGE:3443950 3' similar to contains |
| 104B10 | 6 | 412 | BF058599 | NA | 1.00E-177 | 1 | cDNA clone IMAGE:3477311 3' |
| 331A12 | 13 | 164 | BF059133 | NA | 1.00E-72 | 1 | cDNA clone IMAGE:3480249 3' |
| 40H1 | 81 | 507 | BF060725 | NA | 0 | 1 | 7j59h07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone |
| 464F1 | 1 | 510 | BF061421 | NA | 0 | 1 | 7j52c11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone |
| 71E11 | 1 | 441 | BF105172 | NA | 0 | 1 | cDNA clone IMAGE:4042560 5' |
| 129D7 | 92 | 561 | BF116224 | NA | 0 | 2 | cDNA clone IMAGE:3570793 3' |
| 145E10 | 83 | 624 | BF131060 | NA | 0 | 1 | cDNA clone IMAGE:4051731 5' |
| 113B6 | 105 | 410 | BF194880 | NA | 1.00E-157 | 1 | cDNA clone IMAGE:3643600 3' |
| 157E9 | 102 | 308 | BF197153 | NA | 1.00E-108 | 2 | cDNA clone IMAGE:3561933 3' |
| 127H8 | 1 | 173 | BF197762 | NA | 3.00E-92 | 1 | cDNA clone IMAGE:3653139 3' |
| 462D1 | 29 | 177 | BF221780 | NA | 7.00E-78 | 1 | cDNA clone IMAGE:3578603 3' |
| 472B8 | 7 | 229 | BF306204 | NA | 9.00E-70 | 1 | cDNA clone IMAGE:4138980 5' |
| 62A3 | 187 | 612 | BF309911 | NA | 1.00E-162 | 1 | cDNA clone IMAGE:4138171 5' |
| 476G4 | 316 | 487 | BF330908 | NA | 5.00E-66 | 1 | BT0333 cDNA |
| 524D1 | 86 | 258 | BF339088 | NA | 8.00E-88 | 1 | cDNA clone IMAGE:4182956 5' |
| 58G4 | 13 | 606 | BF341359 | NA | 0 | 2 | cDNA clone IMAGE:4149195 5' |
| 480E7 | 68 | 288 | BF357523 | NA | 4.00E-97 | 1 | HT0945 cDNA |
| 116C9 | 8 | 170 | BF364413 | NA | 2.00E-81 | 1 | NN1068 cDNA |
| 168F4 | 11 | 595 | BF369763 | NA | 0 | 1 | GN0120 cDNA |
| 495F1 | 1 | 318 | BF373638 | NA | 1.00E-108 | 2 | FT0176 cDNA |
| 98E1 | 81 | 499 | BF377518 | NA | 0 | 2 | TN0115 cDNA |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|-----|-----|----------|----|-----------|---|---|
| 169C5 | 17 | 500 | BF380732 | NA | 0 | 1 | UT0073 cDNA |
| 464E11 | 12 | 272 | BF432643 | NA | 1.00E-129 | 1 | cDNA clone IMAGE:3406531 3' |
| 183G2 | 119 | 548 | BF433058 | NA | 1.00E-112 | 1 | cDNA clone IMAGE:3565500 3' |
| 473F9 | 21 | 411 | BF433353 | NA | 0 | 1 | cDNA clone IMAGE:3703678 3' |
| 117C9 | 179 | 462 | BF433657 | NA | 2.00E-99 | 1 | cDNA clone IMAGE:3702965 3' similar to contains |
| 514A3 | 170 | 245 | BF435621 | NA | 2.00E-34 | 2 | Lupski_sciatic_nerve cDNA clone IMAGE:3394901 3' similar to |
| 459G8 | 78 | 417 | BF445405 | NA | 1.00E-179 | 1 | cDNA clone IMAGE:3699337 3' |
| 483D10 | 12 | 474 | BF447885 | NA | 0 | 1 | cDNA clone IMAGE:3706147 3' |
| 519H12 | 319 | 394 | BF449068 | NA | 3.00E-27 | 1 | cDNA clone IMAGE:3579069 3' |
| 584H11 | 78 | 487 | BF475501 | NA | 7.00E-50 | 1 | Lupski_sciatic_nerve cDNA clone IMAGE:3396242 3' |
| 471G8 | 214 | 400 | BF478238 | NA | 9.00E-61 | 1 | cDNA clone IMAGE:3700476 3' similar to contains |
| 109F10 | 20 | 329 | BF507849 | NA | 1.00E-172 | 1 | UI-H-BI4-apv-h-02-0-UI.s1 NCI_CGAP_Sub8 cDNA clone IMAGE:3088755 3' |
| 173E10 | 147 | 231 | BF510393 | NA | 1.00E-39 | 1 | UI-H-BI4-aon-h-07-0-UI.s1 NCI_CGAP_Sub8 cDNA clone IMAGE:3085669 3' |
| 464D1 | 32 | 460 | BF513602 | NA | 1.00E-106 | 1 | UI-H-BW1-amt-a-11-0-UI.s1 NCI_CGAP_Sub7 cDNA clone IMAGE:3070773 3' |
| 118D9 | 106 | 248 | BF514341 | NA | 4.00E-46 | 1 | UI-H-BW1-and-h-10-0-UI.s1 NCI_CGAP_Sub7 cDNA clone IMAGE:3082218 3' |
| 462E3 | 29 | 197 | BF515538 | NA | 1.00E-87 | 1 | UI-H-BW1-anq-b-09-0-UI.s1 NCI_CGAP_Sub7 cDNA clone IMAGE:3083081 3' |
| 459C7 | 70 | 661 | BF525720 | NA | 0 | 1 | cDNA clone IMAGE:4212877 5' |
| 462F8 | 151 | 684 | BF526421 | NA | 0 | 1 | cDNA clone IMAGE:4213536 5' |
| 174H6 | 1 | 367 | BF530382 | NA | 0 | 1 | cDNA clone IMAGE:4214327 5' |
| 477C5 | 183 | 689 | BF569545 | NA | 0 | 1 | cDNA clone IMAGE:4310435 5' |
| 46C3 | 2 | 626 | BF571362 | NA | 0 | 1 | cDNA clone IMAGE:4252059 5' |
| 465B1 | 350 | 508 | BF591040 | NA | 3.00E-39 | 1 | cDNA clone IMAGE:3319177 3' |
| 477G7 | 6 | 127 | BF592138 | NA | 2.00E-57 | 1 | cDNA clone IMAGE:3573334 3' |
| 180B2 | 53 | 264 | BF593930 | NA | 1.00E-114 | 1 | nab48e03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone |
| 185F12 | 139 | 578 | BF663116 | NA | 0 | 1 | cDNA clone IMAGE:4308392 5' |
| 471F9 | 77 | 590 | BF667621 | NA | 0 | 1 | cDNA clone IMAGE:4278888 5' |
| 41D10 | 16 | 664 | BF668050 | NA | 0 | 2 | cDNA clone IMAGE:4279827 5' |
| 491G6 | 87 | 275 | BF670567 | NA | 1.00E-97 | 1 | cDNA clone IMAGE:4290961 5' |
| 112B4 | 17 | 303 | BF671020 | NA | 1.00E-120 | 1 | cDNA clone IMAGE:4292143 5' |
| 194H6 | 6 | 196 | BF678298 | NA | 1.00E-100 | 1 | cDNA clone IMAGE:4248916 5' |
| 514H9 | 96 | 179 | BF691178 | NA | 2.00E-32 | 1 | cDNA clone IMAGE:4332544 5' |
| 99H1 | 146 | 327 | BF691895 | NA | 2.00E-69 | 1 | cDNA clone IMAGE:4333460 5' |
| 465E12 | 29 | 681 | BF725383 | NA | 0 | 1 | cDNA (Un-normalized, unamplified): BX cDNA clone |
| 69B10 | 17 | 96 | BF726114 | NA | 3.00E-37 | 1 | cDNA (Un-normalized, unamplified): BY cDNA clone |
| 151H10 | 18 | 366 | BF732404 | NA | 0 | 1 | cDNA clone IMAGE:3434918 3' |
| 124D2 | 36 | 378 | BF736784 | NA | 1.00E-179 | 1 | KT0018 cDNA |
| 463H5 | 30 | 152 | BF740663 | NA | 3.00E-56 | 1 | HB0031 cDNA |
| 469D2 | 164 | 398 | BF744387 | NA | 6.00E-74 | 1 | BT0636 cDNA |
| 72E1 | 17 | 128 | BF749089 | NA | 1.00E-44 | 3 | BN0386 cDNA |
| 98C3 | 9 | 515 | BF758480 | NA | 0 | 1 | CT0539 cDNA |
| 46E11 | 26 | 162 | BF773126 | NA | 5.00E-57 | 1 | IT0048 cDNA |
| 124C8 | 32 | 257 | BF773393 | NA | 1.00E-115 | 1 | IT0039 cDNA |
| 166G8 | 312 | 549 | BF797348 | NA | 1.00E-108 | 1 | cDNA clone IMAGE:4340490 5' |
| 146D8 | 222 | 288 | BF805164 | NA | 5.00E-29 | 1 | CI0173 cDNA |
| 49G4 | 99 | 460 | BF813798 | NA | 0 | 5 | CI0084 cDNA |
| 469F8 | 31 | 455 | BF816700 | NA | 4.00E-88 | 1 | CI0128 cDNA |
| 98C1 | 37 | 375 | BF818594 | NA | 1.00E-163 | 1 | CI0184 cDNA |
| 62C9 | 166 | 359 | BF821451 | NA | 3.00E-28 | 1 | RT0038 cDNA |
| 51F8 | 28 | 367 | BF827734 | NA | 1.00E-175 | 1 | HN0025 cDNA |
| 56F7 | 15 | 429 | BF845167 | NA | 9.00E-84 | 1 | HT1035 cDNA |
| 476D11 | 1 | 303 | BF869167 | NA | 1.00E-165 | 2 | ET0119 cDNA |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|-----|-----|----------|----|-----------|---|---|
| 476H4 | 12 | 262 | BF875575 | NA | 1.00E-131 | 2 | ET0100 cDNA |
| 68D6 | 242 | 452 | BF877979 | NA | 3.00E-98 | 1 | ET0109 cDNA |
| 37C10 | 1 | 381 | BF897042 | NA | 0 | 3 | MT0179 cDNA |
| 465B3 | 63 | 193 | BF898285 | NA | 5.00E-60 | 1 | MT0229 cDNA |
| 331C7 | 274 | 485 | BF899464 | NA | 3.00E-83 | 1 | MT0211 cDNA |
| 72D8 | 50 | 334 | BF904425 | NA | 1.00E-152 | 1 | MT0245 cDNA |
| 159F6 | 333 | 417 | BF906114 | NA | 2.00E-35 | 1 | MT0267 cDNA |
| 108H5 | 6 | 409 | BF926187 | NA | 0 | 1 | NT0193 cDNA |
| 71F9 | 192 | 286 | BF928644 | NA | 1.00E-43 | 1 | NT0216 cDNA |
| 481D4 | 27 | 334 | BF938959 | NA | 1.00E-102 | 1 | cDNA clone IMAGE:3706689 3' |
| 189B11 | 69 | 183 | BF939014 | NA | 4.00E-29 | 1 | cDNA clone IMAGE:3706658 3' |
| 115G2 | 85 | 399 | BF940103 | NA | 1.00E-177 | 1 | cDNA clone IMAGE:3439383 3' |
| 463B3 | 304 | 449 | BF940291 | NA | 8.00E-62 | 1 | cDNA clone IMAGE:3577096 3' |
| 122G1 | 8 | 339 | BF950968 | NA | 1.00E-170 | 1 | NN1186 cDNA |
| 470B4 | 251 | 320 | BF962743 | NA | 2.00E-28 | 1 | NN0045 cDNA |
| 516D5 | 39 | 208 | BF962934 | NA | 5.00E-69 | 1 | NN0045 cDNA |
| 593G10 | 242 | 597 | BF965068 | NA | 1.00E-177 | 2 | cDNA clone IMAGE:4356776 5' |
| 101A1 | 6 | 356 | BF965438 | NA | 1.00E-132 | 1 | cDNA clone IMAGE:4356453 5' |
| 477F3 | 25 | 653 | BF965960 | NA | 0 | 1 | cDNA clone IMAGE:4365102 5' |
| 588E4 | 67 | 562 | BF966028 | NA | 1.00E-134 | 1 | cDNA clone IMAGE:4364887 5' |
| 467F10 | 11 | 282 | BF966049 | NA | 1.00E-122 | 1 | cDNA clone IMAGE:4364941 5' |
| 59E12 | 81 | 355 | BF966269 | NA | 1.00E-144 | 1 | cDNA clone IMAGE:4375212 5' |
| 480E11 | 416 | 755 | BF968628 | NA | 8.00E-41 | 1 | cDNA clone IMAGE:4359351 5' |
| 37H8 | 200 | 500 | BF968963 | NA | 1.00E-148 | 1 | cDNA clone IMAGE:4358390 5' |
| 98H5 | 396 | 397 | BF969990 | NA | 1.00E-133 | 1 | cDNA clone IMAGE:4360614 5' |
| 597C3 | 15 | 571 | BF971075 | NA | 0 | 1 | cDNA clone IMAGE:4358911 5' |
| 101F1 | 188 | 305 | BF971984 | NA | 6.00E-42 | 1 | cDNA clone IMAGE:4329095 5' |
| 464H5 | 246 | 602 | BF980139 | NA | 0 | 1 | cDNA clone IMAGE:4373963 3' |
| 63B6 | 130 | 597 | BF981080 | NA | 0 | 1 | cDNA clone IMAGE:4401411 5' |
| 167A3 | 223 | 418 | BF981263 | NA | 1.00E-101 | 1 | cDNA clone IMAGE:4400757 5' |
| 512C12 | 1 | 494 | BF981634 | NA | 0 | 1 | cDNA clone IMAGE:4397101 5' |
| 187H7 | 26 | 433 | BF997765 | NA | 1.00E-180 | 2 | GN0127 cDNA |
| 458E4 | 54 | 242 | BG006820 | NA | 3.00E-62 | 1 | GN0227 cDNA |
| 106A7 | 1 | 604 | BG024761 | NA | 0 | 1 | cDNA clone IMAGE:4363858 5' |
| 459H6 | 1 | 524 | BG026279 | NA | 0 | 1 | cDNA clone IMAGE:4386607 5' |
| 460B9 | 264 | 512 | BG028577 | NA | 1.00E-105 | 1 | cDNA clone IMAGE:4387518 5' |
| 49E9 | 100 | 537 | BG033909 | NA | 0 | 1 | cDNA clone IMAGE:4402729 5' |
| 54C10 | 1 | 582 | BG033953 | NA | 0 | 2 | cDNA clone IMAGE:4402647 5' |
| 182B3 | 1 | 489 | BG034799 | NA | 0 | 1 | cDNA clone IMAGE:4413514 5' |
| 166F8 | 13 | 586 | BG036101 | NA | 0 | 1 | cDNA clone IMAGE:4414135 5' |
| 104A12 | 56 | 240 | BG054966 | NA | 1.00E-100 | 1 | cDNA clone IMAGE:3441756 3' |
| 171H10 | 4 | 269 | BG056668 | NA | 3.00E-85 | 1 | cDNA clone IMAGE:4169714 3' |
| 146G11 | 13 | 522 | BG057282 | NA | 0 | 5 | cDNA clone IMAGE:4140477 3' similar to contains |
| 472A11 | 69 | 358 | BG057892 | NA | 1.00E-145 | 1 | 7f76e08.x1 Lupski_dorsal_root_ganglion cDNA clone |
| 513B4 | 2 | 418 | BG058599 | NA | 0 | 1 | cDNA clone IMAGE:4141266 3' |
| 134B4 | 201 | 519 | BG058739 | NA | 1.00E-75 | 4 | cDNA clone IMAGE:4140551 3' |
| 163E7 | 83 | 327 | BG110599 | NA | 1.00E-126 | 1 | cDNA clone IMAGE:4368492 5' |
| 118A7 | 180 | 577 | BG110835 | NA | 0 | 1 | cDNA clone IMAGE:4366502 5' |
| 37F12 | 38 | 649 | BG111212 | NA | 0 | 5 | cDNA clone IMAGE:4369233 5' |
| 464A10 | 57 | 673 | BG111773 | NA | 0 | 1 | cDNA clone IMAGE:4372861 5' |
| 464A7 | 56 | 411 | BG118529 | NA | 1.00E-167 | 1 | cDNA clone IMAGE:4443519 5' |
| 458D8 | 186 | 715 | BG121288 | NA | 0 | 1 | cDNA clone IMAGE:4450407 5' |
| 166H12 | 25 | 339 | BG149747 | NA | 1.00E-177 | 1 | cDNA clone IMAGE:3367325 3' |
| 51H4 | 4 | 224 | BG149986 | NA | 1.00E-121 | 1 | cDNA clone IMAGE:3406766 3' |
| 75G3 | 70 | 280 | BG150273 | NA | 1.00E-115 | 4 | cDNA clone IMAGE:3442930 3' |
| 500F10 | 18 | 677 | BG163237 | NA | 0 | 3 | cDNA clone IMAGE:4446802 5' |
| 519E4 | 39 | 575 | BG164898 | NA | 0 | 3 | cDNA clone IMAGE:4453661 5' |
| 119E5 | 21 | 276 | BG165998 | NA | 1.00E-120 | 1 | cDNA clone IMAGE:4456017 5' |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|-----|-----|----------|----|-----------|----|--|
| 519B8 | 29 | 214 | BG166279 | NA | 5.00E-86 | 1 | cDNA clone IMAGE:4455496 5' |
| 103B8 | 377 | 499 | BG170647 | NA | 1.00E-45 | 1 | cDNA clone IMAGE:4426826 5' |
| 470F8 | 184 | 307 | BG180098 | NA | 4.00E-63 | 1 | cDNA clone IMAGE:4430875 5' |
| 585C4 | 4 | 98 | BG230563 | NA | 5.00E-46 | 1 | cDNA clone IMAGE:4143330 3' similar to contains |
| 48G7 | 2 | 298 | BG231557 | NA | 1.00E-119 | 1 | cDNA clone IMAGE:4142471 3' |
| 73C4 | 188 | 430 | BG231805 | NA | 1.00E-130 | 1 | cDNA clone IMAGE:4142814 3' |
| 148H4 | 2 | 525 | BG231961 | NA | 1.00E-133 | 12 | cDNA clone IMAGE:4143104 3' |
| 484B5 | 364 | 533 | BG235942 | NA | 5.00E-81 | 1 | cDNA clone IMAGE:4141389 3' |
| 137B5 | 97 | 523 | BG236015 | NA | 6.00E-87 | 1 | cDNA clone IMAGE:4141365 3' |
| 489B11 | 12 | 294 | BG236084 | NA | 4.00E-75 | 2 | cDNA clone IMAGE:4141856 3' similar to |
| 45H2 | 1 | 492 | BG249224 | NA | 1.00E-139 | 1 | cDNA clone IMAGE:4470038 5' |
| 172F1 | 1 | 562 | BG254117 | NA | 0 | 1 | cDNA clone IMAGE:4475233 5' |
| 588F3 | 66 | 202 | BG254292 | NA | 9.00E-43 | 1 | cDNA clone IMAGE:4477042 5' |
| 583B5 | 8 | 183 | BG272304 | NA | 7.00E-45 | 1 | cDNA clone IMAGE:4257371 |
| 73A4 | 119 | 311 | BG282346 | NA | 3.00E-42 | 1 | cDNA clone IMAGE:4545131 5' |
| 586A2 | 99 | 511 | BG283706 | NA | 1.00E-160 | 1 | cDNA clone IMAGE:4519866 5' |
| 152F12 | 1 | 676 | BG286649 | NA | 0 | 5 | cDNA clone IMAGE:4499224 5' |
| 479A12 | 228 | 601 | BG286817 | NA | 1.00E-142 | 1 | cDNA clone IMAGE:4500259 5' |
| 99B4 | 1 | 449 | BG288308 | NA | 0 | 2 | cDNA clone IMAGE:4512706 5' |
| 584G2 | 54 | 468 | BG288554 | NA | 0 | 1 | cDNA clone IMAGE:4517068 5' |
| 464E2 | 244 | 549 | BG289048 | NA | 1.00E-159 | 2 | cDNA clone IMAGE:4512868 5' |
| 113H1 | 149 | 436 | BG289347 | NA | 1.00E-161 | 1 | cDNA clone IMAGE:4516241 5' |
| 39G6 | 1 | 503 | BG290577 | NA | 0 | 1 | cDNA clone IMAGE:4517986 5' |
| 48D8 | 38 | 440 | BG291970 | NA | 0 | 1 | cDNA clone IMAGE:4517457 5' |
| 60E7 | 1 | 398 | BG319445 | NA | 0 | 4 | Keratinocyte Subtraction Library- Downregulated Transcripts Homo |
| 168C2 | 3 | 221 | BG319498 | NA | 1.00E-111 | 2 | Keratinocyte Subtraction Library- Downregulated Transcripts Homo |
| 461B12 | 1 | 393 | BG387694 | NA | 0 | 2 | cDNA clone IMAGE:4521084 5' |
| 174G11 | 3 | 542 | BG391695 | NA | 0 | 1 | cDNA clone IMAGE:4537243 5' |
| 597A4 | 164 | 612 | BG396292 | NA | 0 | 2 | cDNA clone IMAGE:4581548 5' |
| 190B10 | 469 | 667 | BG397564 | NA | 3.00E-62 | 2 | cDNA clone IMAGE:4564968 5' |
| 593C3 | 35 | 461 | BG403635 | NA | 0 | 1 | cDNA clone IMAGE:4526364 5' |
| 57H10 | 121 | 495 | BG413494 | NA | 0 | 1 | 7j54e06.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone |
| 155G11 | 119 | 347 | BG424974 | NA | 3.00E-52 | 1 | cDNA clone IMAGE:4591378 5' |
| 45G3 | 17 | 332 | BG427404 | NA | 1.00E-159 | 1 | cDNA clone IMAGE:4612518 5' |
| 185C9 | 16 | 185 | BG432194 | NA | 3.00E-62 | 1 | cDNA clone IMAGE:4610035 5' |
| 331D4 | 60 | 386 | BG434865 | NA | 1.00E-179 | 1 | cDNA clone IMAGE:4605025 5' |
| 464H12 | 97 | 295 | BG438232 | NA | 1.00E-105 | 1 | cDNA clone IMAGE:4622433 5' |
| 521F2 | 280 | 534 | BG468330 | NA | 1.00E-111 | 1 | cDNA clone IMAGE:4644153 5' |
| 56F6 | 167 | 582 | BG473228 | NA | 0 | 2 | cDNA clone IMAGE:4646938 5' |
| 61G3 | 8 | 185 | BG473813 | NA | 2.00E-95 | 1 | cDNA clone IMAGE:4647416 5' |
| 119E9 | 7 | 377 | BG482798 | NA | 1.00E-178 | 3 | cDNA clone IMAGE:4616253 5' |
| 125F8 | 47 | 318 | BG489375 | NA | 1.00E-149 | 1 | cDNA clone IMAGE:4636634 5' |
| 73H3 | 55 | 154 | BG493253 | NA | 5.00E-49 | 1 | cDNA clone IMAGE:4672787 5' |
| 111H9 | 79 | 754 | BG497765 | NA | 0 | 1 | cDNA clone IMAGE:4665582 5' |
| 171A10 | 74 | 476 | BG501063 | NA | 0 | 1 | cDNA clone IMAGE:4668643 5' |
| 471G1 | 65 | 197 | BG501895 | NA | 1.00E-63 | 1 | cDNA clone IMAGE:4654344 5' |
| 111E1 | 16 | 181 | BG503693 | NA | 4.00E-85 | 2 | cDNA clone IMAGE:4657381 5' |
| 121B6 | 77 | 553 | BG505271 | NA | 0 | 2 | cDNA clone IMAGE:4664028 5' |
| 599F2 | 379 | 484 | BG505379 | NA | 3.00E-45 | 1 | cDNA clone IMAGE:4657121 5' |
| 105C1 | 208 | 646 | BG505961 | NA | 0 | 1 | cDNA clone IMAGE:4072795 5' |
| 521E10 | 23 | 440 | BG506168 | NA | 0 | 4 | cDNA clone IMAGE:4072226 5' |
| 119A5 | 188 | 596 | BG506472 | NA | 1.00E-103 | 1 | cDNA clone IMAGE:4070820 5' |
| 479D7 | 34 | 308 | BG527060 | NA | 1.00E-121 | 1 | cDNA clone IMAGE:4685209 5' |
| 71H3 | 27 | 542 | BG527658 | NA | 0 | 1 | cDNA clone IMAGE:4685854 5' |
| 186A7 | 2 | 336 | BG531486 | NA | 5.00E-96 | 1 | cDNA clone IMAGE:4699409 5' |
| 187H11 | 186 | 662 | BG532345 | NA | 0 | 1 | cDNA clone IMAGE:4699954 5' |
| 64G4 | 166 | 650 | BG532470 | NA | 0 | 1 | cDNA clone IMAGE:4699923 5' |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|----------|----|-----------|---|--|
| 486E6 | 224 | 561 | BG533994 | NA | 1.00E-168 | 5 | cDNA clone IMAGE:4663102 5' |
| 116F9 | 188 | 392 | BG536394 | NA | 7.00E-67 | 1 | cDNA clone IMAGE:4689645 5' |
| 75C7 | 1 | 452 | BG536641 | NA | 0 | 2 | cDNA clone IMAGE:4691078 5' |
| 175D10 | 3 | 114 | BG537502 | NA | 2.00E-49 | 1 | cDNA clone IMAGE:4690780 5' |
| 599E1 | 356 | 659 | BG538731 | NA | 1.00E-111 | 1 | cDNA clone IMAGE:4691392 5' |
| 191H9 | 80 | 631 | BG541679 | NA | 0 | 1 | cDNA clone IMAGE:4695805 5' |
| 466A4 | 1 | 408 | BG542394 | NA | 0 | 1 | cDNA clone IMAGE:4696046 5' |
| 67G12 | 29 | 698 | BG547561 | NA | 0 | 3 | cDNA clone IMAGE:4703738 5' |
| 467B6 | 60 | 234 | BG547627 | NA | 3.00E-93 | 2 | cDNA clone IMAGE:4703608 5' |
| 488F8 | 2041 | 2132 | D10495 | NA | 9.00E-31 | 1 | mRNA for protein kinase C delta-type, complete cds Length = 2163 |
| 525B6 | 21 | 222 | D17042 | NA | 1.00E-100 | 2 | HepG2 partial cDNA, clone hmd3f07m5 Length = 222 |
| 471E4 | 2287 | 2877 | D17391 | NA | 0 | 2 | mRNA for alpha 4(IV) collagen, C-terminal Length = 3558 |
| 134D8 | 561 | 694 | D28589 | NA | 2.00E-59 | 1 | mRNA (KIAA00167), partial sequence Length = 792 |
| 112D1 | 1614 | 2159 | D30036 | NA | 0 | 1 | mRNA for phosphatidylinositol transfer protein (PI-TPalpha), complete |
| 98H4 | 1 | 357 | F11941 | NA | 1.00E-180 | 1 | brain cDNA cDNA clone c-33f05 |
| 585G7 | 15 | 264 | F13765 | NA | 1.00E-136 | 1 | (1992) cDNA clone FII112 3' |
| 47D11 | 1 | 296 | F35665 | NA | 1.00E-146 | 1 | cDNA clone sH5-000005-0/E06 |
| 465F5 | 34 | 225 | H03298 | NA | 1.00E-70 | 1 | cDNA clone IMAGE:151865 5' |
| 481A6 | 43 | 362 | H51796 | NA | 1.00E-123 | 1 | spleen 1NFLS cDNA clone IMAGE:194250 5' |
| 100E3 | 116 | 205 | H56344 | NA | 1.00E-37 | 1 | spleen 1NFLS cDNA clone IMAGE:203711 5' similar to |
| 464F9 | 10 | 398 | H57221 | NA | 5.00E-45 | 2 | spleen 1NFLS cDNA clone IMAGE:204710 5' |
| 66C3 | 10 | 77 | H78395 | NA | 8.00E-28 | 1 | liver spleen 1NFLS cDNA clone IMAGE:233597 3' |
| 105D11 | 63 | 365 | H81660 | NA | 1.00E-154 | 1 | 2NbHM cDNA clone IMAGE:249138 5' |
| 60G10 | 1 | 189 | H86841 | NA | 1.00E-100 | 1 | cDNA clone IMAGE:220310 5' similar to SP:S44265 |
| 470D6 | 1 | 314 | H92914 | NA | 1.00E-146 | 1 | Soares_pineal_gland_N3HPG cDNA clone IMAGE:231988 3' |
| 483E5 | 839 | 944 | K02885 | NA | 1.00E-26 | 1 | T-cell receptor active beta-chain V-D-J-beta-1.2-C-beta-1 (TCRB) mRNA, |
| 516F5 | 1753 | 2047 | L11284 | NA | 1.00E-131 | 1 | Homosapiens ERK activator kinase (MEK1) mRNA Length = 2222 |
| 525E11 | 105 | 738 | L40557 | NA | 1.00E-112 | 1 | perforin (PRF1) mRNA, 3' end Length = 818 |
| 74F1 | 661 | 826 | M11124 | NA | 5.00E-41 | 1 | MHC HLA DQ alpha-chain mRNA from DRw9 cell line Length = 835 |
| 121E3 | 1323 | 1870 | M12824 | NA | 0 | 4 | T-cell differentiation antigen Leu-2/T8 mRNA, partial cds Length = 197 |
| 66H2 | 713 | 1190 | M17783 | NA | 0 | 1 | glia-derived nexin (GDN) mRNA, 5' end Length = 1191 |
| 41A9 | 698 | 883 | M32577 | NA | 4.00E-28 | 1 | MHC HLA-DQ beta mRNA, complete cds Length = 1104 |
| 478D10 | 436 | 605 | M55674 | NA | 4.00E-33 | 1 | (clone M212) phosphoglycerate mutase 2 (muscle specific isozyme) (PGAM) |
| 469B8 | 5 | 377 | N20190 | NA | 0 | 1 | 2NbHM cDNA clone IMAGE:264340 3' |
| 109E4 | 21 | 449 | N23307 | NA | 0 | 2 | 2NbHM cDNA clone IMAGE:267836 3' |
| 171D9 | 80 | 381 | N25486 | NA | 1.00E-147 | 1 | 2NbHM cDNA clone IMAGE:264068 5' |
| 73H12 | 1 | 398 | N27575 | NA | 1.00E-144 | 2 | 2NbHM cDNA clone IMAGE:264499 5' |
| 490A11 | 25 | 475 | N31700 | NA | 0 | 1 | 2NbHM cDNA clone IMAGE:267025 5' |
| 599D6 | 185 | 483 | N34261 | NA | 1.00E-150 | 1 | 2NbHM cDNA clone IMAGE:267967 5' |
| 188F3 | 112 | 357 | N36787 | NA | 1.00E-107 | 1 | 2NbHM cDNA clone IMAGE:273145 3' |
| 465B10 | 7 | 558 | N49836 | NA | 0 | 1 | yz08a11.s1 Soares_multiple_sclerosis_2NbHMSP cDNA |
| 40D4 | 199 | 575 | N58136 | NA | 1.00E-153 | 1 | spleen 1NFLS cDNA clone IMAGE:247587 3' |
| 183E2 | 227 | 366 | N80578 | NA | 2.00E-53 | 1 | Soares_fetal_lung_NbHL19W cDNA clone IMAGE:300873 3' similar to |
| 139G6 | 9 | 269 | N94511 | NA | 1.00E-125 | 1 | zb80g04.s1 Soares_senescent_fibroblasts_NbHSF cDNA |
| 126B8 | 1 | 256 | N99577 | NA | 1.00E-137 | 2 | spleen 1NFLS cDNA clone IMAGE:295067 5' |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----|-----------|---|---|
| 118A10 | 893 | 5056 | NC_001807 | NA | 0 | 7 | mitochondrion, complete genome Length = 16568 |
| 41B2 | 1 | 471 | NM_000873 | NA | 0 | 1 | intercellular adhesion molecule 2 (ICAM2), mRNA Length = 1035 |
| 62A8 | 1877 | 1958 | NM_000958 | NA | 1.00E-37 | 4 | prostaglandin E receptor 4 (subtype EP4) (PTGER4), mRNA |
| 179H10 | 53 | 265 | NM_000983 | NA | 1.00E-44 | 1 | ribosomal protein L22 (RPL22), mRNA Length = 602 |
| 331D3 | 71 | 343 | NM_001024 | NA | 1.00E-144 | 5 | ribosomal protein S21 (RPS21), mRNA Length = 343 |
| 41G10 | 3162 | 3565 | NM_001243 | NA | 3.00E-47 | 1 | tumor necrosis factor receptor superfamily, member 8 (TNFRSF8), mRNA |
| 591E9 | 1027 | 1483 | NM_002211 | NA | 0 | 2 | integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 |
| 497C6 | 4946 | 5064 | NM_002460 | NA | 9.00E-36 | 2 | interferon regulatory factor 4 (IRF4), mRNA Length = 5065 |
| 597D8 | 1232 | 1461 | NM_005356 | NA | 2.00E-48 | 1 | lymphocyte-specific protein tyrosine kinase (LCK), mRNA Length = 2032 |
| 166G2 | 50 | 319 | NM_005745 | NA | 2.00E-90 | 1 | accessory proteins BAP31/BAP29 (DXS1357E), mRNA Length = 1314 |
| 468D2 | 3245 | 3480 | NM_011086 | NA | 8.00E-63 | 1 | similar to Mus phosphoinositide kinase, fyve-containing (Pikfyve), mRNA |
| 599A4 | 1335 | 1630 | NM_014644 | NA | 2.00E-69 | 1 | KIAA0477 gene product (KIAA0477), mRNA Length = 5676 |
| 69C2 | 818 | 1361 | NM_014905 | NA | 0 | 3 | glutaminase (GLS), mRNA Length = 4606 |
| 495C6 | 622 | 838 | NM_015435 | NA | 1.00E-104 | 1 | double ring-finger protein, Dorfin (DORFIN), mRNA Length = 1640 |
| 463D11 | 480 | 632 | NM_015995 | NA | 1.00E-77 | 1 | Kruppel-like factor 13 (KLF13), mRNA Length = 1079 |
| 49C10 | 817 | 964 | NM_019604 | NA | 3.00E-28 | 1 | class-I MHC-restricted T cell associated molecule (CRTAM), mRNA |
| 188E4 | 390 | 643 | NM_019997 | NA | 6.00E-79 | 1 | similar to Mus musculus cDNA sequence AB041581 (AB041581) |
| 103H2 | 1421 | 1662 | NM_021432 | NA | 3.00E-66 | 1 | similar to Mus RIKEN cDNA 1110020M21 gene (1110020M21Rik) |
| 465G11 | 1685 | 1761 | NM_021777 | NA | 1.00E-34 | 1 | a disintegrin and metalloproteinase domain 28 (ADAM28), transcript var |
| 166D8 | 1265 | 1951 | NM_022152 | NA | 0 | 1 | PP1201 protein (PP1201), mRNA Length = 2309 |
| 459G6 | 1 | 123 | NM_024567 | NA | 2.00E-36 | 1 | hypothetical protein FLJ21616 (FLJ21616), mRNA Length = 1858 |
| 461G2 | 667 | 1182 | NM_025977 | NA | 1.00E-28 | 1 | similar to Mus RIKEN cDNA 2510048L02 gene (2510048L02Rik) |
| 62A5 | 759 | 1200 | NM_030780 | NA | 0 | 1 | folate transporter/carrier (LOC81034), mRNA Length = 2534 |
| 52C11 | 1277 | 1954 | NM_030788 | NA | 0 | 1 | DC-specific transmembrane protein (LOC81501), mRNA Length = 1974 |
| 108A7 | 910 | 3014 | NM_031419 | NA | 0 | 4 | molecule possessing ankyrin repeats induced by lipopolysaccharide |
| 74E11 | 47 | 464 | NM_031435 | NA | 0 | 1 | hypothetical protein DKFZp564I0422 (DKFZP564I0422), mRNA |
| 56B3 | 1518 | 1962 | NM_031453 | NA | 1.00E-176 | 1 | hypothetical protein MGC11034 (MGC11034), mRNA Length = 3301 |
| 46F2 | 118 | 663 | NM_031480 | NA | 1.00E-105 | 1 | hypothetical protein AD034 (AD034), mRNA Length = 2495 |
| 192B3 | 51 | 290 | R11456 | NA | 1.00E-105 | 1 | spleen 1NFLS cDNA clone IMAGE:129880 5' similar to |
| 458B9 | 43 | 359 | R64054 | NA | 1.00E-159 | 1 | cDNA clone IMAGE:139969 5' |
| 169F11 | 1 | 429 | R85137 | NA | 0 | 1 | brain N2b4HB55Y cDNA clone IMAGE:180492 5' |
| 465B5 | 16 | 392 | R88126 | NA | 1.00E-164 | 1 | cDNA clone IMAGE:186850 5' |
| 477F8 | 1 | 525 | T77017 | NA | 0 | 1 | 1NIB cDNA clone IMAGE:23326 5' |
| 39G11 | 162 | 455 | T80378 | NA | 1.00E-145 | 1 | 1NIB cDNA clone IMAGE:24693 5' |
| 107D7 | 1 | 371 | T80654 | NA | 0 | 1 | spleen 1NFLS cDNA clone IMAGE:108950 5' |
| 465A1 | 6 | 314 | T85880 | NA | 1.00E-114 | 1 | spleen 1NFLS cDNA clone IMAGE:112441 5' |
| 48D12 | 2300 | 2533 | U08015 | NA | 1.00E-128 | 1 | NF-ATc mRNA, complete cds Length = 2743 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|------|------|-----------|----|-----------|---|--|
| 121F1 | 13 | 380 | U46388 | NA | 1.00E-150 | 1 | cell line Patu 8988t cDNA clone xs425 |
| 127B12 | 3 | 330 | U52054 | NA | 0 | 4 | S6 H-8 mRNA expressed in chromosome 6-suppressed melanoma cells |
| 487C2 | 4054 | 4187 | U52682 | NA | 2.00E-28 | 1 | lymphocyte specific interferon regulatory factor/interferon regulatory |
| 110B3 | 1404 | 2081 | U53530 | NA | 0 | 1 | cytoplasmic dynein 1 heavy chain mRNA, partial cds Length = 2694 |
| 466C8 | 34 | 175 | U75805 | NA | 3.00E-47 | 1 | cDNA clone f46 |
| 148G12 | 1513 | 1639 | U87954 | NA | 1.00E-27 | 1 | erbB3 binding protein EBP1 mRNA, complete cds Length = 1648 |
| 70A4 | 564 | 1381 | U94359 | NA | 0 | 2 | glycogenin-2 like mRNA sequence Length = 4066 |
| 158E4 | 843 | 945 | U97075 | NA | 1.00E-33 | 1 | FLICE-like inhibitory protein short form mRNA, complete cds |
| 459A1 | 227 | 446 | W00466 | NA | 1.00E-60 | 1 | 2NbHM cDNA clone IMAGE:291193 5' |
| 459A2 | 60 | 350 | W00491 | NA | 1.00E-126 | 1 | 2NbHM cDNA clone IMAGE:291255 5' similar to |
| 459B1 | 76 | 551 | W02600 | NA | 0 | 1 | spleen 1NFLS cDNA clone IMAGE:296099 5' |
| 166C10 | 10 | 415 | W16552 | NA | 0 | 1 | Soares_fetal_lung_NbHL19W cDNA clone IMAGE:301703 5' |
| 471C6 | 3 | 383 | W19201 | NA | 1.00E-149 | 1 | Soares_fetal_lung_NbHL19W cDNA clone IMAGE:303118 5' similar to |
| 520A8 | 75 | 382 | W19487 | NA | 1.00E-154 | 1 | zb36f09.r1 Soares_parathyroid_tumor_NbHPA cDNA clone |
| 459B7 | 57 | 158 | W25068 | NA | 9.00E-50 | 1 | Soares_fetal_lung_NbHL19W cDNA clone IMAGE:308696 5' |
| 188D3 | 39 | 283 | W26193 | NA | 2.00E-91 | 1 | randomly primed sublibrary cDNA |
| 75B12 | 8 | 386 | W27656 | NA | 1.00E-166 | 1 | randomly primed sublibrary cDNA |
| 163F8 | 74 | 330 | W47229 | NA | 1.00E-117 | 1 | zc39c01.r1 Soares_senescent_fibroblasts_NbHSF cDNA |
| 478E6 | 2 | 322 | W56487 | NA | 3.00E-51 | 1 | zc59c07.r1 Soares_parathyroid_tumor_NbHPA cDNA clone |
| 73H4 | 76 | 297 | W72392 | NA | 1.00E-121 | 1 | Soares_fetal_heart_NbHH19W cDNA clone IMAGE:345661 3' |
| 66D5 | 1 | 457 | W74397 | NA | 0 | 3 | Soares_fetal_heart_NbHH19W cDNA clone IMAGE:345236 5' |
| 496D4 | 85 | 450 | W79598 | NA | 0 | 1 | Soares_fetal_heart_NbHH19W cDNA clone IMAGE:347020 5' |
| 165D1 | 108 | 287 | W80882 | NA | 4.00E-94 | 1 | Soares_fetal_heart_NbHH19W cDNA clone IMAGE:347240 5' |
| 463G1 | 5 | 406 | W86427 | NA | 0 | 1 | zh61c11.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA |
| 469G11 | 1276 | 1621 | X06180 | NA | 0 | 1 | mRNA for CD7 antigen (gp40) Length = 1656 |
| 113E11 | 126 | 885 | X65318 | NA | 0 | 1 | Cloning vector pGEMEX-2 Length = 3995 |
| 482E1 | 921 | 1168 | X79536 | NA | 1.00E-102 | 1 | mRNA for hnRNPcore protein A1 Length = 1198 |
| 123G8 | 408 | 848 | XM_002068 | NA | 8.00E-73 | 1 | glutamate-ammonia ligase (glutamine synthase) (GLUL), mRNA |
| 185E1 | 508 | 734 | XM_002158 | NA | 1.00E-27 | 1 | proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA |
| 71A9 | 1131 | 1252 | XM_002269 | NA | 4.00E-29 | 1 | ARP3 (actin-related protein 3, yeast) homolog (ACTR3), mRNA |
| 49G7 | 1 | 257 | XM_003189 | NA | 1.00E-142 | 3 | similar to eukaryotic translation initiation factor 4A, isoform 2 (H) |
| 128B5 | 783 | 980 | XM_003304 | NA | 6.00E-41 | 1 | toll-like receptor 2 (TLR2), mRNA Length = 2600 |
| 185G10 | 853 | 1057 | XM_003507 | NA | 2.00E-26 | 1 | small inducible cytokine subfamily B (Cys-X-Cys), member 5 (epithelial |
| 41C9 | 588 | 1221 | XM_003593 | NA | 0 | 1 | CD38 antigen (p45) (CD38), mRNA Length = 1227 |
| 156C4 | 127 | 270 | XM_004020 | NA | 6.00E-71 | 1 | ribosomal protein S23 (RPS23), mRNA Length = 488 |
| 66E2 | 1344 | 1577 | XM_004500 | NA | 1.00E-46 | 1 | CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD |
| 61C6 | 474 | 987 | XM_004611 | NA | 2.00E-80 | 1 | Ras homolog enriched in brain 2 (RHEB2), mRNA Length = 987 |
| 184A7 | 971 | 1361 | XM_004720 | NA | 0 | 1 | hypothetical protein FLJ11000 (FLJ11000), mRNA Length = 1680 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|--------|-------|-------|-----------|----|-----------|---|--|
| 128E6 | 580 | 741 | XM_004839 | NA | 5.00E-38 | 1 | pre-B-cell colony-enhancing factor (PBEF), mRNA Length = 2377 |
| 55A11 | 1096 | 1305 | XM_005162 | NA | 1.00E-60 | 1 | GTP-binding protein overexpressed in skeletal muscle (GEM), mRNA |
| 519C4 | 1307 | 1441 | XM_005543 | NA | 1.00E-69 | 1 | aquaporin 3 (AQP3), mRNA Length = 1441 |
| 129F1 | 1854 | 2367 | XM_005693 | NA | 0 | 1 | inositol polyphosphate-5-phosphatase, 40kD (INPP5A), mRNA |
| 522C10 | 700 | 916 | XM_005698 | NA | 7.00E-53 | 1 | programmed cell death 4 (PDCD4), mRNA Length = 1622 |
| 180G6 | 1884 | 2290 | XM_005799 | NA | 1.00E-166 | 1 | integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 |
| 55F4 | 2573 | 2748 | XM_005883 | NA | 4.00E-73 | 1 | early growth response 2 (Krox-20 (Drosophila) homolog) (EGR2), mRNA |
| 492H7 | 976 | 1176 | XM_005980 | NA | 4.00E-33 | 1 | proteoglycan 1, secretory granule (PRG1), mRNA Length = 1176 |
| 476B4 | 1541 | 1918 | XM_006741 | NA | 0 | 1 | hypothetical protein FLJ10701 (FLJ10701), mRNA Length = 2299 |
| 493H5 | 145 | 379 | XM_006881 | NA | 2.00E-56 | 1 | interleukin 22 (IL22), mRNA Length = 676 |
| 499B4 | 11117 | 11410 | XM_007156 | NA | 3.00E-34 | 1 | spastic ataxia of Charlevoix-Saguenay (sacsin) (SACS), mRNA |
| 183D7 | 4270 | 4376 | XM_007189 | NA | 5.00E-37 | 1 | forkhead box O1A (rhabdomyosarcoma) (FOXO1A), mRNA Length = 5037 |
| 115B6 | 4151 | 4408 | XM_007606 | NA | 2.00E-50 | 2 | thrombospondin 1 (THBS1), mRNA Length = 5719 |
| 587B4 | 31 | 264 | XM_007650 | NA | 1.00E-114 | 3 | beta-2-microglobulin (B2M), mRNA Length = 918 |
| 598H5 | 206 | 300 | XM_008062 | NA | 1.00E-31 | 1 | ribosomal protein S15a (RPS15A), mRNA Length = 435 |
| 73E4 | 3252 | 3505 | XM_008082 | NA | 1.00E-119 | 1 | adaptor-related protein complex 1, gamma 1 subunit (AP1G1), mRNA |
| 64F7 | 186 | 334 | XM_008449 | NA | 1.00E-47 | 1 | small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4) |
| 585E1 | 904 | 1020 | XM_009533 | NA | 1.00E-26 | 1 | CGI-06 protein (LOC51604), mRNA Length = 2146 |
| 75B8 | 710 | 1406 | XM_009574 | NA | 0 | 1 | nucleolar protein (KKE/D repeat) (NOP56), mRNA Length = 1910 |
| 467A5 | 210 | 620 | XM_009641 | NA | 0 | 1 | v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), |
| 44A3 | 480 | 854 | XM_009917 | NA | 0 | 1 | splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA Length = 2614 |
| 114D12 | 2269 | 2491 | XM_009929 | NA | 7.00E-56 | 1 | LIM domain kinase 2 (LIMK2), mRNA Length = 3699 |
| 52F6 | 1 | 230 | XM_010593 | NA | 2.00E-36 | 1 | signaling lymphocytic activation molecule (SLAM), mRNA Length = 1791 |
| 185E5 | 1576 | 1695 | XM_010897 | NA | 3.00E-32 | 1 | neural precursor cell expressed, developmentally down-regulated 5 (NED |
| 106C3 | 1359 | 1824 | XM_011080 | NA | 0 | 1 | T cell activation, increased late expression (TACTILE), mRNA |
| 56H11 | 40 | 617 | XM_011082 | NA | 0 | 1 | interleukin 21 (IL21), mRNA Length = 617 |
| 53B2 | 2711 | 2839 | XM_011714 | NA | 3.00E-29 | 1 | neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF |
| 47A3 | 896 | 1231 | XM_011865 | NA | 1.00E-55 | 1 | isopentenyl-diphosphate delta isomerase (IDI1), mRNA Length = 1835 |
| 159E9 | 17 | 178 | XM_011914 | NA | 1.00E-73 | 1 | ribosomal protein S24 (RPS24), mRNA Length = 515 |
| 39E6 | 339 | 535 | XM_012059 | NA | 1.00E-44 | 1 | hypothetical protein MDS025 (MDS025), mRNA Length = 1225 |
| 142F6 | 623 | 745 | XM_012328 | NA | 2.00E-40 | 1 | granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine ester |
| 118D4 | 329 | 765 | XM_012649 | NA | 1.00E-114 | 1 | small inducible cytokine A7 (monocyte chemotactic protein 3) (SCYA7), |
| 168H9 | 2502 | 2616 | XM_015180 | NA | 2.00E-33 | 1 | apolipoprotein L, 6 (APOL6), mRNA Length = 2915 |
| 58D2 | 1582 | 1742 | XM_015921 | NA | 2.00E-30 | 1 | putative chemokine receptor; GTP-binding protein (HM74), mRNA |
| 466H9 | 86 | 440 | XM_016138 | NA | 2.00E-45 | 1 | hypothetical protein FLJ12439 (FLJ12439), mRNA Length = 1614 |

Table 3A, Candidate nucleotide sequences identified using differential cDNA hybridization analysis

| | | | | | | | |
|-------|------|------|-----------|----|-----------|---|---|
| 184G1 | 2651 | 3584 | XM_016481 | NA | 0 | 3 | hypothetical protein (DJ328E19.C1.1), mRNA Length = 3603 |
| 107G9 | 8199 | 8786 | XM_016721 | NA | 0 | 1 | zinc finger protein 106 (ZFP106), mRNA Length = 10462 |
| 39F11 | 2719 | 3671 | XM_016972 | NA | 0 | 2 | similar to hypothetical protein (H. sapiens) (LOC82646), mRNA |
| 159A7 | 19 | 561 | XM_018498 | NA | 1.00E-167 | 3 | ribosomal protein L5 (RPL5), mRNA Length = 984 |
| 459H2 | 2956 | 3450 | Y16414 | NA | 0 | 1 | mRNA for exportin (tRNA) Length = 3497 |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| Example Clone | Genome Start | End | Accession | Probability | Number Clones | Genbank Description |
|---------------|--------------|--------|-----------|-------------|---------------|--|
| 172H5 | 12457 | 13616 | AC000015 | 0 | 2 | chromosome 4 clone B271E1 map 4q25, complete sequence L |
| 464A9 | 21144 | 21280 | AC000068 | 2.00E-70 | 1 | Chromosome 22q11.2 Cosmid Clone 102g9 In DGCR Region, c |
| 472B10 | 20340 | 20745 | AC000087 | 2.00E-67 | 1 | Chromosome 22q11.2 Cosmid Clone 83c5 In DGCR Region, co |
| 103C4 | 93389 | 93611 | AC000119 | 0 | 5 | BAC clone RG104I04 from 7q21-7q22, complete sequence [H] |
| | 119111 | 119521 | AC000119 | | | |
| | 119522 | 119890 | AC000119 | | | |
| | 119989 | 121059 | AC000119 | | | |
| 514A3 | 201218 | 201293 | AC000353 | 5.00E-34 | 2 | Chromosome 11q13 BAC Clone 18h3, complete sequence Leng |
| 524A9 | 24315 | 24820 | AC002073 | 0 | 3 | PAC clone RP3-515N1 from 22q11.2-q22, complete sequence |
| | 24879 | 25274 | AC002073 | | | |
| 458D10 | 28080 | 28625 | AC002297 | 0 | 1 | Genomic sequence from 9q34, complete sequence [Homo sap |
| 476D3 | 106080 | 106289 | AC002302 | 1.00E-86 | 1 | Chromosome 16 BAC clone CIT987-SKA-345G4 ~complete geno |
| 471D10 | 34638 | 34885 | AC002306 | 1.00E-118 | 2 | DNA from chromosome 19-cosmid R33799, genomic sequence, |
| 596F6 | 75526 | 76327 | AC002467 | 0 | 1 | BAC clone CTA-364P16 from 7q31, complete sequence [Homo |
| 473F3 | 74912 | 75540 | AC002549 | 0 | 2 | Xp22 BAC GS-377014 (Genome Systems BAC library) complet |
| 111E12 | 24581 | 24992 | AC003086 | 0 | 1 | BAC clone CTB-104F4 from 7q21-q22, complete sequence Le |
| 471E9 | 39706 | 40014 | AC003103 | 1.00E-151 | 1 | chromosome 17, clone HCIT268N12, complete sequence Leng |
| 526B9 | 39477 | 39615 | AC003695 | 3.00E-29 | 1 | chromosome 17, clone hRPC.859_O_20, complete sequence L |
| 331A3 | 47793 | 48492 | AC003976 | 1.00E-164 | 5 | chromosome 17, clone hCIT.91_J_4, complete sequence Len |
| 105C1 | 115642 | 116079 | AC004067 | 0 | 1 | chromosome 4 clone B366O24 map 4q25, complete sequence |
| 469H8 | 35828 | 35976 | AC004080 | 5.00E-71 | 1 | PAC clone RP1-170O19 from 7p15-p21, complete sequence L |
| 55F9 | 114263 | 114415 | AC004169 | 3.00E-46 | 1 | chromosome 4 clone C0236G06 map 4p16, complete sequence |
| 487F9 | 35319 | 35718 | AC004187 | 0 | 1 | clone UWGC:y17c131 from 6p21, complete sequence Length |
| 459H7 | 13409 | 13739 | AC004190 | 1.00E-166 | 1 | from UWGC:y18c282 from 6p21, complete sequence Length = |
| 464D1 | 28530 | 29042 | AC004221 | 1.00E-106 | 1 | DNA from chromosome 19, cosmid R29144 (LLNLR-252D12) an |
| 468A7 | 53111 | 53416 | AC004386 | 5.00E-80 | 2 | Homo Sapiens Chromosome X clone bWXD691, complete seque |
| 188F1 | 859 | 1200 | AC004520 | 0 | 1 | BAC clone CTB-119C2 from 7p15, complete sequence Length |
| 523F5 | 38269 | 38756 | AC004644 | 3.00E-38 | 1 | chromosome 16, cosmid clone 367E12 (LANL), complete seq |
| 142E4 | 113118 | 114014 | AC004686 | 0 | 14 | chromosome 17, clone hRPC.1073_F_15, complete sequence |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | | |
|--------|--------|--------|----------|-----------|---|---|
| | 117050 | 117275 | AC004686 | | | |
| 135F10 | 39469 | 39637 | AC004762 | 3.00E-75 | 1 | chromosome 20, P1 clone 28 (LBNL H134), complete sequen |
| 472C8 | 120427 | 120603 | AC004838 | 6.00E-92 | 1 | PAC clone RP4-589D8 from 7q31.1-q31.3, complete sequenc |
| 464F11 | 64853 | 65242 | AC004849 | 5.00E-59 | 2 | PAC clone RP4-659J6 from 7q33-q35, complete sequence Le |
| 460D2 | 54796 | 55320 | AC004854 | 0 | 1 | PAC clone RP4-673M15 from 7p13-p11.2, complete sequence |
| 513B4 | 94866 | 95147 | AC004858 | 2.00E-57 | 1 | PAC clone RP4-687K1 from 14, complete sequence Length = |
| 463C7 | 53959 | 54083 | AC004906 | 1.00E-44 | 1 | PAC clone RP5-852O24 from 7p22, complete sequence Lengt |
| 584D3 | 56155 | 56311 | AC004913 | 5.00E-36 | 1 | clone DJ0876A24, complete sequence Length = 98870 |
| 171B1 | 23796 | 24098 | AC004918 | 1.00E-145 | 1 | PAC clone RP5-894A10 from 7q32-q32, complete sequence L |
| 463B10 | 33758 | 34061 | AC004923 | 1.00E-135 | 1 | PAC clone RP5-901A4, complete sequence Length = 94851 |
| 101A1 | 50075 | 50425 | AC004997 | 1.00E-129 | 1 | PAC clone RP1-130H16 from 22q12.1-qter, complete sequen |
| 465G8 | 28181 | 28635 | AC005014 | 0 | 1 | BAC clone GS1-166A23 from 7p21, complete sequence Lengt |
| 470C3 | 93162 | 93469 | AC005068 | 1.00E-160 | 1 | BAC clone CTB-137N13 from 7, complete sequence Length = |
| 119E5 | 28806 | 29061 | AC005156 | 1.00E-119 | 1 | PAC clone RP5-1099C19 from 7q21-q22, complete sequence |
| 98C3 | 24385 | 25049 | AC005192 | 0 | 1 | BAC clone CTB-163K11 from 7q31, complete sequence Lengt |
| 140G6 | 37679 | 37878 | AC005280 | 6.00E-85 | 1 | PAC clone RP1-240K6 from 14, complete sequence Length = |
| 476A10 | 12753 | 12826 | AC005306 | 8.00E-33 | 1 | chromosome 19, cosmid R27216 (LLNLR-232D4) and 3' overl |
| 331A12 | 34177 | 34328 | AC005391 | 2.00E-72 | 1 | chromosome 19, cosmid R29942, complete sequence Length |
| 111H11 | 85156 | 86081 | AC005488 | 0 | 2 | clone NH0313P13, complete sequence Length = 185737 |
| 472H11 | 22517 | 22813 | AC005531 | 1.00E-150 | 1 | PAC clone RP4-701O16 from 7q33-q36, complete sequence L |
| 139G6 | 96577 | 97117 | AC005540 | 0 | 3 | clone RP11-533I8, complete sequence Length = 133761 |
| | 116180 | 116836 | AC005540 | | | |
| 472F4 | 70951 | 71038 | AC005593 | 3.00E-41 | 1 | chromosome 5, P1 clone 1369f10 (LBNL H28), complete seq |
| 469D4 | 27949 | 28457 | AC005667 | 0 | 1 | chromosome 17, clone hRPK.329_E_11, complete sequence L |
| 463A7 | 127455 | 127799 | AC005740 | 1.00E-154 | 1 | chromosome 5p, BAC clone 50g21 (LBNL H154), complete se |
| 126B8 | 27782 | 28073 | AC005837 | 1.00E-160 | 2 | chromosome 17, clone hRPK.318_A_15, complete sequence L |
| 479D2 | 202167 | 202536 | AC005859 | 2.00E-46 | 1 | Xp22-83 BAC GSHB-324M7 (Genome Systems BAC Library) com |
| 39G6 | 62582 | 63099 | AC005920 | 0 | 1 | chromosome 17, clone hRPK.700_H_6, complete sequence Le |
| 63E1 | 39129 | 39250 | AC006006 | 3.00E-59 | 1 | PAC clone RP4-813F11 from 7q32-q34, complete sequence L |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | | |
|--------|--------|--------|----------|-----------|---|---|
| 461B11 | 140287 | 140770 | AC006010 | 1.00E-154 | 2 | clone DJ0935K16 |
| 119G10 | 81312 | 81740 | AC006033 | 0 | 1 | BAC clone RP11-121A8 from 7p14-p13, complete sequence L |
| 64A2 | 109063 | 109613 | AC006050 | 0 | 2 | chromosome 17, clone hRPK.268_F_2, complete sequence Le |
| 459B7 | 13630 | 14294 | AC006077 | 0 | 1 | chromosome 5, P1 clone 254f11 (LBNL H62), complete sequ |
| 37H4 | 58820 | 59068 | AC006111 | 1.00E-67 | 1 | chromosome 16 clone RP11-461A8, complete sequence Lengt |
| 512E3 | 39935 | 40123 | AC006139 | 3.00E-94 | 1 | clone UWGC:y55c068 from 6p21, complete sequence Length |
| 171H10 | 33704 | 33969 | AC006165 | 8.00E-78 | 1 | clone UWGC:y54c125 from 6p21, complete sequence Length |
| 72A1 | 106659 | 106958 | AC006207 | 1.00E-149 | 1 | 12p13.3 BAC RPCI3-488H23 (Roswell Park Cancer Institute |
| 195H12 | 38763 | 38930 | AC006323 | 2.00E-61 | 1 | clone RP5-1151M5, complete sequence Length = 86267 |
| 113B6 | 36330 | 36635 | AC006344 | 1.00E-157 | 1 | PAC clone RP4-726N20 from 7q32-q34, complete sequence L |
| 588G6 | 174012 | 174265 | AC006449 | 2.00E-93 | 1 | chromosome 17, clone hCIT.58_E_17, complete sequence Le |
| 463B2 | 65534 | 66031 | AC006483 | 0 | 1 | BAC clone CTB-161C1 from 7, complete sequence Length = |
| 115F11 | 71976 | 72094 | AC006511 | 8.00E-60 | 1 | 12p13.1 (17.1-21.3 cM) BAC RPCI11-69M1 (Roswell Park Ca |
| 187H11 | 34068 | 34544 | AC006536 | 0 | 1 | chromosome 14 clone BAC257P13 map 14q31, complete seque |
| 477E6 | 106567 | 106656 | AC007009 | 6.00E-30 | 1 | BAC clone RP11-560C1 from 7p22-p21, complete sequence L |
| 53E10 | 123408 | 123785 | AC007040 | 0 | 1 | BAC clone RP11-298H3 from 2, complete sequence Length = |
| 462C8 | 164080 | 164223 | AC007068 | 4.00E-72 | 2 | 12p BAC RPCI11-75L1 (Roswell Park Cancer Institute BAC |
| 478C7 | 174303 | 174379 | AC007068 | | | |
| | 27207 | 27305 | AC007097 | 4.00E-43 | 1 | BAC clone RP11-332E22 from 7q35-q36, complete sequence |
| 181A8 | 4600 | 4798 | AC007201 | 5.00E-59 | 2 | chromosome 19, cosmid R34383, complete sequence Length |
| 159F6 | 111852 | 112188 | AC007263 | 1.00E-151 | 1 | chromosome 14 clone RP11-79J20 containing gene for chec |
| 163F10 | 94927 | 95303 | AC007283 | 1.00E-126 | 2 | BAC clone RP11-536I18 from 2, complete sequence Length |
| 124G4 | 192082 | 192785 | AC007318 | 0 | 3 | clone RP11-420C9, complete sequence Length = 204230 |
| 331A5 | 117939 | 118047 | AC007383 | 3.00E-51 | 1 | BAC clone RP11-310K15 from 2, complete sequence Length |
| 463C5 | 101528 | 101815 | AC007444 | 9.00E-41 | 1 | clone RP11-340F1 from 7p14-15, complete sequence Length |
| 485D5 | 94681 | 95267 | AC007458 | 1.00E-152 | 8 | 12q15 BAC RPCI11-444B24 (Roswell Park Cancer Institute |
| | 95517 | 95826 | AC007458 | | | |
| | 95858 | 96487 | AC007458 | | | |
| | 96742 | 96838 | AC007458 | | | |
| | 187608 | 187732 | AC007458 | | | |
| 181B6 | 95554 | 96149 | AC007488 | 0 | 2 | 3q27 BAC RPCI11-246B7 (Roswell Park Cancer Institute BA |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | | |
|--------|--------|--------|----------|-----------|----|---|
| 102E12 | 12533 | 12977 | AC007540 | 4.00E-93 | 1 | 12q24.1 BAC RPCI11-128P10 (Roswell Park Cancer Institut |
| 471C6 | 9877 | 10401 | AC007561 | 1.00E-160 | 1 | clone RP11-394E1, complete sequence Length = 106093 |
| 471C1 | 27629 | 27769 | AC007676 | 1.00E-27 | 1 | clone RP11-9B17, complete sequence Length = 152138 |
| 40D4 | 120766 | 121349 | AC007882 | 0 | 1 | BAC clone RP11-499D5 from 7p11.2-q11.2, complete sequen |
| 166C10 | 90374 | 90790 | AC007899 | 0 | 1 | BAC clone RP11-531C11 from 2, complete sequence Length |
| 492A7 | 11200 | 11376 | AC007911 | 7.00E-57 | 1 | chromosome 18, clone RP11-520K18, complete sequence Len |
| 459B3 | 65768 | 66232 | AC008009 | 0 | 2 | 3q26.2-27 BAC RPCI11-436A20 (Roswell Park Cancer Instit |
| 463F10 | 127622 | 127783 | AC008083 | 3.00E-85 | 1 | 12 BAC RP11-493L12 (Roswell Park Cancer Institute BAC L |
| 585C4 | 176255 | 176348 | AC008124 | 6.00E-38 | 1 | Chromosome 12q13-62.7-72 BAC RPCI11-352M15 (Roswell Par |
| 468E6 | 134033 | 134685 | AC008279 | 0 | 2 | BAC clone RP11-427F22 from 2, complete sequence Length |
| 112E9 | 37565 | 37926 | AC008408 | 0 | 4 | chromosome 5 clone CTC-278H1, complete sequence Length |
| | 37996 | 38360 | AC008408 | | | |
| 145C5 | 131866 | 132484 | AC008592 | 1.00E-141 | 8 | chromosome 5 clone CTC-576H9, complete sequence Length |
| | 134190 | 134862 | AC008592 | | | |
| 458D8 | 82521 | 83080 | AC008623 | 0 | 1 | chromosome 19 clone CTB-14D10, complete sequence Length |
| 584G2 | 44371 | 44929 | AC008723 | 0 | 2 | chromosome 5 clone CTB-95B16, complete sequence Length |
| 144F7 | 73662 | 74295 | AC008750 | 2.00E-54 | 2 | chromosome 19 clone CTD-2616J11, complete sequence Leng |
| 149G2 | 99171 | 99875 | AC008760 | 1.00E-121 | 6 | chromosome 19 clone CTD-3128G10, complete sequence Leng |
| 194H6 | 52930 | 53250 | AC008795 | 5.00E-89 | 2 | chromosome 5 clone CTD-2052F19, complete sequence Lengt |
| | 57088 | 57263 | AC008795 | | | |
| 117H9 | 101321 | 102169 | AC008860 | 0 | 11 | chromosome 5 clone CTD-2185A1, complete sequence Length |
| | 102715 | 102980 | AC008860 | | | |
| | 103113 | 103402 | AC008860 | | | |
| 155D6 | 34277 | 34517 | AC008982 | 1.00E-103 | 1 | chromosome 19 clone LLNLF-172E10, complete sequence Len |
| 458E4 | 33802 | 34039 | AC008985 | 8.00E-77 | 1 | chromosome 19 clone LLNLF-198H7, complete sequence Leng |
| 176A6 | 170428 | 170746 | AC009073 | 1.00E-138 | 1 | chromosome 16 clone RP11-31O11, complete sequence Lengt |
| 146D8 | 11633 | 11699 | AC009086 | 1.00E-28 | 1 | chromosome 16 clone RP11-368N21, complete sequence Leng |
| 458B8 | 176406 | 176888 | AC009120 | 0 | 1 | chromosome 16 clone RP11-484E3, complete sequence Lengt |
| 73C4 | 136885 | 137479 | AC009299 | 0 | 1 | BAC clone RP11-26B22 from 2, complete sequence Length = |
| 54F4 | 202039 | 202564 | AC009312 | 0 | 1 | clone RP11-425F6, complete sequence Length = 204834 |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | | |
|--------|--------|--------|----------|-----------|---|---|
| 480E2 | 143559 | 143986 | AC009313 | 0 | 1 | BAC clone RP11-440P12 from 2, complete sequence Length |
| 519E9 | 13492 | 13848 | AC009404 | 1.00E-178 | 1 | BAC clone RP11-28H22 from 2, complete sequence Length = |
| 129D12 | 81260 | 81769 | AC009466 | 1.00E-151 | 1 | chromosome 11, clone RP11-87N22, complete sequence Leng |
| 37E10 | 124522 | 125457 | AC009477 | 0 | 3 | BAC clone RP11-209H16 from 2, complete sequence Length |
| 129A12 | 6750 | 7331 | AC009506 | 0 | 1 | clone RP11-542H1, complete sequence Length = 191764 |
| 515H10 | 5494 | 5990 | AC009812 | 3.00E-69 | 4 | chromosome 3, clone RP11-48B3, complete sequence Length |
| | 74019 | 74540 | AC009812 | | | |
| 165D1 | 53879 | 54343 | AC009951 | 0 | 1 | clone RP11-107E5, complete sequence Length = 159791 |
| 53D8 | 30308 | 30860 | AC010132 | 1.00E-159 | 1 | BAC clone RP11-111K18 from 7p11.2-p2, complete sequence |
| 487F11 | 16839 | 17267 | AC010480 | 1.00E-130 | 3 | chromosome 5 clone CTD-2315M5, complete sequence Length |
| 461G10 | 8988 | 9327 | AC010677 | 1.00E-163 | 1 | BAC clone CTD-2304L4 from 7, complete sequence Length = |
| 115H2 | 19073 | 19679 | AC010789 | 4.00E-97 | 2 | chromosome 10, clone RP11-190J1, complete sequence Leng |
| | 126247 | 126428 | AC010789 | | | |
| 168A9 | 78976 | 79540 | AC010877 | 0 | 2 | BAC clone RP11-218F6 from Y, complete sequence Length = |
| 468G6 | 98034 | 98744 | AC010878 | 1.00E-107 | 3 | clone RP11-230E20, complete sequence Length = 154115 |
| 477B12 | 167367 | 167895 | AC010913 | 0 | 1 | BAC clone RP11-44N22 from 2, complete sequence Length = |
| 192E1 | 10683 | 11328 | AC011245 | 0 | 1 | clone RP11-498O5, complete sequence Length = 56793 |
| 467C2 | 4521 | 4890 | AC011462 | 1.00E-178 | 1 | chromosome 19 clone CTC-435M10, complete sequence Lengt |
| 189F3 | 12090 | 12208 | AC011495 | 8.00E-60 | 1 | chromosome 19 clone CTB-33G10, complete sequence Length |
| 144C9 | 38166 | 38421 | AC011500 | 1.00E-62 | 1 | chromosome 19 clone CTB-60E11, complete sequence Length |
| 162E8 | 41387 | 41499 | AC012005 | 8.00E-30 | 1 | clone RP11-533E23, complete sequence Length = 189557 |
| 158G6 | 70285 | 70462 | AC012170 | 3.00E-95 | 1 | chromosome 15 clone RP11-562A8 map 15q21.1, complete se |
| 189B11 | 19127 | 19241 | AC013436 | 8.00E-29 | 3 | BAC clone RP11-105B9 from 7, complete sequence Length = |
| | 23196 | 23655 | AC013436 | | | |
| 98C9 | 178883 | 179326 | AC015651 | 1.00E-107 | 1 | chromosome 17, clone RP11-55A13, complete sequence Leng |
| 69F8 | 57839 | 58168 | AC015819 | 0 | 1 | chromosome 18, clone RP11-405M12, complete sequence Len |
| 47F9 | 3198 | 3826 | AC016395 | 0 | 1 | chromosome 10 clone RP11-153K11, complete sequence Leng |
| 480E3 | 39766 | 40155 | AC016623 | 2.00E-35 | 1 | chromosome 5 clone CTD-2345N17, complete sequence Lengt |
| 196G12 | 59552 | 60523 | AC016637 | 0 | 2 | chromosome 5 clone RP11-34J15, complete sequence Length |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | | |
|--------|--------|--------|----------|-----------|---|--|
| 518A8 | 61011 | 61433 | AC016751 | 0 | 1 | BAC clone RP11-504O20 from 2, complete sequence Length |
| 36C11 | 54765 | 54868 | AC017002 | 2.00E-30 | 2 | clone RP11-68E19, complete sequence Length = 205662 |
| 489H9 | 108513 | 109049 | AC017003 | 0 | 2 | clone RP11-78C11, complete sequence Length = 118385 |
| 479H6 | 142657 | 142930 | AC017020 | 8.00E-45 | 1 | BAC clone RP11-185K15 from Y, complete sequence Length |
| 483D10 | 99413 | 99875 | AC017101 | 0 | 1 | clone RP11-556A11, complete sequence Length = 195635 |
| 112B4 | 87464 | 88155 | AC018511 | 1.00E-129 | 2 | chromosome 10 clone RP11-77G23, complete sequence Length |
| | 117653 | 117940 | AC018511 | | | |
| 171F2 | 157933 | 158203 | AC018673 | 2.00E-96 | 1 | clone RP11-145A4, complete sequence Length = 187099 |
| 166H12 | 116351 | 116665 | AC018682 | 1.00E-177 | 1 | clone RP11-417F21, complete sequence Length = 181405 |
| 123F8 | 140561 | 141314 | AC018904 | 0 | 3 | chromosome 15 clone RP11-50C13 map 15q21.3, complete se |
| 116C9 | 191414 | 191866 | AC019206 | 0 | 1 | BAC clone RP11-401N16 from 2, complete sequence Length |
| 472E9 | 148765 | 149172 | AC020550 | 1.00E-140 | 1 | BAC clone RP11-198M19 from 2, complete sequence Length |
| 129D1 | 66284 | 67154 | AC020595 | 0 | 3 | BAC clone RP11-358M9 from 2, complete sequence Length = |
| 465H10 | 82476 | 83166 | AC020629 | 0 | 2 | 12q BAC RP11-76E16 (Roswell Park Cancer Institute BAC L |
| 182E2 | 83346 | 83465 | AC020716 | 1.00E-33 | 2 | clone RP11-449G13, complete sequence Length = 171805 |
| | 84373 | 84451 | AC020716 | | | |
| 37G8 | 35257 | 35957 | AC020750 | 0 | 1 | chromosome 3 clone RP11-105H19 map 3p, complete sequenc |
| 125F8 | 43854 | 44125 | AC022007 | 1.00E-149 | 1 | chromosome 3 clone RP11-481H17 map 3p, complete sequenc |
| 523A8 | 2991 | 3475 | AC022149 | 0 | 1 | chromosome 19 clone CTD-3093B17, complete sequence Leng |
| 459E7 | 90726 | 91104 | AC022173 | 0 | 1 | chromosome 7 clone RP11-29B3, complete sequence Length |
| 469F8 | 53281 | 53724 | AC022336 | 6.00E-92 | 1 | 3 BAC RP11-71H17 (Roswell Park Cancer Institute BAC Lib |
| 463H5 | 75118 | 75256 | AC022382 | 5.00E-72 | 1 | chromosome 3 clone RP11-266J6 map 3p, complete sequence |
| 466G7 | 20276 | 20522 | AC023058 | 2.00E-53 | 2 | 3 BAC CTB-187G23 (CalTech BAC Library B) complete seque |
| | 21327 | 21875 | AC023058 | | | |
| 470B8 | 127894 | 128301 | AC024568 | 1.00E-169 | 1 | chromosome 5 clone CTD-2179L22, complete sequence Lengt |
| 473E11 | 21558 | 21818 | AC024939 | 1.00E-117 | 1 | 12 BAC RP11-485K18 (Roswell Park Cancer institute BAC L |
| 470E1 | 150190 | 150573 | AC025165 | 1.00E-171 | 1 | 12 BAC RP11-571M6 (Roswell Park Cancer Institute BAC Li |
| 480B5 | 107499 | 107766 | AC025253 | 9.00E-66 | 1 | 12 BAC RP11-499A10 (Roswell Park Cancer Institute BAC L |
| 583B5 | 27783 | 27958 | AC025257 | 1.00E-44 | 1 | 12 BAC RP11-56G10 (Roswell Park Cancer Institute BAC Li |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | | |
|--------|--------|--------|----------|-----------|---|--|
| 37H8 | 86118 | 86418 | AC026425 | 1.00E-148 | 1 | chromosome 5 clone CTD-2183D23, complete sequence Length |
| 166A9 | 119110 | 119797 | AC026794 | 0 | 1 | chromosome 5 clone CTD-2276B5, complete sequence Length |
| 103D4 | 105697 | 105794 | AC034240 | 5.00E-40 | 2 | chromosome 5 clone CTD-2335C11, complete sequence Length |
| 117H4 | 49581 | 49962 | AC053513 | 0 | 1 | clone RP11-359J14, complete sequence Length = 155958 |
| 459B8 | 64143 | 64709 | AC066580 | 0 | 1 | chromosome 3 clone RP11-109J15 map 3p, complete sequence |
| 174D1 | 41807 | 42055 | AC067945 | 2.00E-69 | 2 | clone RP11-629B4, complete sequence Length = 162471 |
| 178F5 | 115078 | 115365 | AC067945 | | | |
| | 105048 | 105223 | AC068492 | 7.00E-37 | 1 | BAC clone RP11-809C23 from 2, complete sequence Length |
| 66E6 | 2116 | 2578 | AC068499 | 1.00E-135 | 2 | chromosome 19, cosmid R26574 (LLNL-R_225F10), complete |
| 178C12 | 15618 | 15959 | AC068789 | 0 | 1 | 12 BAC RP11-1049A21 (Roswell Park Cancer Institute BAC |
| 145F12 | 110468 | 110647 | AC069298 | 3.00E-89 | 4 | chromosome 3 clone RP11-56K23, complete sequence Length |
| | 110779 | 111202 | AC069298 | | | |
| | 141211 | 141790 | AC069298 | | | |
| 519F3 | 159763 | 160355 | AC069304 | 0 | 1 | BAC clone RP11-632K21 from 7, complete sequence Length |
| 464B11 | 52608 | 53051 | AC073347 | 0 | 1 | BAC clone RP11-775L16 from 7, complete sequence Length |
| 469E12 | 85540 | 85930 | AC073917 | 0 | 2 | 12q BAC RP11-415D21 (Roswell Park Cancer Institute BAC |
| 118C12 | 141407 | 141495 | AC083868 | 6.00E-70 | 3 | chromosome 7 clone RP11-148L5, complete sequence Length |
| | 142293 | 142607 | AC083868 | | | |
| 168G5 | 6632 | 7097 | AC087065 | 0 | 2 | chromosome 22q11 clone cos6, complete sequence Length = |
| 479G12 | 127024 | 127342 | AC090942 | 1.00E-119 | 1 | chromosome 3 clone RP11-220D14 map 3p, complete sequence |
| 122G1 | 41957 | 42383 | AC091118 | 0 | 1 | chromosome 16 clone CTC-510K1, complete sequence Length |
| 479D7 | 153992 | 154141 | AF001549 | 6.00E-29 | 1 | Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequ |
| 461H7 | 21977 | 22331 | AF015262 | 2.00E-69 | 1 | chromosome 21 clone Pac 255P7 map 21q-AML, complete seq |
| 463E9 | 27006 | 27615 | AF015725 | 0 | 1 | chromosome 21 clone cosmid clone D68F9 map 21q22.2, com |
| 480D9 | 15848 | 16252 | AF027207 | 1.00E-123 | 1 | chromosome 21 clone cosmid D13C2 map 21q22.2, complete |
| 465E9 | 296143 | 296800 | AF131216 | 0 | 1 | chromosome 8 map 8p23-p22 clones CTB-164D9, CTB-169o5, |
| 469D2 | 23811 | 24045 | AF161800 | 2.00E-78 | 1 | chromosome 8q21.2 BAC 189m5, complete sequence Length = |
| 37G7 | 200214 | 200755 | AJ003147 | 0 | 2 | complete genomic sequence between D16S3070 and D16S3275 |
| | 201078 | 201309 | AJ003147 | | | |
| 459A1 | 36969 | 37402 | AL008730 | 8.00E-82 | 2 | DNA sequence from PAC 487J7 on chromosome 6q21-22.1. Co |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | | |
|--------|----------------|----------------|----------------------|-----------|---|---|
| 480C8 | 37929 | 38457 | AL008733 | 0 | 1 | DNA sequence from clone RP1-163G9 on chromosome 1p36.2- |
| 462D9 | 36712 | 37037 | AL021878 | 0 | 2 | DNA sequence from clone RP1-257I20 on chromosome 22q13. |
| 182H1 | 40603 30506 | 40772 30760 | AL021878 AL022238 | 3.00E-96 | 2 | DNA sequence from clone RP5-1042K10 on chromosome 22q13 |
| 166F6 | 75035 | 75547 | AL022240 | 0 | 1 | DNA sequence from clone 328E19 on chromosome 1q12-21.2 |
| 165C12 | 179455 | 179766 | AL022329 | 1.00E-175 | 1 | DNA sequence from clone CTA-407F11 on chromosome 22q12 |
| 465A12 | 26329 | 26834 | AL022331 | 0 | 1 | DNA sequence from clone CTA-440B3 on chromosome 22q12.1 |
| 524D1 | 70719 | 70891 | AL022394 | 2.00E-87 | 1 | DNA sequence from clone RP3-511B24 on chromosome 20q11. |
| 53E3 | 129077 | 129538 | AL022396 | 0 | 1 | DNA sequence from PAC 380E11 on chromosome 6p22.3-p24. |
| 126D1 | 69809 | 70220 | AL031178 | 0 | 1 | DNA sequence from clone RP3-341E18 on chromosome 6p11.2 |
| 466A9 | 103757 | 104346 | AL031277 | 0 | 1 | DNA sequence from clone 1177E19 on chromosome 1p36.12-3 |
| 472E11 | 41594 | 41778 | AL031595 | 9.00E-97 | 1 | DNA sequence from clone RP4-671O14 on chromosome 22q13. |
| 462E8 | 72042 | 72629 | AL031672 | 0 | 1 | DNA sequence from clone RP4-691N24 on chromosome 20p11. |
| 478C2 | 29633 | 29708 | AL031708 | 9.00E-28 | 1 | DNA sequence from clone LA16-315G5 on chromosome 16, co |
| 53B1 | 30963 | 31311 | AL031729 | 1.00E-163 | 1 | DNA sequence from clone RP1-159A19 on chromosome 1p36.1 |
| 178B2 | 38674 | 38800 | AL033383 | 3.00E-27 | 1 | DNA sequence from clone RP5-1013A10 on chromosome 6p24. |
| 104A7 | 40604 | 41062 | AL033397 | 0 | 1 | DNA sequence from clone 27K12 on chromosome 6p11.2-12.3 |
| 190F11 | 77693 | 78285 | AL033519 | 0 | 1 | DNA sequence from clone RP3-340B19 on chromosome 6p21.2 |
| 121A11 | 15252 | 15679 | AL034344 | 9.00E-52 | 1 | DNA sequence from clone RP1-118B18 on chromosome 6p24.1 |
| 173B5 | 102500 | 102752 | AL034384 | 7.00E-58 | 1 | chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, |
| 121A12 | 34566 | 34684 | AL034397 | 6.00E-47 | 1 | DNA sequence from clone 159A1 on chromosome Xq12-13.3. |
| 104B10 | 73639 | 74045 | AL034418 | 1.00E-176 | 1 | DNA sequence from clone RP5-1049G16 on chromosome 20q12 |
| 471F1 | 37083 | 37364 | AL034553 | 1.00E-150 | 1 | DNA sequence from clone RP5-914P20 on chromosome 20q13. |
| 463H8 | 97563 | 97753 | AL035405 | 1.00E-102 | 1 | DNA sequence from clone 21O18 on chromosome 1p35.1-36.2 |
| 472E6 | 20949 | 21271 | AL035413 | 1.00E-155 | 1 | DNA sequence from clone RP4-657E11 on chromosome 1p35.1 |
| 121F1 | 65029 | 65503 | AL035455 | 0 | 1 | DNA sequence from clone RP5-1018E9 on chromosome 20q13. |
| 465B1 | 37269 | 37445 | AL035530 | 2.00E-47 | 1 | DNA sequence from clone RP1-111C20 on chromosome 6q25.3 |
| 482C9 | 64837 | 65129 | AL035662 | 1.00E-163 | 1 | DNA sequence from clone RP4-599F21 on chromosome 20q12- |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | | |
|--------|--------|--------|----------|-----------|----|---|
| 166B9 | 39808 | 39976 | AL049715 | 1.00E-87 | 1 | DNA sequence from clone RP4-646P11 on chromosome 1, com |
| 591D6 | 65470 | 65892 | AL049795 | 0 | 1 | DNA sequence from clone RP4-622L5 on chromosome 1p34.2- |
| 72G1 | 82160 | 82440 | AL049829 | 1.00E-148 | 1 | chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-12 |
| 112H3 | 2111 | 2535 | AL050330 | 0 | 2 | DNA sequence from clone RP1-3E1 on chromosome 6p21.23-2 |
| 479G5 | 18853 | 19244 | AL096712 | 1.00E-125 | 1 | DNA sequence from clone RP4-744I24 on chromosome 6p12.1 |
| 464C10 | 80145 | 80583 | AL096773 | 4.00E-85 | 1 | DNA sequence from clone 1000E10 on chromosome 1p12-13.3 |
| 123D11 | 34999 | 35510 | AL096808 | 1.00E-166 | 1 | genomic region containing hypervariable minisatellites |
| 129F10 | 1148 | 2507 | AL109616 | 0 | 95 | chromosome 21 Cosmid LLNLc116L1110, complete sequence L |
| 469B8 | 13155 | 13527 | AL109755 | 0 | 1 | DNA sequence from clone RP3-340H11 on chromosome 6q24.1 |
| 105F4 | 57995 | 58306 | AL109758 | 5.00E-98 | 1 | chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-87 |
| 465H5 | 136248 | 136356 | AL109847 | 7.00E-29 | 1 | chromosome 14 DNA sequence BAC R-603H7 of library RPCI- |
| 60G8 | 84706 | 84959 | AL109914 | 1.00E-135 | 1 | DNA sequence from clone RP11-27F12 on chromosome 6p22.3 |
| 102A8 | 169378 | 169473 | AL109918 | 2.00E-34 | 1 | DNA sequence from clone RP1-152L7 on chromosome 6p11.2- |
| 471D6 | 63862 | 64021 | AL117186 | 4.00E-80 | 1 | chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-29 |
| 176E10 | 145991 | 146554 | AL117258 | 3.00E-63 | 1 | chromosome 14 DNA sequence BAC R-244E17 of library RPCI |
| 480E7 | 2975 | 3356 | AL117352 | 1.00E-153 | 1 | DNA sequence from clone RP5-876B10 on chromosome 1q42.1 |
| 110D3 | 48631 | 48886 | AL121573 | 3.00E-65 | 2 | DNA sequence from clone RP1-306F2 on chromosome 6p12.1- |
| 40B2 | 106788 | 107123 | AL121657 | 2.00E-42 | 1 | BAC sequence from the SPG4 candidate region at 2p21-2p2 |
| 52B9 | 56473 | 56690 | AL121899 | 1.00E-104 | 2 | DNA sequence from clone RP11-128M1 on chromosome 20. Co |
| 485A6 | 5475 | 7084 | AL121985 | 1.00E-138 | 7 | DNA sequence from clone RP11-404F10 on chromosome 1q23. |
| | 15867 | 16574 | AL121985 | | | |
| | 17098 | 17504 | AL121985 | | | |
| | 24037 | 24292 | AL121985 | | | |
| 40E4 | 54176 | 54528 | AL121998 | 1.00E-179 | 1 | DNA sequence from clone RP5-1103B4 on chromosome 1 Cont |
| 118H12 | 21398 | 21744 | AL132838 | 0 | 1 | chromosome 14 DNA sequence BAC R-85G20 of library RPCI- |
| 599F11 | 153822 | 154345 | AL133153 | 0 | 1 | chromosome 14 DNA sequence BAC R-895M11 of library RPCI |
| 478G8 | 115784 | 116115 | AL133243 | 1.00E-120 | 1 | BAC sequence from the SPG4 candidate region at 2p21-2p2 |
| 107H8 | 119760 | 120729 | AL133330 | 0 | 22 | DNA sequence from clone RP1-68D18 on chromosome 11p12-1 |
| | 121182 | 121863 | AL133330 | | | |
| | 122773 | 122940 | AL133330 | | | |
| | 143751 | 144379 | AL133330 | | | |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | | |
|--------|--------|--------|----------|-----------|---|---|
| | 146057 | 147016 | AL133330 | | | |
| | 159262 | 159639 | AL133330 | | | |
| 471E7 | 127891 | 128013 | AL133340 | 6.00E-46 | 1 | DNA sequence from clone RP11-204H22 on chromosome 20. C |
| 118H5 | 3922 | 4021 | AL133392 | 1.00E-38 | 2 | DNA sequence from clone CITF22-45C1 on chromosome 22 Co |
| | 4557 | 5184 | AL133392 | | | |
| 40A3 | 96202 | 96785 | AL133412 | 0 | 3 | DNA sequence from clone RP11-131A5 on chromosome 9q22.1 |
| | 97177 | 97568 | AL133412 | | | |
| 482A5 | 28668 | 29037 | AL133415 | 3.00E-34 | 4 | DNA sequence from clone RP11-124N14 on chromosome 10. C |
| | 51083 | 51210 | | | | |
| 54G9 | 54866 | 55153 | AL135783 | 1.00E-154 | 1 | DNA sequence from clone RP3-527F8 on chromosome Xq25-27 |
| 515C12 | 72222 | 72601 | AL135818 | 1.00E-146 | 2 | chromosome 14 DNA sequence BAC C-2547L24 of library Cal |
| 109A9 | 53171 | 53447 | AL136320 | 1.00E-137 | 1 | DNA sequence from clone RP3-323N1 on chromosome 10. Con |
| 476H10 | 127150 | 127680 | AL137017 | 0 | 1 | DNA sequence from clone RP11-120J1 on chromosome 9 Cont |
| 192C3 | 122511 | 122837 | AL137100 | 1.00E-117 | 1 | chromosome 14 DNA sequence BAC R-108M12 of library RPCI |
| 55G3 | 38923 | 39058 | AL137142 | 7.00E-44 | 2 | DNA sequence from clone RP11-173P16 on chromosome 13q12 |
| | 42456 | 42686 | AL137142 | | | |
| 466G2 | 24290 | 24402 | AL137144 | 9.00E-42 | 1 | DNA sequence from clone RP11-210E23 on chromosome 13q31 |
| 140F9 | 27354 | 27715 | AL137798 | 8.00E-82 | 1 | DNA sequence from clone RP5-1182A14 on chromosome 1 Con |
| 37A2 | 134590 | 134750 | AL137800 | 3.00E-69 | 1 | DNA sequence from clone RP1-127C7 on chromosome 1q25.1- |
| 493C2 | 734 | 1052 | AL138714 | 1.00E-157 | 1 | DNA sequence from clone RP11-121J7 on chromosome 13q32. |
| 468B9 | 1911 | 2509 | AL138717 | 9.00E-70 | 1 | DNA sequence from clone RP11-11D8 on chromosome 6 Conta |
| 194F9 | 46595 | 46814 | AL138755 | 6.00E-94 | 1 | DNA sequence from clone RP11-48M17 on chromosome 9p24.1 |
| 483D12 | 80220 | 80755 | AL138776 | 1.00E-157 | 1 | DNA sequence from clone RP11-20H6 on chromosome 1q25.1- |
| 464G9 | 14032 | 14659 | AL139020 | 0 | 1 | chromosome 14 DNA sequence BAC R-164H13 of library RPCI |
| 59G1 | 34476 | 34936 | AL139274 | 0 | 1 | DNA sequence from clone RP11-393I2 on chromosome 6, com |
| 129D3 | 65447 | 65661 | AL139289 | 1.00E-107 | 2 | DNA sequence from clone RP1-92O14 on chromosome 1p33-34 |
| | 66950 | 67158 | AL139289 | | | |
| 464C2 | 55616 | 56289 | AL139328 | 0 | 1 | DNA sequence from clone RP11-84N7 on chromosome 13. Con |
| 57H10 | 155342 | 155810 | AL139330 | 0 | 2 | DNA sequence from clone RP11-266C7 on chromosome 6q25.2 |
| 470G6 | 44695 | 44978 | AL139399 | 1.00E-130 | 1 | DNA sequence from clone RP11-574A21 on chromosome Xq21. |
| 476F5 | 42969 | 43159 | AL139801 | 5.00E-98 | 1 | DNA sequence from clone RP11-247M1 on chromosome 13, co |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | | |
|--------|--------|--------|----------|-----------|---|---|
| 107G11 | 139776 | 140378 | AL157402 | 0 | 2 | DNA sequence from clone RP11-553K8 on chromosome 1q31.2 |
| 172B12 | 136072 | 136492 | AL157768 | 1.00E-155 | 1 | DNA sequence from clone RP11-481A22 on chromosome 13 Co |
| 149A11 | 438 | 663 | AL157776 | 1.00E-123 | 1 | DNA sequence from clone RP11-68J15 on chromosome 6, com |
| 165E7 | 66361 | 67034 | AL157789 | 0 | 1 | chromosome 14 DNA sequence BAC R-880O3 of library RPCI- |
| 192B3 | 51907 | 52253 | AL157938 | 1.00E-176 | 1 | DNA sequence from clone RP11-544A12 on chromosome 9q34. |
| 50A11 | 5753 | 5886 | AL158136 | 1.00E-59 | 1 | DNA sequence from clone RP1-44N23 on chromosome 6 Conta |
| 472F9 | 84638 | 85232 | AL158159 | 0 | 1 | DNA sequence from clone RP11-498N2 on chromosome 9, com |
| 462G12 | 132520 | 132708 | AL160155 | 2.00E-95 | 1 | DNA sequence from clone RP11-461N23 on chromosome 13, c |
| 117H6 | 1976 | 2518 | AL160233 | 0 | 1 | chromosome 14 DNA sequence BAC C-2373J19 of library Cal |
| 460B9 | 207 | 739 | AL160408 | 1.00E-104 | 2 | DNA sequence from clone RP4-781K5 on chromosome 1q42.1- |
| | 2023 | 2537 | AL160408 | | | |
| 467F10 | 8461 | 8829 | AL161627 | 1.00E-122 | 1 | DNA sequence from clone RP11-287A8 on chromosome 9, com |
| 469A10 | 81966 | 82313 | AL161781 | 1.00E-175 | 1 | DNA sequence from clone RP11-297B17 on chromosome 9, co |
| 598H2 | 222231 | 222679 | AL162151 | 0 | 1 | chromosome 14 DNA sequence *** IN PROGRESS *** BAC C-31 |
| 466C5 | 147064 | 147687 | AL162578 | 0 | 1 | DNA sequence from clone RP11-2J18 on chromosome 6, comp |
| 467C9 | 216403 | 216544 | AL163303 | 3.00E-38 | 1 | chromosome 21 segment HS21C103 Length = 340000 |
| 462H9 | 63385 | 63502 | AL163853 | 6.00E-59 | 1 | chromosome 14 DNA sequence BAC R-248B10 of library RPCI |
| 464A10 | 63421 | 63807 | AL353744 | 2.00E-55 | 1 | clone RP13-100-A9 on chromosome X |
| 99E10 | 6789 | 7153 | AL353804 | 0 | 1 | DNA sequence from clone RP13-216E22 on chromosome Xq13. |
| 477D10 | 49708 | 50171 | AL354716 | 4.00E-96 | 1 | DNA sequence from clone RP11-86F4 on chromosome 6, comp |
| 518F10 | 3379 | 3602 | AL354891 | 2.00E-94 | 1 | DNA sequence from clone RP11-44I7 on chromosome 13, com |
| 464D8 | 122494 | 122702 | AL354977 | 1.00E-87 | 2 | DNA sequence from clone RP11-509J21 on chromosome 9, co |
| 459H6 | 109525 | 109864 | AL355520 | 1.00E-179 | 1 | DNA sequence from clone RP4-595C2 on chromosome 1q24.1- |
| 196C6 | 21603 | 21783 | AL355615 | 7.00E-96 | 2 | DNA sequence from clone RP11-33E24 on chromosome 6, com |
| 110B8 | 11907 | 12312 | AL355797 | 1.00E-145 | 1 | DNA sequence from clone RP1-9E2 on chromosome 6, comple |
| 180B2 | 142517 | 142726 | AL355871 | 1.00E-72 | 1 | DNA sequence from clone RP11-47K11 on chromosome 1, com |
| 464H5 | 50106 | 50463 | AL356276 | 0 | 2 | DNA sequence from clone RP11-367J7 on chromosome 1. Con |
| 105H4 | 32156 | 32236 | AL356379 | 2.00E-27 | 2 | DNA sequence from clone RP1-63P18 on chromosome 1. Cont |
| | 32440 | 32804 | AL356379 | | | |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | | |
|--------|--------|--------|-----------|-----------|----|---|
| 113H1 | 22550 | 22837 | AL356481 | 1.00E-160 | 1 | DNA sequence from clone RP11-216B9 on chromosome 9, com |
| 170F7 | 46442 | 46855 | AL357374 | 0 | 1 | DNA sequence from clone RP11-353C18 on chromosome 20 Co |
| 522D3 | 113148 | 113424 | AL360182 | 1.00E-127 | 1 | DNA sequence from clone RP11-549L6 on chromosome 10, co |
| 36E9 | 38157 | 38346 | AL390196 | 4.00E-47 | 9 | clone RP11-60E24 on chromosome 6 |
| 587E3 | 15704 | 16062 | AL442128 | 1.00E-173 | 2 | DNA sequence from clone RP11-365P13 on chromosome 13, c |
| 468E8 | 52779 | 53344 | AL445201 | 1.00E-123 | 1 | DNA sequence from clone RP11-358L16 on chromosome 10, c |
| 39G11 | 106047 | 106169 | AL445687 | 2.00E-26 | 1 | clone RP11-567B20 on chromosome 1 |
| 101F1 | 1538 | 1656 | AL449244 | 5.00E-44 | 2 | Novel human gene mapping to chromosome 22 Length = 2315 |
| | 1676 | 2096 | AL449244 | | | |
| 466D1 | 56761 | 56929 | AL450344 | 5.00E-85 | 1 | DNA sequence from clone RP11-136K14 on chromosome 6 Con |
| 142E9 | 116227 | 116568 | AL590763 | 0 | 8 | chromosome X sequence from 6 PACs 1 BAC and 1 cosmid, r |
| | 116669 | 117358 | AL590763 | | | |
| | 154792 | 155165 | AL590763 | | | |
| 459E9 | 26826 | 26890 | AP000471 | 2.00E-27 | 1 | genomic DNA, chromosome 21q22.3, clone:B2308H15 Length |
| 472C1 | 95646 | 96035 | AP000501 | 1.00E-101 | 1 | genomic DNA, chromosome 8p11.2, clone:91h23 to 9-41 Len |
| 464A7 | 7930 | 8285 | AP000526 | 1.00E-178 | 1 | genomic DNA, chromosome 22q11.2, Cat Eye Syndrome regio |
| 165E11 | 643 | 1244 | AP000554 | 1.00E-147 | 2 | genomic DNA, chromosome 22q11.2, BCRL2 region, clone:KB |
| 72D8 | 27091 | 27486 | AP000555 | 0 | 1 | genomic DNA, chromosome 22q11.2, BCRL2 region, clone:KB |
| 470B4 | 15634 | 15703 | AP001429 | 5.00E-28 | 1 | genomic DNA, chromosome 21q22.2, clone:T1212, LB7T-ERG |
| 59E12 | 59103 | 59520 | AP001574 | 1.00E-144 | 2 | genomic DNA, chromosome 8q23, clone: KB1991G8 Length = |
| | 60671 | 61189 | AP001574 | | | |
| 138G5 | 313261 | 313931 | AP001693 | 1.00E-31 | 27 | genomic DNA, chromosome 21q, section 37/105 Length = 34 |
| | 315877 | 315967 | AP001693 | | | |
| | 319062 | 319564 | AP001693 | | | |
| | 319957 | 320293 | AP001693 | | | |
| | 320563 | 321212 | AP001693 | | | |
| | 328757 | 329184 | AP001693 | | | |
| 158G11 | 107888 | 108375 | AP001721 | 0 | 1 | genomic DNA, chromosome 21q, section 65/105 Length = 34 |
| 462F9 | 330129 | 330645 | AP001728 | 1.00E-133 | 1 | genomic DNA, chromosome 21q, section 72/105 Length = 34 |
| 479A12 | 74529 | 74902 | AP002907 | 1.00E-141 | 1 | genomic DNA, chromosome 8q23, clone: KB431C1 Length = 9 |
| 470B2 | 123506 | 123689 | AP003117 | 4.00E-72 | 2 | genomic DNA, chromosome 8q23, clone: KB1958F4 Length = |
| 46D1 | 79174 | 79657 | AP003471 | 1.00E-164 | 2 | genomic DNA, chromosome 8q23, clone: KB1552D7 Length = |
| | 83490 | 84099 | AP003471 | | | |
| 496C4 | 745790 | 746197 | NT_004406 | 0 | 1 | chromosome 1 working draft sequence segment |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | | |
|--------|--------|---------|-----------|-----------|---|---|
| 468E10 | 2015 | 2118 | NT_004452 | 2.00E-32 | 2 | chromosome 1 working draft sequence segment |
| 479H12 | 394087 | 394676 | NT_004480 | 0 | 1 | chromosome 1 working draft sequence segment |
| 472G2 | 268543 | 268642 | NT_004525 | 3.00E-42 | 1 | chromosome 1 working draft sequence segment |
| 477D9 | 231154 | 231469 | NT_004531 | 1.00E-177 | 1 | chromosome 1 working draft sequence segment |
| 460F7 | 786014 | 786511 | NT_004623 | 0 | 1 | chromosome 1 working draft sequence segment |
| 171F11 | 1E+06 | 1036701 | NT_004658 | 1.00E-26 | 1 | chromosome 1 working draft sequence segment |
| 184H1 | 2E+06 | 1770512 | NT_004698 | 0 | 4 | chromosome 1 working draft sequence segment |
| | 2E+06 | 1822054 | NT_004698 | | | |
| | 2E+06 | 1832854 | NT_004698 | | | |
| 514H9 | 289858 | 289941 | NT_004705 | 1.00E-29 | 1 | chromosome 1 working draft sequence segment |
| 463G1 | 175158 | 175615 | NT_004725 | 0 | 1 | chromosome 1 working draft sequence segment |
| 466C9 | 543567 | 544240 | NT_004753 | 0 | 1 | chromosome 1 working draft sequence segment |
| 496D7 | 2E+06 | 1515549 | NT_004754 | 0 | 1 | chromosome 1 working draft sequence segment |
| 583G8 | 733247 | 733667 | NT_004771 | 1.00E-128 | 1 | chromosome 1 working draft sequence segment |
| 124D2 | 107397 | 107739 | NT_004916 | 1.00E-178 | 1 | chromosome 1 working draft sequence segment |
| 479A8 | 285973 | 286345 | NT_005130 | 1.00E-165 | 1 | chromosome 2 working draft sequence segment |
| 165F7 | 1E+06 | 1435537 | NT_005151 | 1.00E-125 | 1 | chromosome 2 working draft sequence segment |
| 465F7 | 773772 | 774502 | NT_005166 | 0 | 2 | chromosome 2 working draft sequence segment |
| 73A3 | 80919 | 81448 | NT_005182 | 0 | 2 | chromosome 2 working draft sequence segment |
| | 81502 | 81742 | NT_005182 | | | |
| 124G7 | 2E+06 | 1859389 | NT_005204 | 1.00E-180 | 1 | chromosome 2 working draft sequence segment |
| 479G6 | 552674 | 553005 | NT_005229 | 1.00E-141 | 5 | chromosome 2 working draft sequence segment |
| | 1E+06 | 1122605 | NT_005229 | | | |
| 194C2 | 481052 | 481444 | NT_005230 | 1.00E-101 | 1 | chromosome 2 working draft sequence segment |
| 159F11 | 795978 | 796616 | NT_005275 | 0 | 1 | chromosome 2 working draft sequence segment |
| 472B1 | 1013 | 1410 | NT_005311 | 0 | 1 | chromosome 2 working draft sequence segment |
| 470G7 | 375182 | 375594 | NT_005399 | 0 | 1 | chromosome 2 working draft sequence segment |
| 100C3 | 803712 | 804094 | NT_005420 | 0 | 2 | chromosome 2 working draft sequence segment |
| | 970577 | 971108 | NT_005420 | | | |
| 98H4 | 2E+06 | 1829143 | NT_005423 | 0 | 1 | chromosome 2 working draft sequence segment |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | | |
|--------|--------|---------|-----------|-----------|---|---|
| 105A10 | 1E+06 | 1144092 | NT_005435 | 1.00E-167 | 2 | chromosome 2 working draft sequence segment |
| 465C3 | 13444 | 13890 | NT_005471 | 0 | 1 | chromosome 2 working draft sequence segment |
| 112E5 | 3169 | 3793 | NT_005485 | 0 | 1 | chromosome 2 working draft sequence segment |
| 111H6 | 146878 | 146999 | NT_005499 | 2.00E-55 | 1 | chromosome 3 working draft sequence segment |
| 467G7 | 198880 | 199329 | NT_005505 | 0 | 1 | chromosome 3 working draft sequence segment |
| 182F12 | 140059 | 140193 | NT_005516 | 1.00E-144 | 3 | chromosome 3 working draft sequence segment |
| 112B5 | 140754 | 141039 | NT_005516 | | | |
| | 137689 | 138300 | NT_005529 | 0 | 4 | chromosome 3 working draft sequence segment |
| 64B3 | 55213 | 55793 | NT_005535 | 0 | 1 | chromosome 3 working draft sequence segment |
| 465E12 | 866776 | 867258 | NT_005769 | 0 | 2 | chromosome 3 working draft sequence segment |
| | 1E+06 | 1021292 | NT_005769 | | | |
| 470D5 | 1E+06 | 1395364 | NT_005795 | 1.00E-147 | 3 | chromosome 3 working draft sequence segment |
| | 2E+06 | 1749621 | NT_005795 | | | |
| 479G2 | 294179 | 294607 | NT_005910 | 0 | 1 | chromosome 3 working draft sequence segment |
| 112E1 | 392884 | 393490 | NT_005973 | 0 | 1 | chromosome 3 working draft sequence segment |
| 466H5 | 339511 | 340153 | NT_005985 | 0 | 2 | chromosome 3 working draft sequence segment |
| 189A8 | 22414 | 22869 | NT_005991 | 1.00E-110 | 1 | chromosome 3 working draft sequence segment |
| 45H8 | 1E+06 | 1012040 | NT_006098 | 1.00E-113 | 1 | chromosome 4 working draft sequence segment |
| 104D1 | 282259 | 282753 | NT_006102 | 0 | 2 | chromosome 4 working draft sequence segment |
| 459G8 | 367701 | 368248 | NT_006111 | 0 | 1 | chromosome 4 working draft sequence segment |
| 480E11 | 486179 | 486804 | NT_006114 | 0 | 1 | chromosome 4 working draft sequence segment |
| 115G2 | 4E+06 | 3514655 | NT_006204 | 1.00E-177 | 1 | chromosome 4 working draft sequence segment |
| 479G3 | 71744 | 72258 | NT_006258 | 0 | 1 | chromosome 4 working draft sequence segment |
| 461H11 | 378023 | 378482 | NT_006397 | 0 | 1 | chromosome 4 working draft sequence segment |
| 462F11 | 80360 | 81081 | NT_006410 | 0 | 1 | chromosome 4 working draft sequence segment |
| 463A5 | 2E+06 | 1609976 | NT_006489 | 1.00E-138 | 1 | chromosome 5 working draft sequence segment |
| 464C5 | 190095 | 190533 | NT_006611 | 0 | 2 | chromosome 5 working draft sequence segment |
| 109H9 | 89260 | 89769 | NT_006946 | 0 | 3 | chromosome 5 working draft sequence segment |
| 137B5 | 2E+06 | 1613357 | NT_006951 | 1.00E-86 | 4 | chromosome 5 working draft sequence segment |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | |
|--------|--------|---------|---------------------|----|--|
| 73H4 | 992358 | 992685 | NT_007288 0 | 1 | chromosome 6 working draft sequence segment |
| 174H6 | 431672 | 432054 | NT_007308 0 | 1 | chromosome 6 working draft sequence segment |
| 124C8 | 282413 | 283138 | NT_007951 0 | 1 | chromosome 7 working draft sequence segment |
| 174G11 | 829762 | 830370 | NT_007972 0 | 1 | chromosome 8 working draft sequence segment |
| 471H11 | 613132 | 613314 | NT_007978 9.00E-96 | 1 | chromosome 8 working draft sequence segment |
| 471G8 | 189279 | 189630 | NT_008012 1.00E-147 | 1 | chromosome 8 working draft sequence segment |
| 67C5 | 287017 | 287563 | NT_008037 0 | 2 | chromosome 8 working draft sequence segment |
| 479H4 | 90555 | 90944 | NT_008047 1.00E-174 | 1 | chromosome 8 working draft sequence segment |
| 100D7 | 64180 | 64371 | NT_008050 1.00E-134 | 6 | chromosome 8 working draft sequence segment |
| 45B9 | 331150 | 331412 | NT_008050 | 12 | chromosome 8 working draft sequence segment |
| | 479878 | 480193 | NT_008060 1.00E-165 | | |
| 169F11 | 489788 | 490607 | NT_008060 | 1 | chromosome 8 working draft sequence segment |
| | 291836 | 292284 | NT_008081 0 | | |
| 468H11 | 106661 | 106897 | NT_008128 1.00E-121 | 2 | chromosome 8 working draft sequence segment |
| 470H6 | 110374 | 110691 | NT_008128 | 1 | chromosome 8 working draft sequence segment |
| | 520107 | 520754 | NT_008139 0 | | |
| 471F9 | 392744 | 393279 | NT_008157 0 | 1 | chromosome 8 working draft sequence segment |
| 469G8 | 433686 | 434156 | NT_008338 0 | 1 | chromosome 9 working draft sequence segment |
| 193E6 | 1E+06 | 1228306 | NT_008445 6.00E-56 | 1 | chromosome 9 working draft sequence segment |
| 480D2 | 90407 | 90990 | NT_008484 0 | 1 | chromosome 9 working draft sequence segment |
| 58G4 | 1E+06 | 1055972 | NT_008513 1.00E-139 | 1 | chromosome 9 working draft sequence segment |
| 490F10 | 669853 | 669980 | NT_008653 5.00E-39 | 2 | chromosome 10 working draft sequence segment |
| 463B3 | 743459 | 744217 | NT_008653 | 1 | chromosome 10 working draft sequence segment |
| | 1E+06 | 1369815 | NT_008682 0 | | |
| 116E10 | 1E+06 | 1462064 | NT_008769 0 | 5 | chromosome 10 working draft sequence segment |
| 190A9 | 2E+06 | 2026887 | NT_008769 | 4 | chromosome 10 working draft sequence segment |
| | 2E+06 | 2027460 | NT_008769 | | |
| | 2E+06 | 2028265 | NT_008769 | | |
| | 806672 | 807345 | NT_008774 0 | | |
| 473B7 | 75339 | 75524 | NT_008783 4.00E-72 | 2 | chromosome 10 working draft sequence segment |
| 490A11 | 75869 | 76181 | NT_008783 | 1 | chromosome 10 working draft sequence segment |
| | 484304 | 484753 | NT_008921 0 | | |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | | |
|--------|--------|---------|------------|-----------|--|--|
| 585E10 | 328767 | 329151 | NT_0089780 | 1 | chromosome 11 working draft sequence segment | |
| 458B9 | 955258 | 955846 | NT_0090730 | 1 | chromosome 11 working draft sequence segment | |
| 471F4 | 288811 | 289312 | NT_0091070 | 1 | chromosome 11 working draft sequence segment | |
| 478H7 | 1E+06 | 1255050 | NT_009184 | 1.00E-92 | 1 | chromosome 11 working draft sequence segment |
| 109F10 | 1E+06 | 1136705 | NT_009314 | 1.00E-171 | 1 | chromosome 11 working draft sequence segment |
| 117F1 | 401530 | 402043 | NT_0093340 | 2 | chromosome 11 working draft sequence segment | |
| | 2E+06 | 1600694 | NT_009334 | | | |
| 467B6 | 3E+06 | 3011938 | NT_009338 | 5.00E-93 | 2 | chromosome 11 working draft sequence segment |
| 158H6 | 351515 | 351940 | NT_0094380 | 2 | chromosome 12 working draft sequence segment | |
| 471C2 | 977560 | 977791 | NT_009452 | 1.00E-127 | 1 | chromosome 12 working draft sequence segment |
| 182G2 | 21455 | 21913 | NT_0094580 | 3 | chromosome 12 working draft sequence segment | |
| | 167133 | 167630 | NT_009458 | | | |
| 462B12 | 518389 | 518876 | NT_0094640 | 1 | chromosome 12 working draft sequence segment | |
| 458A3 | 2E+06 | 1890445 | NT_0094710 | 1 | chromosome 12 working draft sequence segment | |
| 470D7 | 9540 | 10050 | NT_0095400 | 1 | chromosome 12 working draft sequence segment | |
| 525F3 | 163261 | 163590 | NT_009616 | 1.00E-125 | 1 | chromosome 12 working draft sequence segment |
| 186E8 | 2E+06 | 1502030 | NT_0097140 | 1 | chromosome 12 working draft sequence segment | |
| 465G2 | 2E+06 | 1787964 | NT_009759 | 1.00E-130 | 2 | chromosome 12 working draft sequence segment |
| 476C1 | 321714 | 322118 | NT_009763 | 1.00E-170 | 1 | chromosome 12 working draft sequence segment |
| 476G8 | 2E+06 | 1609230 | NT_009770 | 6.00E-26 | 1 | chromosome 12 working draft sequence segment |
| 588E4 | 1E+06 | 1136791 | NT_010036 | 1.00E-134 | 1 | chromosome 14 working draft sequence segment |
| 479H5 | 2E+06 | 2151529 | NT_0100620 | 1 | chromosome 14 working draft sequence segment | |
| 178C10 | 6E+06 | 6026576 | NT_0101130 | 1 | chromosome 14 working draft sequence segment | |
| 192C9 | 5E+06 | 5344032 | NT_0101940 | 1 | chromosome 15 working draft sequence segment | |
| 119F12 | 3E+06 | 2680702 | NT_010204 | 1.00E-128 | 1 | chromosome 15 working draft sequence segment |
| 67G10 | 112609 | 112890 | NT_010222 | 1.00E-132 | 2 | chromosome 15 working draft sequence segment |
| 98C1 | 6684 | 7232 | NT_0102370 | 1 | chromosome 15 working draft sequence segment | |
| 458G10 | 478693 | 479052 | NT_010253 | 1.00E-120 | 1 | chromosome 15 working draft sequence segment |
| 459D1 | 2E+06 | 2123962 | NT_0102890 | 1 | chromosome 15 working draft sequence segment | |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | |
|--------|--------|---------|--------------------|---|--|
| 110G1 | 303146 | 303706 | NT_0103080 | 1 | chromosome 15 working draft sequence segment |
| 73A4 | 758542 | 758734 | NT_0103106.00E-42 | 1 | chromosome 15 working draft sequence segment |
| 470F5 | 495497 | 496038 | NT_0103600 | 1 | chromosome 15 working draft sequence segment |
| 469B6 | 1E+06 | 1095404 | NT_0104191.00E-123 | 1 | chromosome 16 working draft sequence segment |
| 479E10 | 468259 | 468674 | NT_0104320 | 1 | chromosome 16 working draft sequence segment |
| 100F5 | 177425 | 177795 | NT_0105051.00E-169 | 1 | chromosome 16 working draft sequence segment |
| 462C5 | 22345 | 22727 | NT_0105230 | 1 | chromosome 16 working draft sequence segment |
| 71H3 | 125549 | 125838 | NT_0105305.00E-77 | 1 | chromosome 16 working draft sequence segment |
| 161E8 | 1E+06 | 1067677 | NT_0106411.00E-123 | 1 | chromosome 17 working draft sequence segment |
| 464D9 | 120516 | 121079 | NT_0106570 | 1 | chromosome 17 working draft sequence segment |
| 114G3 | 385825 | 386329 | NT_0106721.00E-152 | 3 | chromosome 17 working draft sequence segment |
| | 387069 | 387398 | NT_010672 | | |
| | 424808 | 425286 | NT_010672 | | |
| 459E6 | 262663 | 263161 | NT_0107570 | 1 | chromosome 17 working draft sequence segment |
| 134H3 | 583781 | 583868 | NT_0107997.00E-32 | 1 | chromosome 17 working draft sequence segment |
| 467E5 | 1E+06 | 1376833 | NT_0108080 | 1 | chromosome 17 working draft sequence segment |
| 462A11 | 436300 | 437040 | NT_0108160 | 2 | chromosome 17 working draft sequence segment |
| 460C2 | 168998 | 169554 | NT_0108330 | 1 | chromosome 17 working draft sequence segment |
| 467A8 | 480458 | 480865 | NT_0109860 | 1 | chromosome 18 working draft sequence segment |
| 480F8 | 137902 | 138430 | NT_0110290 | 1 | chromosome 18 working draft sequence segment |
| 470F8 | 472324 | 472740 | NT_0111410 | 1 | chromosome 19 working draft sequence segment |
| 100E3 | 445588 | 445677 | NT_0111452.00E-37 | 2 | chromosome 19 working draft sequence segment |
| | 445757 | 446041 | NT_011145 | | |
| 104A12 | 169627 | 169811 | NT_0112402.00E-99 | 1 | chromosome 19 working draft sequence segment |
| 69B10 | 358921 | 359000 | NT_0112456.00E-37 | 1 | chromosome 19 working draft sequence segment |
| 465C7 | 243467 | 243788 | NT_0112690 | 1 | chromosome 19 working draft sequence segment |
| 464E7 | 1E+06 | 1182829 | NT_0115971.00E-107 | 1 | chromosome X working draft sequence segment |
| 61A11 | 67055 | 67582 | NT_0117240 | 1 | chromosome X working draft sequence segment |
| 140G10 | 761394 | 761693 | NT_0158051.00E-138 | 3 | chromosome 2 working draft sequence segment |
| | 761753 | 762151 | NT_015805 | | |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | |
|--------|---------------------------|---------------------------|---------------------------------------|---|---|
| 486C4 | 503899 | 504524 | NT_016354 0 | 2 | chromosome 4 working draft sequence segment |
| 480G4 | 260275 | 260648 | NT_016355 0 | 1 | chromosome 4 working draft sequence segment |
| 461G8 | 276786 | 277233 | NT_016593 0 | 1 | chromosome 4 working draft sequence segment |
| 118D9 | 413201 | 413343 | NT_016968 7.00E-46 | 1 | chromosome 6 working draft sequence segment |
| 68C9 | 2E+06 | 2193260 | NT_017568 1.00E-169 | 1 | chromosome 9 working draft sequence segment |
| 470E5 | 526603 | 527148 | NT_017582 1.00E-131 | 2 | chromosome 9 working draft sequence segment |
| 127H8 | 248872 | 249411 | NT_019390 0 | 1 | chromosome 5 working draft sequence segment |
| 47G6 | 204946 | 205445 | NT_019447 0 | 1 | chromosome 7 working draft sequence segment |
| 467E8 | 210239 | 210638 | NT_021889 1.00E-170 | 1 | chromosome 1 working draft sequence segment |
| 480C6 | 210001 | 210545 | NT_021897 0 | 1 | chromosome 1 working draft sequence segment |
| 69H11 | 94439 | 94993 | NT_021903 1.00E-104 | 1 | chromosome 1 working draft sequence segment |
| 107D7 | 466791 | 467280 | NT_021918 0 | 1 | chromosome 1 working draft sequence segment |
| 471E11 | 418049 | 418124 | NT_021967 8.00E-32 | 1 | chromosome 1 working draft sequence segment |
| 468F11 | 370984 | 371480 | NT_022103 0 | 1 | chromosome 1 working draft sequence segment |
| 464H12 | 1E+06 | 1024449 | NT_022171 1.00E-155 | 1 | chromosome 2 working draft sequence segment |
| 462B11 | 242113 | 242753 | NT_022174 0 | 1 | chromosome 2 working draft sequence segment |
| 196D7 | 65778 | 66218 | NT_022315 0 | 5 | chromosome 2 working draft sequence segment |
| 100E10 | 66514 148157 | 66886 148338 | NT_022315 NT_022358 4.00E-95 | 1 | chromosome 2 working draft sequence segment |
| 142F9 | 193054 | 193433 | NT_022457 0 | 6 | chromosome 3 working draft sequence segment |
| 595A12 | 240726 286545 40034 | 241196 287198 40650 | NT_022457 NT_022457 NT_022488 0 | 2 | chromosome 3 working draft sequence segment |
| 75A2 | 24792 | 25256 | NT_022555 1.00E-133 | 1 | chromosome 3 working draft sequence segment |
| 468G12 | 276616 | 277068 | NT_022751 0 | 1 | chromosome 4 working draft sequence segment |
| 471F6 | 403620 | 404200 | NT_022765 6.00E-89 | 1 | chromosome 4 working draft sequence segment |
| 463H12 | 197991 | 198185 | NT_022795 2.00E-88 | 1 | chromosome 4 working draft sequence segment |
| 473E4 | 408745 | 409322 | NT_022840 1.00E-123 | 2 | chromosome 4 working draft sequence segment |
| 461C8 | 544633 | 545127 | NT_022844 0 | 1 | chromosome 4 working draft sequence segment |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | | |
|--------|--------|---------|-----------|-----------|---|--|
| 470G10 | 148269 | 148781 | NT_022855 | 0 | 1 | chromosome 4 working draft sequence segment |
| 480F3 | 471820 | 472173 | NT_023178 | 1.00E-138 | 1 | chromosome 5 working draft sequence segment |
| 176G2 | 98388 | 98683 | NT_023529 | 1.00E-153 | 1 | chromosome 7 working draft sequence segment |
| 71F2 | 62180 | 62604 | NT_023654 | 0 | 1 | chromosome 8 working draft sequence segment |
| 459F2 | 324390 | 324869 | NT_023660 | 0 | 1 | chromosome 8 working draft sequence segment |
| 124F9 | 275971 | 276413 | NT_023666 | 0 | 1 | chromosome 8 working draft sequence segment |
| 111H9 | 388593 | 389283 | NT_023676 | 0 | 1 | chromosome 8 working draft sequence segment |
| 460D12 | 527418 | 527528 | NT_023703 | 3.00E-43 | 1 | chromosome 8 working draft sequence segment |
| 129D7 | 104058 | 104672 | NT_023833 | 1.00E-170 | 1 | chromosome 8 working draft sequence segment |
| 183G2 | 183398 | 183840 | NT_023923 | 1.00E-112 | 1 | chromosome 9 working draft sequence segment |
| 478G6 | 41677 | 41996 | NT_023945 | 1.00E-137 | 1 | chromosome 9 working draft sequence segment |
| 163E7 | 1E+06 | 1455953 | NT_023959 | 1.00E-126 | 1 | chromosome 9 working draft sequence segment |
| 472G12 | 21182 | 21574 | NT_024016 | 0 | 1 | chromosome 9 working draft sequence segment |
| 466B7 | 471195 | 471690 | NT_024040 | 1.00E-138 | 1 | chromosome 10 working draft sequence segment |
| 459D2 | 315088 | 315482 | NT_024091 | 0 | 1 | chromosome 10 working draft sequence segment |
| 468B10 | 791272 | 792086 | NT_024101 | 0 | 2 | chromosome 10 working draft sequence segment |
| 175D1 | 270651 | 271264 | NT_024115 | 0 | 2 | chromosome 10 working draft sequence segment |
| 472D7 | 16139 | 16549 | NT_024223 | 0 | 1 | chromosome 11 working draft sequence segment |
| 476G3 | 71426 | 71803 | NT_024498 | 1.00E-144 | 1 | chromosome 13 working draft sequence segment |
| 138B6 | 2E+06 | 1638986 | NT_024680 | 0 | 2 | chromosome 15 working draft sequence segment |
| 466A4 | 308514 | 309137 | NT_024767 | 0 | 1 | chromosome 16 working draft sequence segment |
| 583D6 | 551386 | 551654 | NT_024781 | 1.00E-133 | 1 | chromosome 16 working draft sequence segment |
| 468F10 | 91355 | 92043 | NT_024815 | 1.00E-132 | 2 | chromosome 16 working draft sequence segment |
| 461D9 | 406470 | 406916 | NT_024897 | 0 | 2 | chromosome 17 working draft sequence segment |
| | 440400 | 440720 | NT_024897 | | | |
| 520A8 | 168514 | 168868 | NT_024997 | 0 | 1 | chromosome 18 working draft sequence segment |
| 128F5 | 113027 | 113221 | NT_025378 | 6.00E-82 | 1 | chromosome X working draft sequence segment |
| 467B11 | 519341 | 519633 | NT_025635 | 1.00E-113 | 1 | chromosome 1 working draft sequence segment |

Table 3B: Identified Genomic Regions that code for novel human mRNA's

| | | | | | | |
|--------|--------|---------|-----------|-----------|---|---|
| 464E11 | 8932 | 9161 | NT_025657 | 1.00E-126 | 1 | chromosome 2 working draft sequence segment |
| 188C1 | 1E+06 | 1221531 | NT_025823 | 4.00E-72 | 1 | chromosome 10 working draft sequence segment |
| 468B2 | 156035 | 156630 | NT_025900 | 1.00E-150 | 2 | chromosome 16 working draft sequence segment |
| 470F3 | 427484 | 428029 | NT_026379 | 0 | 2 | chromosome 10 working draft sequence segment |
| 36G1 | 483362 | 484059 | NT_026443 | 0 | 1 | chromosome 15 working draft sequence segment |
| 466B5 | 19929 | 20420 | NT_026455 | 1.00E-123 | 1 | chromosome 16 working draft sequence segment |
| 105A8 | 3431 | 3518 | U12202 | 6.00E-34 | 1 | ribosomal protein S24 (rps24) gene, complete cds Length |
| 175D10 | 18139 | 18285 | U18671 | 8.00E-45 | 2 | Stat2 gene, complete cds Length = 18648 |
| 116F9 | 68889 | 69093 | U85199 | 6.00E-69 | 1 | BAC956, complete sequence Length = 105232 |
| 598F3 | 22246 | 22656 | U91318 | 0 | 1 | chromosome 16 BAC clone CIT987SK-A-962B4, complete sequ |
| 471G1 | 1 | 109 | Z56926 | 9.00E-54 | 1 | CpG island DNA genomic Mse1 fragment, clone 153c6, forw |
| 516D5 | 1 | 143 | Z62429 | 4.00E-53 | 1 | CpG island DNA genomic Mse1 fragment, clone 69a1, forwa |
| 107D11 | 81 | 292 | Z63603 | 1.00E-104 | 1 | CpG island DNA genomic Mse1 fragment, clone 87h3, forwa |
| 481D4 | 12379 | 12686 | Z69304 | 1.00E-101 | 1 | DNA sequence from cosmid V311G7, between markers DXS366 |
| 461G6 | 23967 | 24497 | Z69715 | 1.00E-173 | 2 | DNA sequence from clone LL22NC03-74G7 on chromosome 22 |
| 465F5 | 15468 | 15659 | Z77852 | 3.00E-70 | 1 | DNA sequence from cosmid LUCA2 on chromosome 3p21.3 con |
| 459B2 | 26193 | 26772 | Z82248 | 0 | 2 | DNA sequence from clone LL22NC03-44A4 on chromosome 22 |
| 478E5 | 49480 | 49615 | Z83847 | 6.00E-50 | 1 | DNA sequence from clone RP3-496C20 on chromosome 22 Con |
| 469E6 | 4705 | 5229 | Z83851 | 0 | 1 | DNA sequence from clone 989H11 on chromosome 22q13.1-13 |
| 517H5 | 128852 | 129155 | Z85986 | 1.00E-156 | 1 | DNA sequence from clone 108K11 on chromosome 6p21 Conta |
| 114C1 | 15995 | 16486 | Z93016 | 1.00E-121 | 3 | DNA sequence from clone RP1-211D12 on chromosome 20q12- |
| | 77940 | 78185 | Z93016 | | | |
| 118A8 | 117801 | 118272 | Z97989 | 0 | 2 | DNA sequence from PAC 66H14 on chromosome 6q21-22. Cont |
| | 132708 | 132773 | Z97989 | | | |

Table 3C: Table of novel human nucleotide sequences compared to assembled human sequences, depicting putative exon-intron structure

| Clone | Accession | Exon Clone Start | Exon Stop | Genome Start | Genome Stop | Exon Clone Start | Exon Stop | Genome Start | Genome Stop | Exon Clone Start | Exon Stop | Genome Start | Genome Stop | Exon Clone Start | Exon Stop | Genome Start | Genome Stop |
|-------------------------|-----------|------------------------|--------------|-----------------|----------------|------------------------|--------------|-----------------|----------------|------------------------|--------------|-----------------|----------------|------------------------|--------------|-----------------|----------------|
| 47D11 | NT_008060 | 90 | 407 | 480193 | 479876 | 406 | 586 | 478843 | 478662 | | | | | | | | |
| 53G7 | NT_008060 | 4 | 204 | 478642 | 478842 | 204 | 459 | 479917 | 480171 | | | | | | | | |
| 62C9 | NT_015169 | 29 | 224 | 220269 | 220464 | 321 | 384 | 220540 | 220603 | 449 | 518 | 220668 | 220737 | 517 | 774 | 220958 | 221215 |
| 62G9 | NT_006328 | 1 | 145 | 566357 | 566213 | 144 | 219 | 565724 | 565649 | 217 | 315 | 563987 | 563889 | 315 | 418 | 563775 | 563672 |
| 65B1 | NT_006098 | 243 | 454 | 2418134 | 2418345 | 303 | 462 | 2421648 | 2421807 | | | | | | | | |
| 65D10 | NT_025892 | 218 | 401 | 369301 | 369483 | 404 | 541 | 370290 | 370427 | | | | | | | | |
| 65D11 | NT_025892 | 98 | 241 | 367311 | 367453 | 240 | 425 | 369301 | 369486 | 423 | 562 | 370288 | 370427 | 561 | 690 | 376519 | 376648 |
| 65D12 | NT_025892 | 98 | 219 | 367333 | 367453 | 218 | 399 | 369301 | 369483 | 402 | 541 | 370290 | 370427 | | | | |
| 72D4 | NT_008060 | 1 | 198 | 478646 | 478843 | 197 | 489 | 479876 | 480168 | 491 | 585 | 489271 | 489365 | | | | |
| 73A7 | NT_008060 | 1 | 197 | 478646 | 478842 | 197 | 538 | 479917 | 480259 | | | | | | | | |
| 75B12 | NT_010265 | 1 | 171 | 309301 | 309471 | 169 | 267 | 315278 | 315376 | 264 | 441 | 316976 | 317153 | 440 | 588 | 317239 | 317387 |
| <i>cont'd NT_010265</i> | | | | | | | | | | | | | | | | | |
| 100B5 | NT_006098 | 16 | 142 | 556012 | 556138 | 143 | 336 | 560579 | 560772 | 331 | 416 | 561268 | 561353 | | | | |
| 105B11 | NT_022315 | 2 | 226 | 66662 | 66886 | 429 | 491 | 89124 | 89186 | | | | | | | | |
| 170F9 | NT_010194 | 4 | 324 | 6405068 | 6405386 | 323 | 465 | 6407864 | 6408006 | | | | | | | | |
| 144F5 | NT_011595 | 1 | 280 | 125097 | 124818 | 345 | 491 | 120524 | 120378 | 279 | 347 | 123833 | 123765 | 490 | 559 | 118816 | 118747 |
| 166H7 | NT_009729 | 59 | 130 | 537939 | 537868 | 127 | 281 | 537177 | 537023 | 282 | 362 | 529971 | 529891 | 363 | 581 | 495632 | 495414 |
| <i>cont'd NT_009729</i> | | | | | | | | | | | | | | | | | |
| 171A10 | NT_009151 | 2 | 244 | 6556227 | 6556469 | 245 | 396 | 6556693 | 6556846 | | | | | | | | |
| 98E1 | NT_008098 | 12 | 138 | 556012 | 556138 | 139 | 328 | 560579 | 560768 | 330 | 506 | 561271 | 561447 | | | | |
| 134B4 | NT_011512 | 3 | 251 | 12517461 | 12517709 | 252 | 338 | 12519831 | 12519967 | 336 | 448 | 12523936 | 12524048 | | | | |
| 172E5 | NT_009935 | 5 | 449 | 1427508 | 1427952 | 448 | 551 | 1434457 | 1434560 | | | | | | | | |
| 176F12 | NT_011520 | 48 | 309 | 6163505 | 6163766 | 308 | 409 | 6163866 | 6163967 | | | | | | | | |
| 51B9 | NT_021980 | 75 | 578 | 120596 | 121099 | 3 | 79 | 120203 | 120279 | | | | | | | | |
| 51B12 | NT_007140 | 1 | 85 | 309298 | 309214 | 79 | 609 | 300215 | 299684 | | | | | | | | |
| 191F6 | NT_010194 | 7 | 330 | 6405063 | 6405386 | 329 | 473 | 6407864 | 6408008 | | | | | | | | |
| 459F10 | NT_008982 | 1 | 121 | 92783 | 92903 | 116 | 314 | 93005 | 93202 | | | | | | | | |
| 461H12 | NT_023539 | 19 | 94 | 332693 | 332768 | 92 | 166 | 334220 | 334294 | 164 | 298 | 334438 | 334572 | 300 | 470 | 335340 | 335510 |
| 463C3 | NT_010478 | 1 | 186 | 1307774 | 1307960 | 183 | 314 | 1308993 | 1309124 | 315 | 429 | 1309210 | 1309324 | 427 | 559 | 1309492 | 1309625 |
| 465B3 | NT_010222 | 41 | 227 | 700806 | 700992 | 227 | 414 | 701556 | 701743 | | | | | | | | |
| 513G4 | NT_005130 | 1 | 134 | 384702 | 384569 | 133 | 204 | 383722 | 383651 | 202 | 281 | 378695 | 378616 | 287 | 346 | 299615 | 299556 |
| 515E10 | NT_023563 | 1 | 169 | 9743 | 9575 | 169 | 309 | 8111 | 7971 | | | | | | | | |
| 466B10 | NT_006292 | 1 | 331 | 936306 | 935977 | 244 | 745 | 935875 | 935374 | | | | | | | | |
| 466F9 | NT_024872 | 17 | 186 | 64694 | 64525 | 184 | 295 | 61751 | 61640 | 294 | 626 | 59515 | 59185 | | | | |
| 121B6 | NT_023169 | 2 | 98 | 183171 | 183075 | 258 | 455 | 164976 | 164779 | 460 | 576 | 163071 | 162955 | | | | |
| 462D1 | NT_023923 | 139 | 298 | 191231 | 191072 | 297 | 528 | 190168 | 189937 | | | | | | | | |
| 64G9 | NT_025892 | 68 | 210 | 367311 | 367453 | 209 | 394 | 369301 | 369486 | 392 | 531 | 370288 | 370427 | | | | |
| 467C6 | NT_010101 | 1 | 73 | 1265999 | 1266071 | 218 | 330 | 1295695 | 1295807 | 330 | 468 | 1315073 | 1315211 | 467 | 547 | 1315798 | 1315878 |
| <i>cont'd NT_010101</i> | | | | | | | | | | | | | | | | | |
| 467G9 | NT_011157 | 69 | 142 | 917117 | 917044 | 142 | 253 | 916090 | 915979 | | | | | | | | |
| 476G4 | NT_007592 | 58 | 121 | 2382380 | 2382443 | 120 | 362 | 2382598 | 2382840 | | | | | | | | |
| 477E1 | NT_008680 | 1 | 116 | 1185208 | 1185323 | 116 | 472 | 1186107 | 1186462 | | | | | | | | |
| 477A11 | NT_006292 | 1 | 325 | 936300 | 935977 | 238 | 851 | 935875 | 935262 | | | | | | | | |
| 480A3 | NT_010478 | 1 | 99 | 2220394 | 2220492 | 181 | 525 | 2221546 | 2221890 | | | | | | | | |
| 518H1 | NT_005337 | 1 | 73 | 2383056 | 2383128 | 125 | 229 | 2386650 | 2386754 | 227 | 366 | 2393104 | 2393243 | | | | |
| 519A9 | NT_016632 | 64 | 193 | 172305 | 172434 | 191 | 279 | 176990 | 177078 | | | | | | | | |
| 521F2 | NT_023563 | 3 | 107 | 7651 | 7756 | 110 | 254 | 7968 | 8111 | | | | | | | | |
| 597A4 | NT_023563 | 1 | 109 | 7647 | 7755 | 109 | 256 | 7964 | 8111 | 256 | 452 | 9575 | 9771 | | | | |
| 491G11 | NT_010265 | 1 | 127 | 284740 | 284866 | 123 | 242 | 288529 | 288648 | | | | | | | | |
| 494B11 | NT_007343 | 25 | 246 | 3168142 | 3167921 | 244 | 334 | 3162477 | 3162387 | | | | | | | | |
| 479A1 | NT_015169 | 1 | 109 | 293941 | 293833 | 112 | 217 | 289082 | 288977 | 218 | 338 | 285931 | 285811 | | | | |

Table 4: Patient groups and diagnostic gene sets.

Group A represents a patient group with a disease characteristic of interest. This characteristic either exists at the time of the leukocyte expression profile or develops subsequently as noted in the second column. Leukocyte expression profiles from patient in Group A are compared to those from patients in Group B (control subjects). Genes with expression characteristics in leukocytes that distinguish groups A and B form diagnostic gene sets for the condition.

| <u>Group A</u> | <u>Group A Event</u> | <u>Group B</u> | <u>Gene Set</u> |
|---|-----------------------|--|--|
| Atherosclerosis | At time of profile | No atherosclerosis | Diagnostic of disease |
| Restenosis | Subsequent to profile | No restenosis | Predictive of disease occurrence |
| Myocardial infarction | Subsequent to profile | No myocardial infarction | Predictive of disease complications |
| Death from congestive heart failure | Subsequent to profile | No death, congestive heart failure | Prognostic for known disease |
| Transplant allograft rejection | Subsequent to profile | Transplant allograft, no rejection | Risk stratification for disease |
| CHF responsive to beta blocker (improved ejection fraction) | Subsequent to profile | CHF unresponsive to beta blocker | Predictive of drug responsiveness |
| Improvement in angina after smoking cessation | At time of profile | No improvement in angina after smoking cessation | Assessment of efficacy of non-pharmacologic therapy |
| Improvement in angina after pro-angiogenic drug therapy | At time of profile | No improvement in angina after pro-angiogenic drug therapy | Assessment of efficacy of pharmacologic therapy |
| Positive results (atherosclerosis) at angiography | Subsequent to profile | Negative results (atherosclerosis) at angiography | Assessment of selection for further diagnostic testing |
| Active systemic lupus erythematosus (SLE) | At time of profile | Inactive SLE | Diagnosis of disease |

Table 4 (continued): Patient groups and diagnostic gene sets.

| <u>Group A</u> | <u>Group A</u> <u>Event</u> | <u>Group B</u> | <u>Gene Set</u> |
|---|--|--|---|
| Development of cardiac allograft vasculopathy | Subsequent to profile | No development of cardiac allograft vasculopathy | Predictive of disease |
| Patients at time of angioplasty | | Same patients presenting later with restenosis | Identification of pathway genes/targets |
| Endothelial Dysfunction | At time of profile | No endothelial dysfunction | Diagnosis, disease monitoring |
| Unstable angina | At time of profile | Atherosclerosis without unstable angina | Diagnosis of disease complication |

Table 5: Nucleotide sequence databases used for analysis

| Database | Version | <u>Description</u> | Location of file | Threshold of Significance Used |
|-----------------|----------------|--|--|---------------------------------------|
| nr | Release 123.0 | GenBank+EMBL+DDBJ+P DB sequences (but no EST, STS, GSS, or HTGS sequences). No longer "non-redundant". | ftp://ncbi.nlm.nih.gov/blast/nt.Z | Expect value (e) < 10 ⁻²⁵ |
| dbEST | 04/10/01 | Non-redundant Database of GenBank+EMBL+ DDBJ EST Division | ftp://ncbi.nlm.nih.gov/blast/est_human.Z | Expect value (e) < 10 ⁻²⁵ |
| UniGene_unique | Build 132 | One sequence selected from each UniGene cluster (the one with the longest region of high-quality sequence data). | ftp://ncbi.nlm.nih.gov/pub/shuler/unigene/Hs.seq.uniq.Z | Expect value (e) < 10 ⁻²⁵ |
| Human Genome | Build 22 | Sequence data of all contigs used to assemble the human genome | ftp://ncbi.nlm.nih.gov/genomes/H_sapiens/CHR_#/hs_chr#.fa.gz | Expect value (e) < 10 ⁻²⁵ |

Table 6: Algorithms used for exon and polypeptide prediction

| Algorithm | Description | Web address |
|------------------|---|---|
| Genscan | Predicts the locations and exon-intron structures of genes in genomic sequences. | http://genes.mit.edu/GENSCAN.html |
| Genomescan | Incorporates protein homology information when predicting genes. | http://genes.mit.edu/genomescan.html |
| GrailEXP | Predicts exons, genes, promoters, polyAs, CpG islands, EST similarities, and repetitive elements within a DNA sequence. | http://grail.lsd.ornl.gov/grailexp/ |
| G-Known | Predicts genes and features of a DNA sequence at user-specified levels of complexity. Can incorporate extra information supplied by user including gene predictions from other gene finding programs, EST hits, similarities to known proteins, synteny between corresponding genomic regions in related organisms, methylation of the bases, regulatory binding sites, and topology information. | http://www.cse.ucsc.edu/research/compbio/pgf/ |
| FGENES | Uses linear and hidden Markov models for exon prediction | http://genomic.sanger.ac.uk/gf/gf.shtml |

Table 7: Databases and algorithms used for Protein Analysis

| Algorithm | Description | Web address |
|--------------------------------------|--|---|
| BLASTP, version 2.0 | Identification of unknown protein or subunit based on similarity to known proteins or subunits. | http://www.ncbi.nlm.nih.gov/BLAST/ |
| BLASTX | Algorithm for translating a nucleotide query sequence and aligning the translation to sequences in protein databases | http://www.ncbi.nlm.nih.gov/BLAST/ |
| TBLASTN | Algorithm for aligning an unidentified peptide sequence to predicted translations of nucleotide sequences | http://www.ncbi.nlm.nih.gov/BLAST/ |
| SWISS-PROT, release 39.0 | Protein sequence database | http://www.expasy.ch/cgi-bin/sprot-search-de |
| Protein International Resource (PIR) | Protein sequence database | http://www-nbrf.georgetown.edu/pirwww/ |
| GenPept | Amino acid translations from GenBank/EMBL/DDBJ records that are annotated with one or more CDS features | ftp://ncbi.nlm.nih.gov/genbank/genpept.fsa.gz |
| TrEMBL | Contains the translations of all coding sequences present in the EMBL Nucleotide Sequence Database, which are not yet integrated into SWISS-PROT | http://www.ebi.ac.uk/swissprot/ |
| Prosite, release 16.39 | Database of protein families and domains. Consists of biologically significant sites, patterns and profiles. | http://www.expasy.ch/prosite/ |
| Pfam, version 6.2 | Collection of multiple sequence alignments and hidden Markov models covering many common protein domains | http://www.sanger.ac.uk/Software/Pfam/ |
| ProDom, version 2001.1 | Domain arrangements of proteins and protein families | http://protein.toulouse.inra.fr/prodom.html |
| TMpred | Prediction of transmembrane regions to aid in subcellular localization and function predictions | http://www.ch.embnet.org/software/TMPRED_form.html |

Table 8

| SEQ ID | Origin | Unigene | Locus | GI | Nominal Description | Strand | Probe Sequence |
|--------|--------------|-----------|-----------|----------|--|--------|--|
| 1 | cDNA T-cells | Hs.100001 | NM_005074 | 4827009 | solute carrier family 17 (sodium phosphate), member 1 (SLC17A1), EST380899 cDNA /gb=AW968823 | 1 | AGAGCACTTGCAGAGCCTGGGACAA CCTCCTTATTGAAGGGAAGAGGGAC |
| 2 | cDNA T-cells | Hs.104157 | AW968823 | 8158664 | direction unknown | 1 | TGGTCTCAAAGATTTCACATGGCAACA TTCGAAAGTCCCCAGAGAGTCCT |
| 3 | cDNA T-cells | Hs.104157 | AW968823 | 8158664 | Complement of EST380899 cDNA /gb=AW968823 direction unknown | -1 | AGGACTTCTCTGGGGACTTTCGAATG TTGCCATGTAAATCTTTGAGACCA |
| 4 | literature | Hs.1051 | NM_004131 | 7262379 | granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), | 1 | AGGTGCCAGCAACTGAATAAATACCT CTCCAGTGTAATCTGGAGCCAA |
| 5 | cDNA T-cells | Hs.105230 | AA489227 | 2218829 | aa57f07.s1 cDNA, 3' end /clone=IMAGE:825061 strand unknown | 1 | GGGTGTCTTTAAATAGCACTAGCCAA ATCATATCTCCAACACTCCTTA |
| 6 | cDNA T-cells | Hs.105230 | AA489227 | 2218829 | Complement, aa57f07.s1 cDNA, 3' end /clone=IMAGE:825061 strand unknown | -1 | TAAGGAGTGTGGAGATATGTGATTT GGCTAGTGCTATTTAAAGACACCC |
| 7 | cDNA T-cells | Hs.107979 | NM_014313 | 7657594 | small membrane protein 1 (SMP1), mRNA /cds=(99, | 1 | CCCACAGTGCAATTGAGATATGCTC AGGGAATGCCAGCCACCTTGTA |
| 8 | cDNA T-cells | Hs.10888 | AK025212 | 10437679 | cDNA: FLJ21559 fis, clone COL06406 /cds=UNKNOWN | 1 | GCCAAGACAATAAGCTAGGCTACTGG GTCCAGCTACTACTTTGGTGGAT |
| 9 | cDNA T-cells | Hs.10888 | AK025212 | 10437679 | complement cDNA: FLJ21559 fis, clone COL06406 /cds=UNKNOWN | -1 | ATCCCAACCAAGTAGTAGCTGGACCC AGTAGCCTAGCTTATTGTCTTGGC |
| 10 | cDNA T-cells | Hs.1100 | M55654 | 339491 | TATA-binding protein mRNA, complete cds /cds=(241,12 | 1 | AATTTATAACTCTAGGGGTTATTTCT GTGCCAGACACATTCCACCTCTC |
| 11 | cDNA T-cells | Hs.11000 | NM_015344 | 7662509 | MY47_BRAIN MY047 PROTEIN | 1 | ACTAATTGCATTGGCAGCATTTGTGTC TTTGACCTTGATACCTAGCTTTC |
| 12 | cDNA T-cells | Hs.1101 | NM_002698 | 4505958 | POU domain, class 2, transcription factor 2 (P | 1 | AAACCAAAATAATCACAACAGAAAC CAGCTGCCCAAGGAACAGAGG |
| 13 | cDNA T-cells | Hs.11238 | AB014522 | 3327057 | KIAA0622 protein; Drosophila "multiple asters" (Mast)-like homolog 1 | 1 | TCCCACCAGGACTTTGCTAACAATAA TGTTTGAAATAAAGAAAGTGCTCT |
| 14 | cDNA T-cells | Hs.116481 | NM_001792 | 4502682 | CD72, B cell differentiation antigen | 1 | TGACACTCATGCCAACAAGAACCTGT GCCCTCCTTCTAACCTGAGGGC |
| 15 | cDNA T-cells | Hs.295726 | M14648 | 340306 | cell adhesion protein (vitronectin) receptor alpha s Platelets, megakaryocytes | 1 | ACAAATTTTACCCTAACAGTTTACCA CCTAGCAACAGTCATTTCTGAAA |
| 16 | cDNA T-cells | Hs.119155 | AL109786 | 5725475 | mRNA full length insert cDNA clone EUROMAGE 81 | 1 | TTTATTGGTACTTCTTAAAGATAGAGA CTAAAGTCATGGTAGTATTGGCC |
| 17 | cDNA T-cells | Hs.119155 | AL109786 | 5725475 | Complement of mRNA full length insert cDNA clone EUROMAGE 82 | -1 | GGCCAATACTACCATGACTTTAGTCT CTATCTTTAGGAAGTACCAATAAA |
| 18 | cDNA T-cells | Hs.119537 | NM_006559 | 5730026 | GAP-associated tyrosine phosphoprotein p62 (Sam68) | 1 | CCTCCCATTTTGTCTCGGAAGATTA AATGCTACATGTGTAAGTCTGCCT |
| 19 | cDNA T-cells | Hs.121025 | NM_014205 | 7656935 | chromosome 11 open reading frame 5 (C11ORF5), m | 1 | CCGTGCCCGGAACAGGCCGTGGCT AGAGAAGAGCGAGATCATCTTTACC |
| 20 | literature | Hs.126256 | NM_000576 | 10835144 | interleukin 1-beta (IL1B) mRNA, monocytes, macrophages | 1 | GGTCTAATTATTCAAAGGGGGCAAG AAGTAGCAGTGTCTGTAAAGAGC |
| 21 | cDNA T-cells | Hs.126925 | AK023275 | 10435137 | FLJ13213 fis, clone NT2RP4001126, weakly | 1 | AGATGGGTGAATCAGTTGGGTTTGT AAATACCTGTATGTGGGGAAGACA |
| 22 | cDNA T-cells | Hs.1279 | AK024951 | 10437374 | FLJ21298 fis, clone COL02040, highly sim | 1 | TCTCTAGTTGTCACTTTCCTCTTCCAC TTTGATACCATTTGGGTCAATTGAA |
| 23 | cDNA T-cells | Hs.129780 | NM_003327 | 4507578 | OX40 homolog, ACT35 Antigen, TNF receptor superfamily, member 4 | 1 | TCAAAGAAAGCCTTCTGGATGCTGT TAAGATGTACCCCTTCAGGTGAACC |
| 24 | cDNA T-cells | Hs.1309 | M28825 | 180035 | thymocyte antigen CD1a mRNA | 1 | CCCCCTTTCCTTCTAATTTTTCAGCTC CTTCAATGCAAGTACATGTATT |
| 25 | cDNA T-cells | Hs.1349 | NM_000758 | 4503076 | colony stimulating factor 2 (granulocyte-macrophage) (CSF2), | 1 | CCTCCAACCCCGGAACTTCCTGTGC AACCAGACTATACCTTTGAAAG |
| 26 | cDNA T-cells | Hs.136375 | BF513274 | 11598453 | ESTs, Weakly similar to S65824 reverse transcriptase homolog (3' EST read) | 1 | GGAAGGTAGTCTTCATTGCAATCAG GAAAACGAACGTAAAGGCACAGGT |
| 27 | cDNA T-cells | Hs.136375 | BF513274 | 11598453 | Complement of ESTs, Weakly similar to S65824 reverse transcriptase homolog (3' EST read) | -1 | ACCTGTGCCTTTACGTTCTTTTCCT GATTGCAATGAAGACTACCTTCC |
| 28 | cDNA T-cells | Hs.137548 | NM_003874 | 4502686 | CD84 antigen (leukocyte antigen) (CD84) | 1 | TGTTTTCTCACTACATTGTACATGTG GGAATTACAGATAAACGGAAGCC |
| 29 | cDNA T-cells | Hs.1416 | M15059 | 182447 | Fc-epsilon receptor (IgE receptor) mRNA, complete cd | 1 | CAGAGCAAGACCCTGAAGACCCCA ACCACGGCCTAAAGCCCTTTGTG |
| 30 | cDNA T-cells | Hs.142023 | NM_005816 | 5032140 | TACT_T-CELL SURFACE PROTEIN | 1 | GCTTCATATGTATGGCTGTGCTTTG CTTCATGTGTATGGCTATTTGTAT |
| 31 | cDNA T-cells | Hs.1481 | NM_002112 | 4504364 | histidine decarboxylase (EC 4.1.1.22) (HDC), | 1 | CAGATGGGTTTCAGCAGCTGTGTCAGT GAGAAAGGGCCGAGGGTAGACAGG |
| 32 | cDNA T-cells | Hs.150403 | NM_000790 | 4503280 | dopa decarboxylase (aromatic L-amino acid decarboxylase) | 1 | TCCAGGGCAATCAATGTTACGCAAC TTGAAATTATATCTGTGGTCTTCA |
| 33 | cDNA T-cells | Hs.1513 | NM_000629 | 10835182 | interferon (alpha, beta and omega) receptor 1 (IFNAR1), | 1 | TCATCCCGAGAACATTGGCTCCACA TCACAGTATCTACCCCTTACATGGT |
| 34 | literature | Hs.153053 | NM_001774 | 4502662 | leukocyte antigen CD37 | 1 | CGCTCTCGATATTCCTGTGCAGAAAC CTGGACCACGTCTACAACCGGCTC |
| 35 | cDNA T-cells | Hs.153952 | X55740 | 23896 | placental cDNA coding for 5'nucleotidase (EC 3.1.3.5) | 1 | CCTGCTCAGCTCTGCATAAGTAATTC AAGAAATGGGAGGCTTCACCTTAA |

Table 8

| | | | | | | | |
|----|--------------|-----------|-----------|----------|---|----|------------------------------|
| 36 | cDNA T-cells | Hs.155595 | NM_004404 | 4758157 | Neural precursor cell expressed, developmentally down-regulated 5 | 1 | GGAGGACCCACACTGCTACACTTCTG |
| 37 | cDNA T-cells | Hs.1570 | Z34897 | 510295 | H1 histamine receptor | 1 | ATCCCTTTGGTTTTACTACCCAA |
| 38 | cDNA T-cells | Hs.159557 | AK024833 | 10437239 | FLJ21180 fis, clone CAS11176, highly sim | 1 | GAAGAACAGCAGATGGCGGTGATCA |
| 39 | cDNA T-cells | Hs.160417 | NM_013390 | 7019554 | transmembrane protein 2 (TMEM2), mRNA /cds=(14 | 1 | GCAGAGAGATTGAACCTTTGAGGAGG |
| 40 | cDNA T-cells | Hs.16488 | BC007911 | 14043948 | calreticulin | 1 | GGAATTTCTATCTTGCAGCATCCTG |
| 41 | cDNA T-cells | Hs.166120 | NM_004031 | 4809287 | interferon regulatory factor 7 (IRF7), trans | 1 | TAAATAAACATTCAGTCCACCCT |
| 42 | cDNA T-cells | Hs.166975 | NM_006925 | 5902077 | splicing factor, arginine/serine-rich 5 (SFR) | 1 | CCTCAAAGTGCTACCGATAAACCTTT |
| 43 | literature | Hs.167988 | S71824 | 632775 | N-CAM=145 kda neural cell adhesion molecule | 1 | CTAATTGTAAGTGCCCTTACTAAG |
| 44 | cDNA T-cells | Hs.168103 | AF026402 | 2655201 | U5 snRNP 100 kD protein mRNA, cds /cds=(39,2501 | 1 | AGTGGGTCCCAGATTGGCTCACACT |
| 45 | cDNA T-cells | Hs.168132 | U14407 | 540098 | interleukin 15 (IL15) mRNA | 1 | GAGAATGTAAGAACTACAAACAAAA |
| 46 | literature | Hs.168383 | NM_000201 | 4557877 | intercellular adhesion molecule 1 (CD54), rhinovirus receptor (ICAM1), | 1 | CTGTCCAGCGCCAACAGCCTCTATGA |
| 47 | cDNA T-cells | Hs.169191 | U58913 | 4204907 | chemokine (hmrp-2a) mRNA, complete cds /cds=(71,484) | 1 | CGACATCGAGTGCTTCTTATGGA |
| 48 | literature | Hs.169610 | AJ251595 | 6491738 | transmembrane glycoprotein (CD44 gene), | 1 | AAATTCTGGTAAAGTATGTGCTTTTCTG |
| 49 | cDNA T-cells | Hs.170311 | D89678 | 3218539 | 50 for A+U-rich element RNA binding factor, | 1 | TGGGGGTGGGATTTGGAAGGGGG |
| 50 | cDNA T-cells | Hs.170311 | D89678 | 3218539 | 60 for A+U-rich element RNA binding factor, | 1 | ATGGGTGAAGAGAACCGAGCAAAGA |
| 51 | cDNA T-cells | Hs.170311 | D89678 | 3218539 | 70 for A+U-rich element RNA binding factor, | 1 | TCAAAATAAAAGTGACACAGCAGC |
| 52 | cDNA T-cells | Hs.171763 | X59350 | 36090 | mRNA for B cell membrane protein CD22 | 1 | GCTGTGTCCATCTTTGTCACTGAGTG |
| 53 | cDNA T-cells | Hs.171917 | AB037855 | 7243265 | mRNA for KIAA1434 protein, partial cds | 1 | AAATCTCTGTTTTCTATTTCTCTGA |
| 54 | cDNA T-cells | Hs.172089 | AL110202 | 5817121 | cDNA DKFZp586l2022 (from clone DKFZp586l | 1 | ATGTGCTGTCAAAACAAGTTTTTCTGT |
| 55 | cDNA T-cells | Hs.172089 | AL110202 | 5817121 | Complement of cDNA DKFZp586l2022 (from clone DKFZp586l | -1 | CAAGAAGATGATCAGACCTTGGA |
| 56 | literature | Hs.1722 | M28983 | 186279 | 50 interleukin 1 alpha (IL 1) mRNA, macrophages | 1 | CAGTGATCAGGGTCTGCAAGCAGT |
| 57 | literature | Hs.1722 | M28983 | 186279 | 60 interleukin 1 alpha (IL 1) mRNA, macrophages | 1 | GGGGAAGGGGGCCAAGGTATTGGAG |
| 58 | literature | Hs.1722 | M28983 | 186279 | 70 interleukin 1 alpha (IL 1) mRNA, macrophages | 1 | TGGACACACGGATCAAGACCAGGAA |
| 59 | literature | Hs.1724 | X01057 | 33812 | 50 mRNA for interleukin-2 receptor | 1 | GAATTTGAATTTGTCAAGGTGAAGGG |
| 60 | literature | Hs.1724 | X01057 | 33812 | 60 mRNA for interleukin-2 receptor | 1 | AACAGACCCCTCTAGAAATTTTCA |
| 61 | literature | Hs.1724 | X01057 | 33812 | 70 mRNA for interleukin-2 receptor | 1 | GATGCTTCTGGGAGACACCAAAGG |
| 62 | cDNA T-cells | Hs.172631 | J04145 | 189068 | neutrophil adherence receptor alpha-M subunit mRNA | 1 | GTCAGTAGGTGCGGTGTCTAGGGTA |
| 63 | cDNA T-cells | Hs.305870 | NM_003761 | 14043025 | vesicle-associated membrane protein 8 (endob | 1 | GTGAATCCTGTAAGTTCAAATTTAT |
| 64 | cDNA T-cells | Hs.172791 | NM_004182 | 4759297 | ubiquitously-expressed transcript (UXT), mR | 1 | TTTAAAGTTGTGTGGTCAGTAGGTGCG |
| 65 | literature | Hs.173894 | NM_000757 | 4503074 | macrophage-specific colony-stimulating factor (CSF-1) | 1 | GTGTCTAGGGTAGTGAATCCTGTAAG |
| 66 | cDNA T-cells | Hs.174103 | NM_002209 | 4504756 | Integrin, alpha L (CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) | 1 | TTCAAATTTATGATTAGG |
| 67 | cDNA T-cells | Hs.174142 | X03663 | 29899 | c-fms proto-oncogene Monocytes | 1 | GTTTGAGATGGACACACTGGTGTGGA |
| 68 | cDNA T-cells | Hs.169610 | AA156937 | 1728552 | z19c02.s1 | 1 | TTAACCTGCCAGGGAGACAGAGCT |
| 69 | cDNA T-cells | Hs.17483 | NM_000616 | 10835166 | Soares_pregnant_uterus_NbHPU CD4 antigen (p55) (CD4), | 1 | TTGTGACTCTGAATCCCATGTTCTCA |
| 70 | cDNA T-cells | Hs.177559 | U05875 | 463549 | clone pSK1 interferon gamma receptor accessory factor | 1 | AACACTGCTGCCTTCCGAAGTCTG |

Table 8

| | | | | | | | |
|-----|--------------|-----------|-----------|----------|---|---|-----------------------------|
| 71 | cDNA T-cells | Hs.179526 | S73591 | 688296 | brain-expressed HHCPA78 homolog VDUP1 (Gene) | 1 | AAGATGCCCAACCTGTGATCAGAAC |
| 72 | cDNA T-cells | Hs.1799 | J04142 | 619799 | (lambda-gt11ht-5) MHC class I antigen-like gl | 1 | CTCCAAATACTGCCATGAGAAACT |
| 73 | cDNA T-cells | Hs.180804 | AK000271 | 7020240 | cDNA FLJ20264 fis, clone COLF7912 /cds=UNKNOWN | 1 | CAGGAGTTTGTGTGTCCTTTTATAAAA |
| 74 | cDNA T-cells | Hs.180866 | NM_000416 | 4557879 | interferon gamma receptor 1 (IFNGR1), | 1 | GTTTGCCCTGGATGTCATATTGG |
| 75 | cDNA T-cells | Hs.181165 | AK026650 | 10439548 | FLJ22997 fis, clone KAT11962, highly sim | 1 | CCCTGAGTGACAGTCACGACAGAAC |
| 76 | cDNA T-cells | Hs.181357 | NM_002295 | 9845501 | laminin receptor 1 (67kD, ribosomal protein SA | 1 | AAAACCAAGACCAGACCACATTT |
| 77 | cDNA T-cells | Hs.187660 | NM_014504 | 7657495 | Major histocompatibility complex, class I, E (HLA-E) | 1 | CCTTTACATCCAGTAGGTTACCACT |
| 78 | cDNA T-cells | Hs.182740 | NM_001015 | 14277698 | ribosomal protein S11 (RPS11), mRNA /cds=(15,4 | 1 | AACGGAACATATCCAGTACTCCTG |
| 79 | cDNA T-cells | Hs.187660 | NM_014504 | 7657495 | putative Rab5 GDP/GTP exchange factor homologue | 1 | TGCATCGTAAAGCTTCAGAAAGAAA |
| 80 | cDNA T-cells | Hs.197345 | NM_001469 | 4503840 | thyroid autoantigen 70kD (Ku antigen) (G22P1), | 1 | GGAGAAATGTTTTGTGGACCACTT |
| 81 | cDNA T-cells | Hs.198253 | M33906 | 184194 | MHC class II HLA-DQA1 mRNA, complete cds /cds=(43,810) | 1 | GGCCACTGAATGGGTAGGAGCAACC |
| 82 | cDNA T-cells | Hs.197345 | NM_001469 | 4503840 | thyroid autoantigen 70kD (Ku antigen) (G22P1), | 1 | ACTGACTGGTCTTAAGCTGTGCTTG |
| 83 | cDNA T-cells | Hs.198253 | M33906 | 184194 | MHC class II HLA-DQA1 mRNA, complete cds /cds=(43,810) | 1 | TGTAGGGTAAATGTGACTGGAATACA |
| 84 | cDNA T-cells | Hs.1987 | NM_006139 | 5453610 | CD28 antigen (Tp44) (CD28) | 1 | CCTTTGGAACGGAATTCCTTATCA |
| 85 | cDNA T-cells | Hs.336769 | NM_002074 | 11321584 | guanine nucleotide binding protein (G protein) | 1 | AGGCTGGACATCGGCCCGCTCCCCA |
| 86 | cDNA T-cells | Hs.211576 | L10717 | 307507 | T cell-specific tyrosine kinase mRNA, complete | 1 | CAATGAAATAAGTATTTTCTCAT |
| 87 | cDNA T-cells | Hs.336769 | NM_002074 | 11321584 | guanine nucleotide binding protein (G protein) | 1 | TGTAGGGTAAATGTGACTGGAATACA |
| 88 | cDNA T-cells | Hs.2186 | AF119850 | 7770136 | PRO1808 mRNA, complete cds /cds=(1221,2174) / | 1 | CCTTTGGAACGGAATTCCTTATCA |
| 89 | cDNA T-cells | Hs.21907 | NM_007067 | 5901961 | histone acetyltransferase (HBOA), mRNA /cds= | 1 | GTTGCCATGGTGTGTTGATGCCCTC |
| 90 | cDNA T-cells | Hs.2200 | NM_005041 | 4826941 | Perforin 1 (pore forming protein; PRF1) | 1 | CCACTTTGCTGTTCTTACTTTAC |
| 91 | cDNA T-cells | Hs.2233 | NM_000759 | 4503078 | granulocyte colony-stimulating factor 3 (G-CSF) | 1 | CCACCCACCCCTCAATTAAGGCAACA |
| 92 | cDNA T-cells | Hs.2236 | Z29067 | 479172 | NEK3_SERINE/THREONINE-PROTEIN KINASE NEK3 | 1 | ATGAAGTTAATGGATACCCTCTGC |
| 93 | cDNA T-cells | Hs.233936 | NM_006471 | 5453739 | myosin, light polypeptide, regulatory, non-s | 1 | GTTGCCATGGTGTGTTGATGCCCTC |
| 94 | cDNA T-cells | Hs.236449 | NM_024898 | 13376352 | cDNA: FLJ22757 fis, clone KAIA0803 /cds=(92,24 | 1 | CCACTTTGCTGTTCTTACTTTAC |
| 95 | cDNA T-cells | Hs.238648 | NM_003999 | 4557039 | oncostatin-M specific receptor beta subunit (OSMRB) | 1 | CCACCCACCCCTCAATTAAGGCAACA |
| 96 | cDNA T-cells | Hs.238707 | NM_024901 | 13376358 | cDNA: FLJ22457 fis, clone HRC09925 /cds=(56,14 | 1 | ATGAAGTTAATGGATACCCTCTGC |
| 97 | cDNA T-cells | Hs.239138 | NM_005746 | 5031976 | pre-B-cell colony-enhancing factor (PBEF), m | 1 | GCTCACCTATTTGGGTTAAGCATGCC |
| 98 | cDNA T-cells | Hs.239189 | NM_014905 | 7662327 | glutaminase (GLS), | 1 | AATTTAAAGAGACCAAGTGATGT |
| 99 | cDNA T-cells | Hs.241392 | NM_002985 | 4506846 | small inducible cytokine A5 (RANTES) (SCYA5), | 1 | TCCACCTTTTGATTTAATTTTAAAGT |
| 100 | cDNA T-cells | Hs.241567 | NM_016838 | 8400721 | RNA binding motif, single stranded interacting | 1 | CAGTGTACTGCAAGGAAGCTGGA |
| 101 | cDNA T-cells | Hs.241570 | NM_000594 | 10835154 | Tumor necrosis factor (TNF superfamily, member 2 | 1 | CCCTATCCCGCAAAATGGGCTTCCTG |
| 102 | cDNA T-cells | Hs.247885 | NM_022304 | 13435404 | Histamine receptor H2 (HRH2) | 1 | CCTGGGTTTTTCTCTTCTCACAT |
| 103 | cDNA T-cells | Hs.248156 | NM_020530 | 10092620 | oncostatin M (OSM), | 1 | TCCACCTTTTGATTTAATTTTAAAGT |
| 104 | cDNA T-cells | Hs.298469 | NM_000789 | 4503272 | dipeptidyl carboxypeptidase 1 (angiotensin I converting enzyme) (ACE) | 1 | CAGTGTACTGCAAGGAAGCTGGA |
| 105 | cDNA T-cells | Hs.336780 | NM_006088 | 5174734 | tubulin, beta, 2 (TUBB2), mRNA | 1 | AGATCTTCAAGTGAACATCTCTTGCC |
| 106 | cDNA T-cells | Hs.252723 | NM_000981 | 4506808 | ribosomal protein L19 (RPL19), mRNA /cds=(28,6 | 1 | ATCACCTAGCTGCCAGCTGCTTGCC |
| 107 | cDNA T-cells | NA | X53795 | 35832 | R2 mRNA for an inducible membrane protein /cds=(156,95 | 1 | GCTAATTTTAAAGCATGTTCAAGT |
| 108 | literature | Hs.25648 | NM_001250 | 4507580 | Tumor necrosis factor receptor superfamily, member 5 | 1 | ATGACCTCAAGATTTTAAAGGAGA |
| 109 | cDNA T-cells | Hs.258503 | AF160973 | 5616319 | P53 inducible protein | 1 | TGTCTGGCAGGGAAGTGAACCTG |

Table 8

| | | | | | | | |
|-----|--------------|-----------|-----------|----------|--|----|--|
| 110 | cDNA T-cells | Hs.265829 | NM_002204 | 4504746 | integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), | 1 | GGCTGTGTCTTAAGGCCCATTTGAGA AGCTGAGGCTAGTTCAAAAACCT |
| 111 | cDNA T-cells | Hs.271387 | Y16645 | 2916795 | for monocyte chemotactic protein-2 /cds= | 1 | GTGCTCCTGTAAGTCAAATGTGTGCT TTGTAAGTCTGTTGTTGAAATTGA |
| 112 | cDNA T-cells | Hs.272493 | NM_004167 | 14602450 | small inducible cytokine subfamily A (Cys-Cys | 1 | CAGAGACATAAAGAGAAGATGCCAAG GCCCCCTCCTCCACCCACCGCTAA |
| 113 | cDNA T-cells | Hs.176663 | NM_000570 | 10835138 | Fc fragment of IgG, low affinity IIb, receptor for (CD16) (FCGR3B), | 1 | ATGGGAGTAATAAGACAGTGGGAG CAGCATCTCTGAACATTTCTCTGGA |
| 114 | literature | Hs.278443 | NM_004001 | 4557021 | Fc fragment of IgG, low affinity IIb, receptor for (CD32) (FCGR2B), | 1 | CCACTAATCCTGATGAGGCTGACAAA GTTGGGGCTGAGAACACAATCACC |
| 115 | cDNA T-cells | Hs.62954 | J04755 | 182512 | ferritin H processed pseudogene, complete cds /cds=UN | 1 | TGTTGGGGTTTCTTTACCTTTTCTAT AAGTTGTACCAAAACATCCACTT |
| 116 | cDNA T-cells | Hs.279581 | AK000575 | 7020763 | FLJ20568 fis, clone REC00775 /cds=(6,422) | 1 | CAGAGTAGGCATCTGGGCACCAAGA CCTTCCTCAACAGAGGACACTGAG |
| 117 | cDNA T-cells | Hs.279930 | V00522 | 32122 | encoding major histocompatibility complex gene | 1 | CTTTGCGCTAAACCTATGGCCTCCTG TGCATCTGTACTCACCTGTACCA |
| 118 | cDNA T-cells | Hs.181357 | NM_002295 | 9845501 | Laminin receptor 1 (67kD, ribosomal protein SA) | 1 | GGCCACTGAATGGGTAGGAGCAACC ACTGACTGGTCTTAAGCTGTTCTTG |
| 119 | cDNA T-cells | Hs.283722 | NM_020151 | 9910251 | GTT1 protein (GTT1), mRNA /cds=(553,1440) /gb | 1 | TGATTCTGCACTTGGGGTCTGTCTGT ACAGTTACTCATGTCAATTGTAATG |
| 120 | cDNA T-cells | Hs.78961 | NM_014110 | 13699255 | PRO2047 protein (PRO2047), mRNA /cds=(798,968) | 1 | TGTGTAATAGGCCTTTTCATGCTTTAT GTGTAGCTTTTACCTGTAACCT |
| 121 | cDNA T-cells | Hs.334853 | NM_006013 | 5174430 | cDNA DKFZp762B195 (from clone DKFZp762B195) | 1 | AAGTTATCATGTCCATCCGACCAAG CTGCAGAACAAAGGAGCATGTGATT |
| 122 | cDNA T-cells | Hs.334853 | NM_006013 | 5174430 | Complement cDNA DKFZp762B195 (from clone DKFZp762B195) | -1 | AAGTTATCATGTCCATCCGACCAAG CTGCAGAACAAAGGAGCATGTGATT |
| 123 | cDNA T-cells | Hs.284283 | U90552 | 2062705 | butyrophilin (BTF5) mRNA, complete cds /cds=(359,190) | 1 | TGGTGGATGTTAAACCAATATTCCTTT CAACTGCTGCCTGCTAGGGAAAA |
| 124 | cDNA T-cells | Hs.286212 | AK021791 | 10433048 | cDNA FLJ11729 fis, clone HEMBA1005394, modera | 1 | TGAAGTTGCTGAATGTAAGGACAGGCT ACTATGCGTTATAATCTAATCACA |
| 125 | cDNA T-cells | Hs.287369 | NM_020525 | 10092624 | 50 interleukin 22 (IL22), mRNA /cds=(71,610) /gb | 1 | ATTTGACCAGAGCAAAGCTGAAAAAT GAATAACTAACCCCTTTCCCTGC |
| 126 | cDNA T-cells | Hs.287369 | NM_020525 | 10092624 | 60 interleukin 22 (IL22), mRNA /cds=(71,610) /gb | 1 | GCAATTGGAGAACTGGATTGCTGTT TATGTTCTCTGAGAAATGCCTGATT GACCAGAG |
| 127 | cDNA T-cells | Hs.287369 | NM_020525 | 10092624 | 70 interleukin 22 (IL22), mRNA /cds=(71,610) /gb | 1 | TTTGACCAGAGCAAAGCTGAAAAATG AATAACTAACCCCTTTCCCTGCTAG AATAACAATTAGATGCC |
| 128 | cDNA T-cells | Hs.288061 | NM_001101 | 5016088 | actin, beta (ACTB), | 1 | CCCTTTTTGTCCCCCACTTGAGATG TATGAAGGCTTTTGGTCTCCCTGG |
| 129 | cDNA T-cells | Hs.315054 | NM_032921 | 14249707 | hypothetical protein MGC15875 (MGC15875), | 1 | ATTAGACCAGACCAAGTGATTTCTAA AGAAAATCCTGACATGCACACCCA |
| 130 | cDNA T-cells | Hs.289088 | NM_005348 | 13129149 | heat shock 90kD protein 1, alpha (HSPCA), | 1 | GACCCACTGCTGATGATACCAAGTGC TGCTGTAAGTGAAGAAATGCCACC |
| 131 | cDNA T-cells | Hs.29052 | AK000196 | 7020122 | FLJ20189 fis, clone COLF0657 /cds=(122,84) | 1 | ACAGGCAAAGTGACAGGGGAAAAGG AATTAGTCTAAGAGTAAGGGGATGA |
| 132 | cDNA T-cells | Hs.291129 | AA837754 | 2912953 | oe10d02.s1 cDNA /clone=IMAGE:1385475 /gb=AA | 1 | CTTTCCTCTTGCTGCTGGGGCCTAGG TCTTCTTGCTGCTGCTTCTTTTC |
| 133 | cDNA T-cells | Hs.292590 | D59502 | 960608 | HUM041H11A cDNA, 3' end /clone=GEN-041H11 /cl | 1 | AGAGTTTTTGTGGTAGACTGGAGCT GGGATGTTGAATCAACCTCAGGCA |
| 134 | cDNA T-cells | Hs.292590 | D59502 | 960608 | Complement HUM041H11A cDNA, 3' end /clone=GEN-041H11 /cl | -1 | TGCCCTGAGGTTGATTCAACATCCCAG CTCCAGTCTACCAACAAAACTCT |
| 135 | cDNA T-cells | Hs.99858 | X61923 | 36646 | Ribosomal protein L7a Gene with exons /introns | 1 | CTGACGATCAGCTTGGAAACAGCCAAA CAGAATAACGCAACTAATTAACCT |
| 136 | cDNA T-cells | Hs.323463 | AL050141 | 4884352 | cDNA DKFZp586O031 (from clone DKFZp586O0) | 1 | TCCTTTTATGCATTGGAGGAAAAACA TGTTGGCTTTTCTTTCAGCTGGG |
| 137 | cDNA T-cells | Hs.323463 | AL050141 | 4884352 | Complement cDNA DKFZp586O031 (from clone DKFZp586O1 | -1 | CCCACGTCAAGAGAAAAGCCCAATG TTTTTCTCCAATGCATAAAAGGA |
| 138 | cDNA T-cells | Hs.323822 | AB046771 | 10047166 | for KIAA1551 protein, partial cds /cds=(0) | 1 | CTCAGGAAACCCGACAGAAAGAACAT GTAACACAGAACTCAGTCCACTA |
| 139 | cDNA T-cells | NA | AF347015 | 13273284 | Mitochondrial DNA, chyochrome B gene | 1 | ACTCGAGACGTAATAATTATGGCTGAAT CATCCGCTACCTTCACGCCAATGG |
| 140 | cDNA T-cells | Hs.30035 | U61267 | 1418285 | putative splice factor transformer2-beta mRN | 1 | TGCTGTTTTCATTTCTGCATTTGTGTAG TTTGGTCTTTTGTGTTTCAAGTTAA |
| 141 | cDNA T-cells | Hs.30909 | NM_019081 | 11464998 | KIAA0430 gene product (KIAA0430), mRNA /cds=(| 1 | AAAAATGACAAAAGTTATCACCACAAA CCCCCTTTCCCATCTTGCACTGTT |
| 142 | cDNA T-cells | Hs.3195 | NM_002995 | 4506852 | sapiens small inducible cytokine subfamily C, member 1 (lymphotactin) (SCYC1), | 1 | AGCTTTTAACTGCTCCAAATGCTGACC CATGCAATATTTCTCATGTGATC |
| 143 | cDNA T-cells | Hs.322645 | AL050376 | 4914609 | mRNA; cDNA DKFZp586J101 (from clone DKFZp586J1 | 1 | AAAAGAAATGCAGGTTTATTATCCAG CACTGAGAGAGTTAACAGGAGCTG |
| 144 | cDNA T-cells | Hs.324481 | AL050376 | 4914609 | Complement mRNA; cDNA DKFZp586J101 (from clone DKFZp586J2 | -1 | AGAGAGACTTCTCATTGGCTGTGAAG GTAGAGCTTTTGGGGAAATTCCTG |
| 145 | cDNA T-cells | Hs.324481 | AW968541 | 8158382 | Complement EST380617 cDNA /gb=AW968541 unknown coding strand | -1 | CAGGAATTTCCCAAAAGCTCTACCT TCACAGCCAATGAGAAGTCTCTCT |
| 146 | cDNA T-cells | Hs.324481 | AW968541 | 8158382 | EST380617 cDNA /gb=AW968541 unknown coding strand | 1 | AGAGAGACTTCTCATTGGCTGTGAAG GTAGAGCTTTTGGGGAAATTCCTG |

Table 8

| | | | | | | | |
|-----|--------------|-----------|-----------|----------|--|---|----------------------------|
| 147 | cDNA T-cells | Hs.327 | NM_001558 | 4504632 | interleukin-10 receptor mRNA, complete IL10RA | 1 | CATCTCAGCCCTGCCTTTCTCTGGAG |
| 148 | cDNA T-cells | Hs.32970 | NM_003037 | 4506968 | signaling lymphocytic activation molecule (S | 1 | TCATGATAACCTGCAGACCTGATCAA |
| 149 | literature | Hs.334687 | NM_000569 | 12056966 | Fc fragment of IgG, low affinity IIIa, receptor for (CD16) (FCGR3A) | 1 | ATGGGGGTAATAAGACAGTAGCAG |
| 150 | cDNA T-cells | Hs.303649 | M26683 | 184641 | interferon gamma treatment inducible mRNA Monocytes | 1 | GAAATTGCTTTTCTCTTTGAACCACA |
| 151 | cDNA T-cells | Hs.105938 | X53961 | 34415 | lactoferrin /cds=(294,2429) Neutrophils | 1 | GTTCTACCCCTGGGATGTTTTGAG |
| 152 | cDNA T-cells | Hs.36 | D12614 | 219911 | lymphotoxin (TNF-beta), complete cds T-cells, B-cells | 1 | AATTCCTCAGGAAGTAAACCCGAAGA |
| 153 | cDNA T-cells | Hs.278670 | AB034205 | 6899845 | Acid-inducible phosphoprotein | 1 | AGATGGCCAGCTCCCCAAGAAAG |
| 154 | cDNA T-cells | Hs.3886 | NM_002267 | 4504898 | karyopherin alpha 3 (importin alpha 4) (KPNA3) | 1 | AACATCCAAGGAGAAACAGAGACAG |
| 155 | cDNA T-cells | Hs.394 | NM_001124 | 4501944 | adrenomedullin (ADM), | 1 | GCCCAAGAGATGAAGAGTGAGAGGG |
| 156 | literature | Hs.40034 | NM_000885 | 6006032 | integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) (ITGA4) | 1 | TCGTGTGAATCAGACTAAGTGGGATT |
| 157 | cDNA T-cells | Hs.41724 | NM_002190 | 4504650 | interleukin 17 (cytotoxic T-lymphocyte-associated serine esterase 8) | 1 | TCATTTTACAACCTGCTCTACT |
| 158 | cDNA T-cells | Hs.44163 | NM_018838 | 10092656 | 13kDa differentiation-associated protein (L | 1 | GCATATACAGTTGGAAGACTAAAGA |
| 159 | cDNA T-cells | Hs.44926 | X60708 | 35335 | pchDP7 mRNA for liver dipeptidyl peptidase IV /cds=(75 | 1 | GGTGCAATGTGATCTGAGCTGAA |
| 160 | literature | Hs.46 | D10202 | 219975 | for platelet-activating factor receptor, | 1 | TGAGTGTGTTTGTGTGATGAAAGAG |
| 161 | cDNA T-cells | Hs.48433 | NM_014345 | 7657183 | endocrine regulator (HRIHFB2436), mRNA /cds= | 1 | AAAGACTGATTACCTCCTGTGTGG |
| 162 | cDNA T-cells | Hs.50002 | AB000887 | 2189952 | for EB11-ligand chemokine, complete cds | 1 | AGCTGTTCCCAAATTTCTAACGAGT |
| 163 | cDNA T-cells | Hs.50404 | U86358 | 2388626 | chemokine (TECK) mRNA, complete cds /cds=(0,452) /gb | 1 | GGACATTATCACTTTAAAGCCCT |
| 164 | cDNA T-cells | Hs.50964 | NM_001712 | 4502404 | carcinoembryonic antigen-related cell adhesion molecule 1 (CEACAM1) | 1 | ATCAACAGACCAACATTTTCTCTTCC |
| 165 | cDNA T-cells | Hs.301921 | NM_001295 | 4502630 | chemokine (C-C motif) receptor 1 (CCR1), | 1 | TCAAGCAACACTCTAGGCGCTG |
| 166 | cDNA T-cells | Hs.54457 | NM_004356 | 4757943 | CD81 antigen (target of antiproliferative antibody 1) | 1 | TATGACTGATGATCCTCCAAACAAA |
| 167 | cDNA T-cells | Hs.54460 | U46573 | 1280140 | eotaxin precursor mRNA, complete cds /cds=(53,346) / | 1 | AACCACTTACTGCTCGTAAATTC |
| 168 | cDNA T-cells | Hs.54609 | NM_014291 | 7657117 | glycine C-acetyltransferase (2-amino-3-keto | 1 | AAAATACTGATGTTCTAGTGAAAGA |
| 169 | cDNA T-cells | Hs.55921 | NM_004446 | 4758293 | glutamyl-prolyl-tRNA synthetase (EPRS), mRN | 1 | GGCAGCTTGAACCTGAGATGTGAA |
| 170 | cDNA T-cells | Hs.57987 | NM_022898 | 12597634 | B-cell lymphoma/leukaemia 11B (BCL11B), mRNA | 1 | GGAAGACTTTAAACCACTAGTTCTC |
| 171 | cDNA T-cells | Hs.59403 | NM_004863 | 4758667 | serine palmitoyltransferase, long chain base subunit 2 (SPTLC2) | 1 | CCACTGGGGCATCGGTCTAAAGCT |
| 172 | cDNA T-cells | Hs.5985 | NM_020240 | 9910377 | non-kinase Cdc42 effector protein SPEC2 (LOC56990), | 1 | CCCTGTTCCACAAACCATATGTATC |
| 173 | cDNA T-cells | Hs.6179 | BG929114 | 14323637 | Does not hit the NM_ numbers two splice variants. Direction unknown | 1 | CTTTCTCAACCTCCTCTTTCCC |
| 174 | cDNA T-cells | Hs.62192 | J02931 | 339501 | placental tissue factor (two forms) mRNA, complete cd | 1 | GTGTGTGAGTGTGAGTGTGAGCGAG |
| 175 | cDNA T-cells | Hs.62192 | NM_001993 | 10518499 | coagulation factor III (thromboplastin, tissue factor)(F3), mRNA. | 1 | AGGGTGAGTGTGGTCAGAGTAAAGC |
| 176 | literature | Hs.624 | NM_000584 | 10834977 | interleukin 8 (IL8), | 1 | TCTGGTCATTCAAGGATCCCTCCCA |
| 177 | literature | Hs.62954 | NM_002032 | 4503794 | 50 ferritin, heavy polypeptide 1 (FTH1), mRNA /c | 1 | AGGCTATGCTTTTCTATAACTTTT |
| 178 | literature | Hs.62954 | NM_002032 | 4503794 | 60 ferritin, heavy polypeptide 1 (FTH1), mRNA /c | 1 | GGCAGCTCAGGACCACTCCAATGAC |
| 179 | literature | Hs.62954 | NM_002032 | 4503794 | 70 ferritin, heavy polypeptide 1 (FTH1), mRNA /c | 1 | CCACCTAACAGATGAATGAAGTTA |
| 180 | literature | Hs.652 | NM_000074 | 4557432 | tumor necrosis factor (ligand) superfamily, member 5, TNFSF5 | 1 | TGTTCTTCATCTAAGCCTTCTGGTTT |
| 181 | cDNA T-cells | Hs.66053 | AB051540 | 12698050 | mRNA for KIAA1753 protein, partial cds /cds=(0 | 1 | ATGGGTCAGAGTTCGACTGCCA |
| 182 | cDNA T-cells | Hs.66151 | AL157438 | 7018513 | mRNA; cDNA DKFZp434A115 (from clone DKFZp434A1 | 1 | GCCTTCATGCACCTGTCTTTTAAC |
| 183 | cDNA T-cells | Hs.6975 | NM_014086 | 7662589 | PRO1073 protein (PRO1073), | 1 | ACCGCTCGACCTGTGCTGTAATCACA |
| 184 | cDNA T-cells | Hs.70186 | NM_003169 | 4507312 | suppressor of Ty (S.cerevisiae) 5 homolog (SUP | 1 | CTTCCTGTACCTCCTCCCAAGAGT |

Table 8

| | | | | | | | |
|-----|--------------|----------|-----------|----------|---|----|---|
| 185 | cDNA T-cells | Hs.70258 | N21089 | 1126259 | IMAGE:265324 Foreskin 3' read 2.0 kb | 1 | AACCTGCACAAGCATGTAATAAAAGA GCACACTTAAAAACATTCTGACCA |
| 186 | cDNA T-cells | Hs.70258 | N21089 | 1126259 | Complement IMAGE:265324 Foreskin 3' read 2.0 kb | -1 | TGGTCAGAATGTTTTAAGTGTTGCTC TTTTATTACATGCTTGTGCAGGTT |
| 187 | cDNA T-cells | Hs.70258 | AA743863 | 2783214 | IMAGE:1308639 5' read, perfect hit. | 1 | CCTTCTGAAGGTGTATAGATACAGCT TGTCTTGAATGTCTTTCTCCACA |
| 188 | cDNA T-cells | Hs.70258 | AA743863 | 2783214 | Complement IMAGE:1308639 5' read, perfect hit. | -1 | TGTGGAGAAAGACATTTCAAGACAAG CTGTATCTATACACCTTCAGAAGG |
| 189 | cDNA T-cells | Hs.72918 | NM_002981 | 4506832 | small inducible cytokine A1 (I-309, homologous to mouse Tca-3) (SCYA1) | 1 | TGCTAGGTACACAGAGGATCTGCTTGG TCTTGATAAGCTATGTTGTTGCAC |
| 190 | cDNA T-cells | Hs.73165 | U64198 | 1685027 | IL-12 receptor beta2 mRNA, complete cds /cds=(640,322 | 1 | CTAGAGGACCATTTCATGCAATGACTA TTTCTAAAGCACTGCTACACAGC |
| 191 | cDNA T-cells | Hs.737 | NM_004907 | 4758313 | immediate early protein (ETR101), mRNA /cds=(| 1 | GGGAGTTTCTGAGGGTCTGCTTTGTT TACCTTTCTGCGGTTGGATTCTTT |
| 192 | cDNA T-cells | Hs.73742 | NM_001002 | 4506666 | ribosomal protein, large, P0 (RPLP0), | 1 | TCGGAGGAGTCGGACGAGGATATGG GATTTGGTCTCTTTGACTAATCACC |
| 193 | cDNA T-cells | Hs.73792 | J03565 | 181919 | Epstein-Barr virus complement receptor type II (cr2) | 1 | TTCTTCTCCTCGGTGGTGTAAATCATTT CGTTTTTACCTTTACCTTCGGA |
| 194 | cDNA T-cells | Hs.73798 | NM_002415 | 4505184 | macrophage migration inhibitory factor (MIF) | 1 | GTCTACATCAACTATTACGACATGAA CGCGGCCAATGTGGGCTGGAACAA |
| 195 | cDNA T-cells | Hs.738 | NM_003973 | 4506600 | ribosomal protein L14 (RPL14), mRNA /cds=(17,6 | 1 | CAGAAGGGTCAAAAAGCTCCAGCCC AGAAAGCACCTGCTCCAAGGCATC |
| 196 | cDNA T-cells | Hs.73800 | NM_003005 | 6031196 | selectin P (granule membrane protein 140kD, antigen CD62) (SELP) | 1 | GACCTTCTGCCACCAGTCACTGTCC CTCAAAATGACCCAAAGACCAATAT |
| 197 | cDNA T-cells | Hs.73817 | D90144 | 219905 | LD78 alpha precursor, complete cds /c | 1 | GAGATGGGAGGGCTACCACAGAGT TATCCACTTTACAACGGAGACACAG |
| 198 | cDNA T-cells | Hs.73818 | NM_006004 | 5174744 | ubiquinol-cytochrome c reductase hinge prote | 1 | ATGGGTTTGGCTTGAGGCTGGTAGCT TCTATGTAATTGCAATGATTTCCA |
| 199 | cDNA T-cells | Hs.73839 | NM_002935 | 4506550 | ribonuclease, RNase A family, 3 (eosinophil cationic protein) (RNASE3) | 1 | CATCCCTCCATGTACTCTGGGTATCA GCAACTGTCTCATCAGTCTCCAT |
| 200 | cDNA T-cells | Hs.73917 | M13982 | 186334 | interleukin 4 (IL-4) mRNA | 1 | ACCTTACAGGAGATCATCAAACTTT GAACAGCCTCACAGAGCAGAAGAC |
| 201 | cDNA T-cells | Hs.74011 | NM_002286 | 11693297 | lymphocyte-activation gene 3 (LAG3), | 1 | GAGAAGACAGTGGCGACCAAGACGA TTTTCTGCCTTAGAGCAAGGGATT |
| 202 | cDNA T-cells | Hs.74085 | X54870 | 35062 | NKG2-D gene /cds=(338,988) /gb=X54870 /gi=3 | 1 | CAGGGGATCAGTGAAGGAAGAGAAG GCCAGCAGATCAGTGAGAGTGCAAC |
| 203 | cDNA T-cells | Hs.74335 | NM_007355 | 6680306 | heat shock 90kD protein 1, beta (HSPCB), mRNA / | 1 | CCCATTCCTCTCTACTCTTGACAGC AGGATTGGATGTTGTGTATTGTGG |
| 204 | cDNA T-cells | Hs.74621 | NM_000311 | 4506112 | prion protein (p27-30) (Creutzfeld- Jakob dis | 1 | ACTTAATATGTGGGAAACCCCTTTTGC GTGGTCTTAGGCTTACAACTGTGC |
| 205 | cDNA T-cells | Hs.75249 | D31885 | 505097 | ADP-ribosylation factor-like 6 interacting protein | 1 | AAAATACAAGGGCTGTTGGTGAGAGC AGACTTGAGGTGATGATAGTTGGC |
| 206 | cDNA T-cells | Hs.75348 | NM_006263 | 5453989 | proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) (PSME1), | 1 | CCAGATTTTCCCAAACTTGCTTCTG TTGAGATTTTTCCCTCACCTTGCC |
| 207 | cDNA T-cells | Hs.75545 | X52425 | 33833 | interleukin 4 receptor | 1 | ACCTTGGGTTGAGTAATGCTCGTCTG TGTGTTTTAGTTTCATCAGCTGTT |
| 208 | cDNA T-cells | Hs.75596 | NM_000878 | 4504664 | interleukin 2 receptor, beta (IL2RB), | 1 | AAACTCCCTTTCTTGAGGTTGTCTG AGTCTTGGGTCTATGCCTTGA AAA |
| 209 | literature | Hs.75613 | M24795 | 178670 | CD36 antigen mRNA | 1 | CTCAGTGTGGTGTGGTGATGTTGT TGCTTTTATGATTTCATATTGTGC |
| 210 | cDNA T-cells | Hs.75678 | NM_006732 | 5803016 | FBJ murine osteosarcoma viral oncogene homolo | 1 | CTGTATCTTTGACAATTCTGGGTGCG AGTGTGAGAGTGTGAGCAGGGCTT |
| 211 | cDNA T-cells | Hs.75703 | J04130 | 178017 | 50 activation (Act-2) mRNA, complete cds /cds=(108,386) | 1 | GATAAGTGTCTCTATGGGAGTGGTCCA CTGTCACTGTTTCTCTGCTGTTGC |
| 212 | cDNA T-cells | Hs.75703 | J04130 | 178017 | 60 activation (Act-2) mRNA, complete cds /cds=(108,386) | 1 | TTTAGCCAAAGGATAAGTGTCTATG GGGATGGTCCACTGTCACTGTTTCTC |
| 213 | cDNA T-cells | Hs.75703 | J04130 | 178017 | 70 activation (Act-2) mRNA, complete cds /cds=(108,386) | 1 | TGCTGTTG |
| 214 | cDNA T-cells | Hs.75968 | NM_021109 | 11056060 | thymosin, beta 4, X chromosome (TMSB4X), mRNA | 1 | ATTTATATTAGTTTAGCCAAAGGATAA GTGTCCTATGGGGATGGTCCACTGTG |
| 215 | cDNA T-cells | Hs.76506 | NM_002298 | 7382490 | lymphocyte cytosolic protein 1 (L- plastin) (L | 1 | ACTGTTTCTCTGCTGT |
| 216 | cDNA T-cells | Hs.76640 | NM_014059 | 7662650 | RG32 protein (RGC32), mRNA /cds=(146,499) /g | 1 | GAAGGAAGAAGTGGGGTGAAGAAG TGGGGTGGGACGACAGTGAATCTA |
| 217 | cDNA T-cells | Hs.76753 | NM_000118 | 4557554 | endoglin (Osler-Rendu-Weber syndrome 1) (ENG), | 1 | CCATCAATGAGGTATCTTCTTAGTG GTGGTATGTAATGGAACCTAGCCA |
| 218 | cDNA T-cells | Hs.77039 | NM_001006 | 4506722 | ribosomal protein S3A (RPS3A), mRNA /cds=(36,8 | 1 | AAAGACGTGCACTCAACCTTCTACCA GGCCACTCTCAGGCTCACTTAAAC |
| 219 | literature | Hs.77318 | L13385 | 349823 | Miller-Dieker lissencephaly protein (LIS1) | 1 | CCAAGCTGCTTGTCTGGGCTGCC CCTGTGTATTACCACCAATAAATC |
| 220 | cDNA T-cells | Hs.77424 | X14356 | 31331 | high affinity Fc receptor (FcRI) /cds=(36,116 | 1 | CACTGGGACGAGACAGGTGCTAAA GTTGAACGAGCTGATGGATATGAAC |
| 221 | cDNA T-cells | Hs.77502 | BC001854 | 12804818 | , methionine adenosyltransferase II, alpha, c | 1 | CGTTGCTGAAGTGGTAATTGAGGAAA ACAGTTCCCCAGATTGTTAAGAGT |

Table 8

| | | | | | | | |
|-----|--------------|-----------|-----------|----------|--|---|-----------------------------|
| 222 | cDNA T-cells | Hs.77729 | NM_002543 | 4505500 | oxidised low density lipoprotein (lectin-like | 1 | AGAACAACTAAGCCAGGTATGCAAA |
| 223 | cDNA T-cells | Hs.77729 | AB010710 | 2828355 | lectin-like oxidized LDL receptor | 1 | TATCGCTGAATAGAAACAGATGGA |
| 224 | cDNA T-cells | Hs.78146 | M28526 | 189775 | platelet endothelial cell adhesion molecule (PECAM-1) | 1 | AGAACAACTAAGCCAGGTATGCAAA |
| 225 | cDNA T-cells | Hs.78225 | NM_000700 | 4502100 | annexin A1 (ANXA1), mRNA | 1 | TATCGCTGAATAGAAACAGATGGA |
| 226 | literature | Hs.785 | NM_000419 | 6006009 | integrin, alpha 2b (platelet glycoprotein IIb | 1 | GCAATTTCTCCAGGCTAAGCTGCCGGT |
| 227 | cDNA T-cells | Hs.78713 | NM_002635 | 4505774 | solute carrier family 25 (mitochondrial carri | 1 | TCTTAAATCCATCCTGCTCAAGTTA |
| 228 | cDNA T-cells | Hs.78864 | M31932 | 182473 | IgG low affinity Fc fragment receptor (FcRlla) mRNA, c | 1 | TCCTGGTGGCTCTTTGTGGAGGAAAC |
| 229 | cDNA T-cells | Hs.789 | X54489 | 34625 | melanoma growth stimulatory activity (MGSA) | 1 | TAAACATTCCCTTGATGGTCTCAA |
| 230 | literature | Hs.78996 | BC000491 | 12653440 | proliferating cell nuclear antigen | 1 | CTTTGGGTTGGAGCTGTTCCATTGGG |
| 231 | cDNA T-cells | Hs.79008 | NM_012245 | 6912675 | SKI-INTERACTING PROTEIN (SNW1), mRNA /cds=(2 | 1 | TCCTCTTGGTGTCTGTTCCCTCCC |
| 232 | cDNA T-cells | Hs.79022 | U10550 | 762886 | Gem GTPase (gem) mRNA, complete cds /cds=(213,1103) / | 1 | AGAAAAAGCTTGGGTTAACTCAGTAG |
| 233 | cDNA T-cells | Hs.79110 | NM_005381 | 4885510 | nucleolin (NCL), | 1 | TTAGATCAAAGCAAATGTGGACTG |
| 234 | cDNA T-cells | Hs.79197 | NM_004233 | 4757945 | CD83 antigen (activated B lymphocytes, immuno | 1 | ACAGATGTAGCAACATGAGAAACGCT |
| 235 | cDNA T-cells | Hs.79630 | S75217 | 241773 | mb-1=IgM-alpha | 1 | TATGTTACAGGTTACATGAGAGCA |
| 236 | cDNA T-cells | Hs.80358 | NM_004653 | 4759149 | SMC (mouse) homolog, Y chromosome (SMCY), mRNA | 1 | TGTTTAATGGTAGTTTACAGTGTTTC |
| 237 | cDNA T-cells | Hs.80420 | U84487 | 1888522 | CX3C chemokine precursor, mRNA, alternatively splice | 1 | TGGCTTAGAACAAAGGGGCTTAA |
| 238 | cDNA T-cells | Hs.80617 | NM_001020 | 14591912 | ribosomal protein S16 (RPS16), mRNA /cds=(37,4 | 1 | TGCCAGCATATACTGAAGTCTTTTCT |
| 239 | cDNA T-cells | Hs.80642 | L78440 | 1479978 | STAT4 mRNA, complete cds /cds=(81,2327) /gb=L | 1 | GTCACCAAATTTGACCTCTAAGT |
| 240 | cDNA T-cells | Hs.81226 | X60992 | 29817 | CD6 mRNA for T cell glycoprotein CD6 /cds=(120,152 | 1 | GCTGCATATGAGTAAAGTTACCCCAA |
| 241 | cDNA T-cells | Hs.8128 | NM_014338 | 13489111 | phosphatidylserine decarboxylase (PISD), | 1 | CCACAGTGAGGAGGAAGATGTTCA |
| 242 | cDNA T-cells | Hs.81564 | NM_002619 | 4505732 | platelet factor 4 (PF4), mRNA. | 1 | AAACCTCCAGTACTTTGGTTGACCCT |
| 243 | cDNA T-cells | Hs.81665 | X06182 | 34084 | c-kit proto-oncogene mRNA /cds=(21,2951) /gb=X06182 | 1 | TGTATGTCACAGCTCTGCTCTATT |
| 244 | cDNA T-cells | Hs.82132 | NM_002460 | 4505286 | 50 interferon regulatory factor 4 (IRF4), mRNA / | 1 | ACCTGATCAATGACAGAGCCTCTCTGA |
| 245 | cDNA T-cells | Hs.82132 | NM_002460 | 4505286 | 60 interferon regulatory factor 4 (IRF4), mRNA / | 1 | GGACATTCCAAGACAGTATACAGT |
| 246 | cDNA T-cells | Hs.82132 | NM_002460 | 4505286 | 70 interferon regulatory factor 4 (IRF4), mRNA / | 1 | GCCCTTCCCTTCTTGGTTTCCAAAGG |
| 247 | literature | Hs.82359 | X63717 | 28741 | APO-1 cell surface antigen /cds=(220,122 | 1 | CATTATTTGCTGAGTTATATGTTTC |
| 248 | literature | Hs.82401 | NM_001781 | 4502680 | CD69 antigen (p60, early T-cell) Activated B & T cells. | 1 | CTGATTGTAGCAGCCTCGTTAGTGTC |
| 249 | cDNA T-cells | Hs.279841 | NM_006296 | 5454163 | vaccinia related kinase 2 (VRK2), mRNA /cds=(1 | 1 | ACCCCTCCTCCTCGTATCTGTCAG |
| 250 | cDNA T-cells | Hs.82829 | M25393 | 190740 | protein tyrosine phosphatase (PTPase) mRNA, complete | 1 | ACCAAAAAGAAATAGGGAAAAACAAGA |
| 251 | literature | Hs.82848 | NM_000655 | 5713320 | selectin L (lymphocyte adhesion molecule 1) (| 1 | ATTTCACTACTACCTGTGGTCT |
| 252 | cDNA T-cells | Hs.83077 | D49950 | 1405318 | for interferon-gamma inducing activated macrophages | 1 | GACTTTTCCAACCTCATCAACACG |
| 253 | cDNA T-cells | Hs.83086 | L38935 | 1008845 | GT212 mRNA /cds=UNKNOWN /gb=L38935 /gi=100884 | 1 | TCTGTGCCATTTTGTATTTTACTA |
| 254 | cDNA T-cells | Hs.83583 | NM_005731 | 5031598 | actin related protein 2/3 complex, subunit 2 (| 1 | GCTCGCTACAGAAATCCTACCGATA |
| 255 | cDNA T-cells | Hs.83731 | NM_001772 | 4502654 | CD33 antigen (gp67) (CD33), mRNA. | 1 | AGCCCATCGTGACTCAAACTCAC |
| 256 | cDNA T-cells | Hs.838 | NM_005191 | 4885122 | CD80 antigen (CD28 antigen ligand 1, B7-1 antig | 1 | ACCTGAGTCCCAACAACATTTGAACT |
| 257 | literature | Hs.83968 | NM_000211 | 4557885 | integrin, beta 2 (antigen CD18 (p95), macrophage antigen 1 (mac-1) | 1 | GCAATGAAGTCTCCTTATTCTGCT |
| 258 | literature | Hs.84 | D11086 | 303611 | interleukin 2 receptor gamma chain | 1 | AATTGATGAGGATGCTCCTGGGAGG |
| 259 | cDNA T-cells | Hs.845 | U31120 | 1045451 | interleukin-13 (IL-13) precursor gene, activated T cells | 1 | GATGCGTGACTATGTGGTGTCAC |
| 260 | cDNA T-cells | Hs.85258 | M12824 | 339426 | T-cell differentiation antigen Leu-2/T8 mRNA | 1 | TGAAATATGGGAAAGTTGCTGCTATT |

Table 8

| | | | | | | | |
|-----|--------------|-----------|-----------|----------|---|----|-----------------------------|
| 261 | cDNA T-cells | Hs.85266 | X51841 | 33910 | mRNA for integrin beta(4)subunit | 1 | CAGCGGAACCCCTTAGCACCCACATG |
| 262 | literature | Hs.856 | NM_000619 | 10835170 | interferon, gamma (IFNG), mRNA T-cells, NK cells | 1 | GACCAACAGTTCCTCCAACTTGAC |
| 263 | cDNA T-cells | Hs.87149 | M35999 | 183532 | platelet glycoprotein IIIa (GPIIIa) mRNA, complete c | 1 | ATGCCCTGGTGCTTCCAAATATTGTG |
| 264 | cDNA T-cells | Hs.87409 | X14787 | 37464 | thrombospondin /cds=(111,3623) /gb=X14787 | 1 | ACAACCTGTGACTGTACCCAAATGG |
| 265 | cDNA T-cells | Hs.88474 | M59979 | 189886 | prostaglandin endoperoxide synthase | 1 | CCTCTCTCCAAACCCGTTTTCCAACA |
| 266 | cDNA T-cells | Hs.88820 | NM_016649 | 7705402 | HDCMC28P protein (HDCMC28P), | 1 | TTTGTTAATAGTTACGTCTCTCCT |
| 267 | cDNA T-cells | NA | AQ336195 | 4143104 | cDNA clone IMAGE:4143104 blood 3' read | 1 | TCATTTGTTGTGTGACTGAGTAAAGA |
| 268 | literature | Hs.89137 | X13916 | 34338 | LDL-receptor related protein | 1 | ATTTTTGGATCAAGCGGAAAGAGT |
| 269 | cDNA T-cells | Hs.89414 | AF147204 | 6002763 | chemokine receptor CXCR4-Lo (CXCR4) mRNA, alt | 1 | TGAGGATGTAGAGAGAACAGGTGGG |
| 270 | cDNA T-cells | Hs.89476 | M16336 | 180093 | T-cell surface antigen CD2 (T11) mRNA, complete cds, c | 1 | CTGTATTCACGCCATTGGTTGGAAG |
| 271 | cDNA T-cells | Hs.89575 | M89957 | 179311 | immunoglobulin superfamily member B cell receptor co | 1 | GAAATTAATGGGTCCAGGTCTTAA |
| 272 | literature | Hs.89679 | NM_000586 | 10835148 | 50 interleukin 2 (IL2), | 1 | AGAAAGTGCAGAAGAGATGGTCAA |
| 273 | literature | Hs.89679 | NM_000586 | 10835148 | 60 interleukin 2 (IL2), | 1 | AACCACTATCATCTACGGCAACAACT |
| 274 | literature | Hs.89679 | NM_000586 | 10835148 | 70 interleukin 2 (IL2), | 1 | TGCAAAAGCTGTCCACACCATTTT |
| 275 | cDNA T-cells | Hs.89751 | NM_021950 | 11386186 | CD20 antigen | 1 | CCCGTTTTGGGGACGTGAACGTTTTA |
| 276 | cDNA T-cells | Hs.89887 | D38081 | 533325 | thromboxane A2 receptor | 1 | ATAATTTTTGCTGAATCTTTTACA |
| 277 | cDNA T-cells | Hs.93304 | U24577 | 1314245 | LDL-phospholipase A2 mRNA, complete cds /cds=(216,15 | 1 | TCAGTTTTCAGGAGTGGGTTGATTTC |
| 278 | cDNA T-cells | Hs.93649 | NM_003367 | 4507846 | upstream transcription factor 2, c-fos intera | 1 | AGCACCTACAGTGTACAGTCTTGT |
| 279 | literature | Hs.93913 | X04430 | 32673 | IFN-beta 2a mRNA for interferon-beta-2, T-cells, macrophages | 1 | AGCCTATCTGCTTAAGAGACTCTGGA |
| 280 | cDNA T-cells | Hs.960 | NM_000590 | 10834979 | interleukin 9 (IL9), | 1 | GTTTCTATGTGCCCTGGTGACACA |
| 281 | cDNA T-cells | Hs.96023 | M28170 | 862622 | cell surface protein CD19 (CD19) gene, Most B cells | 1 | GAGTAGAAGGACACAGGGCAGCAA |
| 282 | cDNA T-cells | Hs.96487 | BF222826 | 11130003 | ESTs, Highly similar to S08228 ribosomal protein S2, cytosolic | 1 | CTTGAGAGGAGTGAATGTGAAACG |
| 283 | cDNA T-cells | Hs.9663 | NM_013374 | 7019486 | programmed cell death 6-interacting protein (PDCD6IP), | 1 | TGAACCTCCAACAGGGAAGGCTGT |
| 284 | cDNA T-cells | Hs.96731 | AB014555 | 3327123 | mRNA for KIAA1375 protein, partial cds /cds=(0 | 1 | CCAGAAAGGATTGAATGTGAAACG |
| 285 | literature | Hs.99863 | NM_001972 | 4503548 | elastase 2, neutrophil (ELA2), | 1 | TGAAGGAGATGATGAGAATCTTATTC |
| 286 | cDNA T-cells | Hs.99899 | NM_001252 | 4507604 | tumor necrosis factor (ligand) superfamily, member 7 (TNFSF7) | 1 | CAGGGACCAACATTAACACAACCA |
| 287 | literature | Hs.169476 | NM_002046 | 7669491 | 50 Glyceraldehyde-3-phosphate dehydrogenase | 1 | CTCTCTGGAGGTACTGAGACAGGGT |
| 288 | literature | Hs.169476 | NM_002046 | 7669491 | 60 Glyceraldehyde-3-phosphate dehydrogenase | 1 | GCTGATGGGAAGGAGGGGAGCCTTT |
| 289 | literature | Hs.169476 | NM_002046 | 7669491 | 70 Glyceraldehyde-3-phosphate dehydrogenase | 1 | CTCTTCGGCAAATGTAGCATGGGCAC |
| 290 | literature | Hs.169476 | NM_002046 | 7669491 | 50 Complement Glyceraldehyde-3-phosphate dehydrogenase | -1 | CTCAGATTGTTGTTGTTAATGGGC |
| 291 | literature | Hs.169476 | NM_002046 | 7669491 | 60 Complement Glyceraldehyde-3-phosphate dehydrogenase | -1 | TTCCAGAAAGAAAAGATGAGAGGGAT |
| 292 | literature | Hs.169476 | NM_002046 | 7669491 | 70 Complement Glyceraldehyde-3-phosphate dehydrogenase | -1 | GAGAGGCAAGATGAGAGATGAAA |
| 293 | literature | Hs.182937 | NM_021130 | 10863926 | 50 peptidylprolyl isomerase A (cyclophilin A), clone | 1 | GGCCAGCCTGGACCCAATCATGAGG |
| 294 | literature | Hs.182937 | NM_021130 | 10863926 | 60 peptidylprolyl isomerase A (cyclophilin A), clone | 1 | AAGATGCAGACTCTTATGAGAACAT |
| 295 | literature | Hs.182937 | NM_021130 | 10863926 | 70 peptidylprolyl isomerase A (cyclophilin A), clone | 1 | AATGTTTGGCCAGAAATAAAGAAAATA |
| 296 | literature | Hs.182937 | NM_021130 | 10863926 | 50 complement peptidylprolyl isomerase A (cyclophilin A), clone | -1 | AGCTTTGCACACACTCTCAATTCT |

Table 8

| | | | | | | | |
|-----|------------|-----------|-----------|----------|--|----|---|
| 297 | literature | Hs.182937 | NM_021130 | 10863926 | 60 complement peptidylprolyl isomerase A (cyclophilin A), clone | -1 | TATTTTCATAATCATAAACTTAACTCTG CAATCCAGCTAGGCATGGGAGGGAA CAAGGAAA |
| 298 | literature | Hs.182937 | NM_021130 | 10863926 | 70 complement peptidylprolyl isomerase A (cyclophilin A), clone | -1 | TTATTTTCATAATCATAAACTTAACTCT GCAATCCAGCTAGGCATGGGAGGGGA ACAAGGAAAAACATGGAAC |
| 299 | literature | Hs.288883 | NM_005877 | 5032086 | mRNA for splicing factor (SF3A1) (120kD) | 1 | GTCATCCACCTGGCCCTCAAGGAGA GAGGCGGGAGGAAGAAGTAGACAAG |
| 300 | literature | Hs.12084 | NM_003321 | 4507732 | Tu translation elongation factor, mitochondrial (TUFM) | 1 | TGACTGAGGAGGAGAAGAATATCAAA TGGGGTTGAGTGTGCAGATCTCTG |
| 301 | literature | Hs.75887 | NM_004371 | 6996002 | coatamer protein complex, subunit alpha (COPA) | 1 | TGGTTTTCAAAAATGCACACTGCGGG TTATTGATTTGTTCTTTACAACATA |
| 302 | literature | Hs.182278 | NM_001743 | 4502548 | calmodulin 2 (phosphorylase kinase, delta) (CALM2), | 1 | ACTGTGCAGCATGTTGTTGTTGAAGTG TGGAGTTGTAACCTGCGTGGACT |
| 303 | literature | Hs.2795 | NM_005566 | 5031856 | mRNA for lactate dehydrogenase-A (LDH-A, EC 1.1.1.27) | 1 | TGAGTCACATCCTGGGATCCAGTGTA TAAATCCAATATCATGCTTGTGTC |
| 304 | literature | Hs.1708 | NM_005998 | 5174726 | chaperonin containing TCP1, subunit 3 (gamma) (CCT3), | 1 | GTTCTGCTACTGCGAATTGATGACAT CGTTTCAGGCCACAAAAAGAAAGG |
| 305 | literature | Hs.75428 | NM_000454 | 4507148 | superoxide dismutase (SOD-1) mRNA, complete cds | 1 | ACATTCCCTTGGATGTAGTCTGAGGC CCCTTAACATCATCTGTTATCCTGC |
| 306 | literature | Hs.2271 | NM_001955 | 4503460 | Arabidopsis endothelein-1 (EDN1) | 1 | ACTGGCTTCCATCAGTGGTAACTGCT TTGGTCTCTCTTTCATCTGGGGA |
| 307 | literature | NA | X56062 | 16206 | Arabidopsis CAB photosystem 1 chlorophyll a/b-binding protein (500 bp) | 1 | CCATTGGAGAAGCTTGGCACTCACTT GGCGGATCCATGGCACACAACAT |
| 308 | literature | NA | X14212 | 16470 | Arabidopsis RCA RUBISCO activase (513) | 1 | TTTTCTCCTTTGTGTAATTGTGGATTG GATCTTGTCTCTTTTGTCTCCCT |
| 309 | literature | NA | U91966 | 1928871 | Arabidopsis RBCL ribulose-1,5-biophosphate carboxylase/oxygenase large subunit | 1 | TATTCTTTCGTGTGAGGGCTTGAACC AAGTATCCCCGCTTCTTCTACCCC |
| 310 | literature | NA | AF159801 | 8571922 | Arabidopsis lipid transfer protein 4 (527) | 1 | CATCAAGTGAAGTGGGGAATAACGAC ATCATTTGCGCTGAAGAGTATGGTT |
| 311 | literature | NA | AF159803 | 8571926 | Arabidopsis lipid transfer protein 6 (477) | 1 | AATGAGGGCATTTGGTTTGTAGTTGC TAATTGATCAGTGATGTATTGTCA |
| 312 | literature | NA | AF191028 | 6708182 | Arabidopsis papain-type cysteine endopeptidase (507) | 1 | TGGAATCAACAAGATGGCTTCTTTCC CCACCAAAACATAAGTGATCATCAG |
| 313 | literature | NA | AF168390 | 6137137 | Arabidopsis root cap 1 (533) | 1 | TGGACCGTATGAATGAATGTACACG CCATAAACGCCCTTTGTTCGAAGCA |
| 314 | literature | NA | AF198054 | 6649235 | Arabidopsis NAC1 (457) | 1 | CCTCACTCTTGTACCCACGGTAGATT CATGTAAATACCACTTATGACGC |
| 315 | literature | NA | AF247559 | 7839390 | Arabidopsis triosphosphate isomerase (498) | 1 | GGTTAGCGACCTTGTGTTGTTGTTG TGTTCTTACATCTTCTTCTTGAAC |
| 316 | literature | NA | X58149 | 16440 | Arabidopsis PRKase gene for ribulose-5-phosphate kinase (497) | 1 | GGCGAAAAGGACGGTCTTGTCTGTTT GTAATTTGTGTGGAGATAAAAAAGA |
| 317 | literature | Hs.288061 | NM_001101 | 5016088 | actin, beta (ACTB), | 1 | CCCTTTTGTCTCCCACTTGAGATG TATGAAGGCTTTTGGTCTCCCTGG |
| 318 | literature | Hs.77356 | XM_002788 | 4507456 | 50 Transferrin receptor | 1 | TGAAATATCAGACTAGTGACAAGCTC CTGGTCTTGAGATGCTTCTCTGCTT |
| 319 | literature | Hs.77356 | XM_002788 | 4507456 | 60 Transferrin receptor | 1 | GGTTGAGTTACTTCTATCAAGCCAG TACCGTGCTAACAGGCTCAATATTCC |
| 320 | literature | Hs.77356 | XM_002788 | 4507456 | 70 Transferrin receptor | 1 | TGAATGAA GTTGAGTTACTTCTATCAAGCCAGT ACCGTGCTAACAGGCTCAATATTCTT |
| 321 | literature | Hs.77356 | XM_002788 | 4507456 | 50 Complement Transferrin receptor | -1 | GAATGAAATATCAGACTA AACGAGAAGACATCTCAAGACCAGGA GCTTGTCACTAGTCTGATATTTC |
| 322 | literature | Hs.77356 | XM_002788 | 4507456 | 60 Complement Transferrin receptor | -1 | TTCAATCAGGAATATTGAGCCTGTTA GCACGGTACTGGCTTGATAGGAAGTA ACTCAACC |
| 323 | literature | Hs.77356 | XM_002788 | 4507456 | 70 Complement Transferrin receptor | -1 | TAGTCTGATATTTCAATCAGGAATATT GAGCCTGTTAGCACGGTACTGGCTT GATAGGAAGTAACTCAAC |
| 324 | Tabel 3A | NA | | 36E9 | | 1 | TTTCAAGACAGAAAAGTGACGCAGAGA ACCTCCCCGGCCAGTCTCGACGC |
| 325 | Tabel 3A | NA | | 36E9 | | -1 | GCGTCGAGACTGGGCGGGGAGGTT CTCTGCGTCACTTTCTGTCTTGAA |
| 326 | Tabel 3A | NA | | 47D11 | | 1 | CCTAGACACCTGCATCAGTCAAGGTC ATGGATATTGGGAAGACAGACAGC |
| 327 | Tabel 3A | NA | | 47D11 | | -1 | GCTGTCTGTCTTCCCAATATCCATGA CCTTGACTGATGCAGGTGTCTAGG |
| 328 | Tabel 3A | NA | | 53G7 | | 1 | AAATAAGAAGAGGAAAGAGAGAGGC CTGCCCTAACCCACTGTTGTGCTGA |
| 329 | Tabel 3A | NA | | 53G7 | | -1 | TCAGACAACAGTGGGTTAGGGCAG GCCTCTCTCTTCTCTTCTTATTT |
| 330 | Tabel 3A | NA | | 62C9 | | 1 | CTCATGCTGCAAGTGTCTCATGTT GCCCCCTTGGAACTACTTGTTC |
| 331 | Tabel 3A | NA | | 62C9 | | -1 | TTGAACAAGTAATTCCAAGGGGGCAA CATGAGCAGCACTGCAGGCATGAG |
| 332 | Tabel 3A | NA | | 62G9 | | 1 | CCAATTTCTATAATTATTGAACAGCTT TTCGTGGGGCCAGCACAAAGTCT |

Table 8

| | | | | | |
|-----|----------|----|--------|----|--|
| 333 | Tabel 3A | NA | 62G9 | -1 | AGACTTTGTGCTGGCCCCACGAAAAG CTGTTCAATAATTATAGAAATTGG |
| 334 | Tabel 3A | NA | 65B1 | 1 | TGGCTACAAATAGAGTAGAGAACAGA CTCCAGTCTCTCAAAGACTTTTCAGT |
| 335 | Tabel 3A | NA | 65B1 | -1 | ACTGAAAGTCTTTGAGGACTGGAGTC TGTTCTCTACTCTATTTGTAGCCA |
| 336 | Tabel 3A | NA | 65D10 | 1 | AGTTAAGATGGAAGAATATAGAGACC TTCTGAAGAGCACTGTAGCTTGGA |
| 337 | Tabel 3A | NA | 65D10 | -1 | TCCAAGCTACAGTGCTCTTCAGAAGG TCTCTATATCTTCCATCTTAAC |
| 338 | Tabel 3A | NA | 100D7 | 1 | CACCTCTATGGCATGTGGAAGCAGGT CTGAGCAGTGTGCATAGAAGAAAA |
| 339 | Tabel 3A | NA | 100D7 | -1 | TTTTCTTCTATGCACACTGCTCAGAC CTGCTTCCACATGCCATAGGAGTG |
| 340 | Tabel 3A | NA | 107H8 | 1 | GCTCTCCGTTGACAATGGCCAAAGAA TAGAAGCTCTAGACCTTCCTTATT |
| 341 | Tabel 3A | NA | 107H8 | -1 | AATAAGGAAGGTCTAGAGCTTCTATT CTTTGGCCATTGTCAACGGAGAGC |
| 342 | Tabel 3A | NA | 129F10 | 1 | GGCAAAACGCACCTGGCACAACAGA ACGAATAATACAGAAGCTGGATGAC |
| 343 | Tabel 3A | NA | 129F10 | -1 | GTCATCCAGCTTCTGTATTATTCGTTG TGTTGTGCCAGGTGCGTTTTGCCC |
| 344 | Tabel 3A | NA | 137B5 | 1 | TAGCCATTCTTCTGATTGTGCCCTA GTATATCCAGACAGTTTGTCTTCT |
| 345 | Tabel 3A | NA | 137B5 | -1 | AGAAACAACTGTCTGGGATATACTA GGCACAATCAGGAAGAAATGGCTA |
| 346 | Tabel 3A | NA | 139G6 | 1 | GGTTGGAATGGTGATCGGGATGCAG TGAGATACTCTTGTGAGAGGGCAAA |
| 347 | Tabel 3A | NA | 139G6 | -1 | TTTGCCCTCTCACAAGAGTATCTCAC TGCACTCCCGATCACCATTCCAACC |
| 348 | Tabel 3A | NA | 142E4 | 1 | GCCATGAGATTCAACAGTCAACATCA GTCTGATAAGCTACCCGACAAAAGT |
| 349 | Tabel 3A | NA | 142E4 | -1 | ACTTTGTGCGGTAGCTTATCAGACTG ATGTTGACTGTTGAATCTCATGGC |
| 350 | Tabel 3A | NA | 142E9 | 1 | AAGAGGACAAGTTTGAGAGGCAACA CTTAAACACTAGGGCTACTGTGGCA |
| 351 | Tabel 3A | NA | 142E9 | -1 | TGCCACAGTAGCCCTAGTGTTTAAGT GTTGCCTCTCAAACCTTGCCTCTT |
| 352 | Tabel 3A | NA | 142F9 | 1 | ATTGCTTTAAATTGAGTTTCCTTGCC ATTGCACACTCCTATCTTTCTGA |
| 353 | Tabel 3A | NA | 142F9 | -1 | TCAGAAAGATAGGAGTGTGCAATGGC AAGGAAACTCAATTTAAAGCAAAT |
| 354 | Tabel 3A | NA | 331A3 | 1 | AAAAGTCACTACCAGGCTGGCAGGG AATGGGGCAATCTATTCATACTGAT |
| 355 | Tabel 3A | NA | 331A3 | -1 | ATCAGTATGAATAGATTGCCCATTC CCTGCCAGCCTGGTAGTGACTTTT |
| 356 | Tabel 3A | NA | 138G5 | 1 | ATATTGATTTGGATACGGTGAATAAG CTGGACAAGATGTTGAGGAGAGGG |
| 357 | Tabel 3A | NA | 138G5 | -1 | CCCTCTCCTCAACATCTTGTCCAGCT TATTCACCGTATCCAAATCAATAT |
| 358 | Tabel 3A | NA | 145C5 | 1 | AATGTGCAAGGTGAAATGCTTTTGGA TAAACGTAAGCCTATTTTCTGACG |
| 359 | Tabel 3A | NA | 145C5 | -1 | CGTCAGAAAATAGGCTTACGTTTATC CAAAAGCATTTACCTTGACACATT |
| 360 | Tabel 3A | NA | 184H1 | 1 | TTCATCTCTAAGGCACACTTGCTACC CCTCTTTGCTGACCCAGATTGTG |
| 361 | Tabel 3A | NA | 184H1 | -1 | CACAATCTGGGGTCAGCAAAGAGGG GTAGCAAGTGTGCCTTAGAGATGAA |
| 362 | Tabel 3A | NA | 45B9 | 1 | TTCTGGCAAGCTCTTGTATGGTGT CGACACTTCCTCTGTCTTCTTGG |
| 363 | Tabel 3A | NA | 45B9 | -1 | CCAAGAAGACAGAAGGAAGTGTGCA ACACCATGACAAGAGCTTGCCAGAA |
| 364 | Tabel 3A | NA | 112B5 | 1 | GGTCAATGTAGCCAATTATTTGTTTCA ACAGTTGCAGAACAGATATTTCA |
| 365 | Tabel 3A | NA | 112B5 | -1 | TGAAATATCTGTTCTGCAACTGTTGA AACAAATAATTGGCTACATTGACC |
| 366 | Tabel 3A | NA | 117H9 | 1 | TGAAAAGACAGCTAATTTGGTCCAAC AAACATGACTGGGTCTAGGGCACC |
| 367 | Tabel 3A | NA | 117H9 | -1 | GGTGCCCTAGACCCAGTCATGTTGT TGGACCAAATTAGCTGTCTTTTCA |
| 368 | Tabel 3A | NA | 515H10 | 1 | TGGATCATTTGCCCAAAGTTGCACGCA CTGACTCCTTACCTGTGAGGAATG |
| 369 | Tabel 3A | NA | 515H10 | -1 | CATTCTCACAGGTAAGGAGTCAGTG CGTGCAACTTTGGGCAATGATCCA |
| 370 | Tabel 3A | NA | 103C4 | 1 | TTAAAACATTAAAGATTGACTCCACT TTGTGCCAAGCTCTCGGGTAGG |
| 371 | Tabel 3A | NA | 103C4 | -1 | CCTACCCGCAGAGCTTGGCACAAAG TGGAGTCAATCTTTTAATGTTTAA |
| 372 | Tabel 3A | NA | 116E10 | 1 | TGAATTTGGAGTCCCTGGCACATAAA TCTACCTTCAAATCAGAGGTCCTT |

Table 8

| | | | | | | | |
|-----|-----------|-----------|-----------|----------|--|----|--|
| 373 | Tabel 3A | NA | | 116E10 | | -1 | AAGGACCTCTGATTGGAAGGTAGATT TATGTGCCAGGGAAGCTCCAAATTCA |
| 374 | Tabel 3A | NA | | 196D7 | | 1 | TGGGTGACAGACGAAAAAGGGCTATTA TAGGTCAAACATTACAGAAATCA |
| 375 | Tabel 3A | NA | | 196D7 | | -1 | TGATTTCTGTAATGTTTGACCTAATAA TAGCCCTTTTCGTCTCTGACCCA |
| 376 | Tabel 3A | NA | | 524A9 | | 1 | CTGATTTAACAGGTGGTCTCGCGGGC GTCCAGGTCAACATCTTTTTGTCC |
| 377 | Tabel 3A | NA | | 524A9 | | -1 | GGACAAAAGATGTTGACCTGGACG CCCGCAGAACCCCTGTAAATCAG |
| 378 | Tabel 3A | NA | | 485A6 | | 1 | GTCACTTTAGCGAGCGGAAACAAT GGCGGAAAGGAAACCTGGAAAG |
| 379 | Tabel 3A | NA | | 485A6 | | -1 | CTTCCAGGTTTTCCCTTCGCGCAT TGTTTTCCCGCTCGCTAAAGTGAC |
| 380 | Tabel 3A | NA | | 485D5 | | 1 | TAATTAATAGAGCTCACTTAAGATTGC CCATCAAGAAACAGGAGGGTGGT |
| 381 | Tabel 3A | NA | | 485D5 | | -1 | ACCACCTCCTGTTTCTTGATGGGCA ATCTTAAGTGAGCTCTATTAAATTA |
| 382 | Tabel 3A | NA | | 479G6 | | 1 | AGTCTGCTGAATCATTGGTTTATAG AAGACTATCTGGAGGGCTGATAG |
| 383 | Tabel 3A | NA | | 479G6 | | -1 | CTATCAGGCCCTCCAGATAGTCTTCT ATAAACCAATGATTCAGCAGGACT |
| 384 | Tabel 3A | NA | | 482A5 | | 1 | ATGTGATTCCATGATAATCAAATAGT GAATACATTATAAAGTCAGCAACT |
| 385 | db mining | Hs.195219 | W63776 | 1371377 | hypothetical protein FLJ14486 (FLJ14486), mRNA /cds=(80,1615) | 1 | ATATATGGGGCTGGGCTCGGGAC TCTCGCTCTAATAAAGGACTGTAGG |
| 386 | Table 3A | Hs.183454 | AK027789 | 14042727 | cDNA FLJ14883 fis, clone PLACE1003596, moderately similar to OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT /cds=(2,862) | 1 | TTTTGACCCAGATGATGGTTCCTTTA CAGAAACAATAAAATGGCTGAACAT |
| 387 | db mining | Hs.69171 | NM_006256 | 5453973 | protein kinase C-like 2 (PRKCL2), mRNA /cds=(9,2963) | 1 | TGAGCACTGGAACAGTTTCATGGAG TTTAAGTTGAGTGAACATCGGCCA |
| 388 | Table 3A | Hs.131828 | R67468 | 840106 | EST390979 cDNA | 1 | ATGCATTTAGTTTTTGGCACCGTAGT TTAAGGGTGGGATTGCCAGTTTTT |
| 389 | Table 3A | Hs.181297 | AA010282 | 1471308 | tc35a11.x1 cDNA, 3' end /clone=IMAGE:2066588 /clone_end=3' | 1 | GGTTGTGCTCTGGTTTCCCTTTTTC CCCGTGGTTTTAATTTTAAAGAC |
| 390 | Table 3A | Hs.235883 | AA020845 | 1484616 | 602628774F1 cDNA, 5' end /clone=IMAGE:4753483 /clone_end=5' | 1 | GGAGGACACCCCTGTGTGTTGCTGC TGCCCTCCGTGCTGTCTACTGTATC |
| 391 | Table 3A | Hs.330145 | AA044450 | 1522307 | RST29149 cDNA | 1 | GCATCAGAGAGAATATGGAAGGACAT CGACCCTAATTCATCCAGTGAGG |
| 392 | Table 3A | Hs.189468 | AA069335 | 1578904 | tm30a06.x1 cDNA, 3' end /clone=IMAGE:2158066 /clone_end=3' | 1 | ACCATAGCAGACAGGGTCAGATGGA ATATTAGCGGTTAGGTGAAGAACC |
| 393 | Table 3A | Hs.205675 | AA111921 | 1664016 | EST389824 cDNA | 1 | AGACAGAAGACAAGGCCAAATGGGT GTCTCTGGAATGATAGACTTAGAAA |
| 394 | Table 3A | Hs.13659 | AA115345 | 1670525 | mRNA; cDNA DKFZp586F2423 (from clone DKFZp586F2423) /cds=UNKNOWN | 1 | ATCCACATCTTACCTTTGGTAGTCA GGTTTTGGCTACTTTGCAGCTCGCC |
| 395 | Table 3A | Hs.11861 | AA122297 | 1678553 | thyroid hormone receptor-associated protein, 240 kDa subunit (TRAP240), mRNA /cds=(77,6601) | 1 | ATAGCAGTGGATTACCAACACCTTGA CTTCTGTACAGTGCTAACATCTT |
| 396 | Table 3A | Hs.183454 | AA149078 | 1719368 | cDNA FLJ14883 fis, clone PLACE1003596, moderately similar to OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT /cds=(2,862) | 1 | TAGTAAAAGTGAAAGAGAAAGGGTTT TTCTGCCACAGGATATAACTTTT |
| 397 | Table 3A | Hs.124601 | AA203497 | 1799265 | zx58g05.r1 cDNA, 5' end /clone=IMAGE:446744 /clone_end=5' | 1 | AAAGCGGTCGTTTTCCCCACAAGGTGT CCAAGTTTGGGGTACTCACACTTA |
| 398 | Table 3A | Hs.73798 | AA210786 | 1809440 | macrophage migration inhibitory factor (glycosylation-inhibiting factor) (MIF), mRNA /cds=(97,444) | 1 | CTAGGCCCGCCACCCCAACCTTCT GGTGGGAGAAATAAACGGTTTAGA |
| 399 | Table 3A | NA | AA214691 | 1814479 | Express cDNA library cDNA 5' | 1 | TGCACTAAACAGTTGCCCAAAAGAC ATATCTTGTTTAAAGGCCAGACC |
| 400 | Table 3A | NA | AA243144 | 1874139 | cDNA clone IMAGE:685113 5' | 1 | TTGGATGAAGCTGAAAAGACACTAAG ACCTTCTGTGCCTCAGATCCCTGA |
| 401 | Table 3A | Hs.135187 | AA250809 | 1885832 | zs06a08.r1 cDNA, 5' end | 1 | GTGTGGCCTAAGGAACACCTCTGTG GGGAGTAAGAGCCAGCCCTTCTCC |
| 402 | Table 3A | Hs.100651 | AA251184 | 1886149 | golgi SNAP receptor complex member 2 (GOSR2), mRNA /cds=(0,638) | 1 | AAGGATGAAGGACTGATGGAGGGCA GAGGAAGTGAGGCAGCAGGCACAA |
| 403 | Table 3A | NA | AA252909 | 1885512 | cDNA clone IMAGE:669292 5' | 1 | AGATGTCTGTATAAACAAGCTTTGGG TAGCAGGTGGTCACTTAGGCAGGA |
| 404 | Table 3A | Hs.194480 | AA258979 | 1894268 | EST389427 cDNA | 1 | TGCTTGTCTTTTAAACACCTTACAGA TATCATTTGCACCTTGCCAAAGG |
| 405 | Table 3A | Hs.5241 | AA280051 | 1921589 | fatty acid binding protein 1, liver (FABP1), mRNA /cds=(42,425) | 1 | GGGTAGGCAGCTTGACCCAGTTCT CCTTTATCTCACTTATTTCTCTGG |
| 406 | Table 3A | NA | AA282774 | 1925825 | cDNA clone IMAGE:713136 5' | 1 | CCGGTGTCCCTGAGTGAGGGCAAG TTGTAATAACACTTGTCTCTCTT |

Table 8

| | | | | | | | |
|-----|----------|-----------|----------|----------|---|---|---|
| 407 | Table 3A | Hs.89072 | AA283061 | 1926050 | hypothetical protein MGC4618 (MGC4618), mRNA /cds=(107,1621) | 1 | ACGGCGTTCGTGAAATTTAGCACACTG GGAAGTCCACATGGTTCATCTGAA |
| 408 | Table 3A | Hs.291448 | AA290921 | 1938772 | EST388168 cDNA | 1 | AATGAGATCACAGATGGTGACACTGA GCGGAAGGATGCAGTACCTCGGAG |
| 409 | Table 3A | Hs.211866 | AA290993 | 1938989 | wh99f02.x1 cDNA, 3' end /clone=IMAGE:2388891 /clone_end=3' | 1 | TCCTTGCAAAACATTTGGCTAGTGGT GTTGAGAGAAATACCAAAACGTGT |
| 410 | Table 3A | Hs.323950 | AA307854 | 1960203 | zinc finger protein 6 (CMPX1) (ZNF6), mRNA /cds=(1265,3361) | 1 | GGCAAAGGGGAAGGATGATGCCATG TAGATCCTGTTTGACATTTTATGG |
| 411 | Table 3A | Hs.100293 | AA312681 | 1965030 | O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) (OGT), mRNA /cds=(2039,4801) | 1 | ACTGTTAACCATAATTTTGAGCAAGGA GTCTCAAAGGTAATCTGAACCAAG |
| 412 | Table 3A | Hs.217493 | AA314369 | 1966698 | annexin A2 (ANXA2), mRNA /cds=(49,1068) | 1 | ACTAGCAGATTGAATCGATATTCATTA AGTTAGGAATGGTGGTGGTCT |
| 413 | Table 3A | Hs.85844 | AA322158 | 1974484 | neurotrophic tyrosine kinase, receptor, type 1 (NTRK1), mRNA /cds=(0,2390) | 1 | AATTGTGCTTTGTATCAGTCAGTGCT GGAGAAATCTTGAATAGCTTATGT |
| 414 | Table 3A | Hs.260238 | AA332553 | 1984808 | hypothetical protein FLJ10842 (FLJ10842), mRNA /cds=(39,1307) | 1 | AGGAAACCAAGCCCTCACAGGAAAG AAAGCCTGAATCAAGAAAACAAAGT |
| 415 | Table 3A | Hs.323463 | AA360634 | 2012954 | mRNA for KIAA1693 protein, partial cds /cds=(0,2707) | 1 | ACTGAGCAGGACAACCTGACCTGTCTC CTTCACATAGTCCATATCACACA |
| 416 | Table 3A | NA | AA377352 | 2029681 | EST89924 Small intestine II cDNA 5' end | 1 | GCGTAAACGCCAGGGCCATCTTCTT ACTTAAGCCACATCCTGAACCAAGG |
| 417 | Table 3A | Hs.27973 | AA397592 | 2050712 | KIAA0874 protein (KIAA0874), mRNA /cds=(0,8188) | 1 | AGCGACAAGAAGGAATCTGGTGAATT TTAGTCATCCCAGCTTTTATGCT |
| 418 | Table 3A | Hs.343557 | AA401648 | 2056830 | 601500320F1 cDNA, 5' end /clone=IMAGE:3902237 /clone_end=5' | 1 | CTGTTGGGCTGAGAGAGGGTCTGGGT TATCTCCTTCTGATCTTCAAACAA |
| 419 | Table 3A | Hs.186674 | AA402069 | 2056860 | qf56f06.x1 cDNA, 3' end /clone=IMAGE:1754051 /clone_end=3' | 1 | TCATGGACACAAACTTTGGAGTATAA GCGACATCCCTTAAGCAACAGGCT |
| 420 | Table 3A | Hs.301985 | AA412436 | 2071006 | 602435787F1 cDNA, 5' end /clone=IMAGE:4553684 /clone_end=5' | 1 | ATTCAAGTCAGGGCCTCTCTGCCCTT TTCCCTCCAGAAACAAAACCAAGA |
| 421 | Table 3A | Hs.9691 | AA418765 | 2080566 | cDNA: FLJ23249 fis, clone COL04196 /cds=UNKNOWN | 1 | TGTTTGTACCACTAGCATTTCTATGTC TGTAATGAACGTGTAGTTAGCA |
| 422 | Table 3A | Hs.24143 | AA426506 | 2106769 | Wiskott-Aldrich syndrome protein interacting protein (WASPIP), mRNA /cds=(108,1619) | 1 | AATATAGCTCCACTAAAGGACCATAG GGAAGAGCCAGCCTTGCCCTTTCT |
| 423 | Table 3A | Hs.303214 | AA427653 | 2111519 | 7c45b01.x1 cDNA, 3' end /clone=IMAGE:3576912 /clone_end=3' | 1 | GACAGTCCATTAAAGTTGATTCCAGT GGTGAAGGGTCAGACACGCCCTCCC |
| 424 | Table 3A | Hs.89519 | AA429783 | 2112974 | KIAA1046 protein (KIAA1046), mRNA /cds=(577,1782) | 1 | CCTGGGTTGCCCTGTATGAAAAGGG AGATCGAGCCATTGTACCACCTTA |
| 425 | Table 3A | Hs.112071 | AA442585 | 2154463 | zv57f09.r1 cDNA, 5' end /clone=IMAGE:757769 /clone_end=5' | 1 | GTTCACCTGTTTAACAGCCAGAAGCCA GAGCCTGCGTACTAGAAGTGGATG |
| 426 | Table 3A | Hs.8832 | AA454036 | 2167705 | zx48b04.r1 cDNA, 5' end /clone=IMAGE:795439 /clone_end=5' | 1 | TTGTCAAGTGGATCTGCCCAAGGTT TGCTTTGAGGAAACCGGGCTCCCT |
| 427 | Table 3A | Hs.286148 | AA454987 | 2177763 | stromal antigen 1 (STAG1), mRNA /cds=(400,4178) | 1 | CTTGATGGAAACAGATGCTGACAG AATTGTAGACTACCATGCCACACA |
| 428 | Table 3A | Hs.255452 | AA455707 | 2178483 | aa22d09.r1 cDNA, 5' end /clone=IMAGE:814001 /clone_end=5' | 1 | AAATCTAAGACACCCAAACCCCTCTT TGCCCTAAGTAGCCCTAGCCTGG |
| 429 | Table 3A | NA | AA457757 | 2180477 | fetal retina 937202 cDNA clone IMAGE:838756 5' | 1 | AGCTGTTTAATTGAATTGGAATCGCTT CCACTTGAACCCCAAGTTTGAAAA |
| 430 | Table 3A | Hs.82772 | AA460876 | 2185996 | collagen, type XI, alpha 1 (COL11A1), mRNA /cds=(161,5581) | 1 | TTTTCTACGTTATCTCATCTCCTTGT TTTCAGTGTGCTTCAATAATGCA |
| 431 | Table 3A | Hs.292451 | AA461604 | 2185468 | zx51d08.r1 cDNA, 5' end /clone=IMAGE:795759 /clone_end=5' | 1 | CTCCCATCTGCACACCTGGATCAAGG TAGCCTCTCTGCACAAGGGCAGGT |
| 432 | Table 3A | Hs.13809 | AA476568 | 2204779 | mRNA for KIAA1525 protein, partial cds /cds=(0,2922) | 1 | TGTTTTGCTTCCTCAGAACTTTTAA TTGCATCTGCCATCCTTATTGG |
| 433 | Table 3A | Hs.83733 | AA479163 | 10433041 | cDNA FLJ11724 fis, clone HEMBA1005331 /cds=UNKNOWN | 1 | ACAGCCAACTGGAAAGATATAAAAGT TTGGGTCTGTCTCCTCTCCTTCAG |
| 434 | Table 3A | Hs.190154 | AA490796 | 2219969 | td07e03.x1 cDNA, 3' end /clone=IMAGE:2074972 /clone_end=3' | 1 | ACTCCTGCTTTAGAGAGAAGCCACCA TGAAAAGTCTCATCATCAGGGGA |
| 435 | Table 3A | Hs.119960 | AA496483 | 2229804 | mRNA; cDNA DKFZp727G051 (from clone DKFZp727G051); partial cds /cds=(0,1423) | 1 | TCCGTACTGTATGTGATATAGTGCCA TTTTAGTAAGTCTGTACACACA |
| 436 | Table 3A | Hs.75470 | AB000115 | 2564034 | hypothetical protein, expressed in osteoblast (GS3686), mRNA /cds=(241,1482) | 1 | ACTTGCCATTACTTTTCTTCCCACTC TCTCCAACATCACTTCACTTTA |
| 437 | Table 3A | Hs.50002 | AB000887 | 2189952 | small inducible cytokine subfamily A (Cys-Cys), member 19 (SCYA19), mRNA /cds=(138,434) | 1 | GTGAGTGTGAGCGAGAGGGTGAGTG TGGTCAGAGTAAGCTGCTCCACCC |
| 438 | Table 3A | Hs.76730 | AB002299 | 2224542 | mRNA for KIAA0301 gene, partial cds /cds=(0,6144) | 1 | TAATATGCTGGCTTTGACAGAGAATG AAAAGGATGAGTTGGTGTAGCCTT |
| 439 | Table 3A | Hs.7911 | AB002321 | 2224586 | mRNA for KIAA0323 gene, partial cds /cds=(0,2175) | 1 | TTCTTCCCTGGAGGAAGCTTTGGT TGCAGGGCTAAACTTAGAGGCTGC |

Table 8

| | | | | | | | |
|-----|----------|-----------|----------|---------|--|---|------------------------------|
| 440 | Table 3A | Hs.7720 | AB002323 | 2224590 | mRNA for KIAA0325 gene, partial cds /cds=(0,5265) | 1 | TCTGACGGTTGGGAGTGGTGGAAATT |
| 441 | Table 3A | Hs.278671 | AB002334 | 2224612 | KIAA0338 gene product (KIAA0338), mRNA /cds=(253,5004) | 1 | GGAAGGATACCAGGAGGTATTTGG |
| 442 | Table 3A | Hs.23311 | AB002365 | 2224674 | mRNA for KIAA0367 gene, partial cds /cds=(0,2150) | 1 | TGATTACAAAAGGCGTATTCTTTCAT |
| 443 | Table 3A | Hs.3852 | AB002366 | 2224676 | mRNA for KIAA0368 gene, partial cds /cds=(0,4327) | 1 | GGTTTCTGCAATGAGAGGAAGTGT |
| 444 | Table 3A | Hs.70500 | AB002368 | 2224680 | mRNA for KIAA0370 gene, partial cds /cds=(0,2406) | 1 | TCATGCATTGGATTGCTCAGAAATAA |
| 445 | Table 3A | Hs.63302 | AB002369 | 2224682 | myotubularin related protein 3 (MTMR3), mRNA /cds=(247,3843) | 1 | GTGTCTGTTAGACTTCGTTTTGGT |
| 446 | Table 3A | Hs.32556 | AB002377 | 6634024 | mRNA for KIAA0379 protein, partial cds /cds=(0,3180) | 1 | TGACGTTAACACCAGGAATCTCCATG |
| 447 | Table 3A | Hs.101359 | AB002384 | 2224712 | mRNA for KIAA0386 gene, complete cds /cds=(177,3383) | 1 | TTTATTATTTTTCTGTTGAACTCC |
| 448 | Table 3A | Hs.100955 | AB007859 | 6634028 | mRNA for KIAA0399 protein, partial cds /cds=(0,2961) | 1 | TTGCAAAGACTCACGTTTTTGTGTTT |
| 449 | Table 3A | Hs.118047 | AB007881 | 2662082 | 602971981F1 cDNA, 5' end /clone=IMAGE:5111324 /clone_end=5' | 1 | TCTCATCATCCATTGTGATACT |
| 450 | Table 3A | Hs.28578 | AB007888 | 2887430 | muscleblind (Drosophila)-like (MBNL), mRNA /cds=(1414,2526) | 1 | AGCTGTACATATAACCCCTTTCTCCTA |
| 451 | Table 3A | Hs.32168 | AB007902 | 2662164 | KIAA0442 mRNA, partial cds /cds=(0,3519) | 1 | AAGAGGAGTCAGTCAGTGCTCCT |
| 452 | Table 3A | Hs.158286 | AB007915 | 6634034 | mRNA for KIAA0446 protein, partial cds /cds=(3480,4586) | 1 | AGTTCAGGAGATCTCTAAGTGTAGCT |
| 453 | Table 3A | Hs.214646 | AB007916 | 6683704 | mRNA for KIAA0447 protein, partial cds /cds=(233,1633) | 1 | GTAATTTTGGGGTTAATTTGGCT |
| 454 | Table 3A | Hs.28169 | AB007928 | 3413879 | mRNA for KIAA0459 protein, partial cds /cds=(0,461) | 1 | TGTTTGGTTGAGGGGTGCTTTTAGTT |
| 455 | Table 3A | Hs.7764 | AB007938 | 3413899 | KIAA0469 gene product (KIAA0469), mRNA /cds=(184,1803) | 1 | GTGTGGCATTGTATTCAATTGATC |
| 456 | Table 3A | Hs.92381 | AB007956 | 3413930 | mRNA, chromosome 1 specific transcript KIAA0487 /cds=UNKNOWN | 1 | TCAGCCTGAGTGAGTTCAGCGTGAA |
| 457 | Table 3A | Hs.306193 | AB011087 | 9558752 | hypothetical protein (LQFBS-1), mRNA /cds=(0,743) | 1 | AAAGGATGTTAAGCTGTGGGTAAA |
| 458 | Table 3A | Hs.59403 | AB011098 | 3043575 | serine palmitoyltransferase, long chain base subunit 2 (SPTLC2), mRNA /cds=(188,1876) | 1 | AGGGGAAAAGAGGGGAGAAAACAG |
| 459 | Table 3A | Hs.173081 | AB011102 | 3043583 | mRNA for KIAA0530 protein, partial cds /cds=(0,4692) | 1 | GAGTGATGTCATTTCTTTTCATGT |
| 460 | Table 3A | Hs.198891 | AB011108 | 3043595 | mRNA for KIAA0536 protein, partial cds /cds=(0,3087) | 1 | ACTTCTGCTTGTAGTTGCTTAAAT |
| 461 | Table 3A | Hs.62209 | AB011114 | 6635200 | mRNA for KIAA0542 protein, partial cds /cds=(390,4028) | 1 | AAGCAACTGAATCTTCAGCATGTTCT |
| 462 | Table 3A | Hs.13273 | AB011164 | 3043707 | mRNA for KIAA0592 protein, partial cds /cds=(0,4061) | 1 | CATCGGCGGAGCCTCTCTGTGTAA |
| 463 | Table 3A | Hs.20141 | AB011169 | 3043717 | mRNA for KIAA0597 protein, partial cds /cds=(0,2915) | 1 | TGATTGGAGCACTGAGGAACAAGGG |
| 464 | Table 3A | Hs.118087 | AB011182 | 3043743 | DNA sequence from clone RP11-251J8 on chromosome 13 Contains ESTs, STSs, GSSs and a CpG Island. Contains two novel genes with two isoforms each and the KIAA0610 gene with two isoforms /cds=(61,2081) | 1 | GGCTTCCATGTCGGAATCTCTGCTTA |
| 465 | Table 3A | Hs.9075 | AB011420 | 3834353 | serine/threonine kinase 17a (apoptosis-inducing) (STK17A), mRNA /cds=(117,1361) | 1 | AGGTTTTAGGGTACCTTCAGTACT |
| 466 | Table 3A | Hs.120996 | AB011421 | 3834355 | serine/threonine kinase 17b (apoptosis-inducing) (STK17B), mRNA /cds=(261,1379) | 1 | TTTTGGCCAGCTTTCTAGATAAGGT |
| 467 | Table 3A | Hs.180383 | AB013382 | 3869139 | dual specificity phosphatase 6 (DUSP6), transcript variant 1, mRNA /cds=(351,1496) | 1 | TGTATTGCTACTGCAACTAACAAA |
| 468 | Table 3A | Hs.323712 | AB014515 | 3327043 | KIAA0615 gene product (KIAA0615), mRNA /cds=(237,2927) | 1 | CACACATCCTGGTACCCTTGGTCTTC |
| 469 | Table 3A | Hs.11238 | AB014522 | 3327057 | mRNA for KIAA0622 protein, partial cds /cds=(0,3869) | 1 | AAAGGCCATTTCCAGCAGACCCCTC |
| 470 | Table 3A | Hs.12259 | AB014530 | 3327073 | mRNA for KIAA0630 protein, partial cds /cds=(0,1473) | 1 | AAACATGTCTTTTCTCGCCTCAACTT |
| 471 | Table 3A | Hs.31921 | AB014548 | 3327109 | mRNA for KIAA0648 protein, partial cds /cds=(0,2557) | 1 | TATCCACATGAATGTGTGCCCA |
| 472 | Table 3A | Hs.8118 | AB014550 | 3327113 | mRNA for KIAA0650 protein, partial cds /cds=(0,2548) | 1 | TAAGCATAAACCTGACACGTTAAAA |
| 473 | Table 3A | Hs.96731 | AB014555 | 3327123 | mRNA for KIAA0655 protein, partial cds /cds=(0,3253) | 1 | TCCCTGCCCTTTGGTGAGCCCACT |
| 474 | Table 3A | Hs.65450 | AB014558 | 3327129 | reticulon 4a mRNA, complete cds /cds=(141,3719) | 1 | AACCTTGCAITTAGCAGTCATGTTT |
| | | | | | | 1 | CTAATTGACTTACGGGAACTGA |
| | | | | | | 1 | AGGCCTCAGGCCACCTCCAGGAACA |
| | | | | | | 1 | GAACACAGTTTTAAGTTTGATTTTT |
| | | | | | | 1 | TGAGTCTTAGCAATATGGGAGCAGGT |
| | | | | | | 1 | TTTCACTGAATTCTGAGGGTGCCCT |
| | | | | | | 1 | GTTGTCTGCGCACACAGGAGGCGCA |
| | | | | | | 1 | GGCTATGCGTTCGAGGCCAACCTAG |
| | | | | | | 1 | TGGGAACACATAGAAGCTGATGGAGG |
| | | | | | | 1 | CTTTCTCAAGGCCAAGGATAATGT |
| | | | | | | 1 | GGATTGAACAGTTTCAAGTTGTATCTAT |
| | | | | | | 1 | GCCCCACAGTGACCAGTAAAGTCC |
| | | | | | | 1 | CGATGACTCATTACCCAATCCCCATG |
| | | | | | | 1 | AACCTGTTTCAGATTGTCTGTGT |
| | | | | | | 1 | GTGCGAAAGGGGATAATCTGGGAAA |
| | | | | | | 1 | GACACCAAAATCATGGGCTCACTTTA |
| | | | | | | 1 | ACTCAAGCTCACACCTGTACCTGATG |
| | | | | | | 1 | GGAATGAACATAATGTGAAGAAAC |
| | | | | | | 1 | CACCAAAATAGTTATGTTGGCACTGT |
| | | | | | | 1 | GTTTCACAGCGATGGTCCCAACACC |
| | | | | | | 1 | GTGCGCTTCTTTTACAACAAGCCTC |
| | | | | | | 1 | TAGAAACAGATAGTTTCTGAGAAT |
| | | | | | | 1 | GTGTGTATAATGTAAAGTAGTTTTCG |
| | | | | | | 1 | ATATTCTGTGTGTCACATGGGCT |
| | | | | | | 1 | AGGAATCCTTTTCTACATTTGAGCAA |
| | | | | | | 1 | ATACTGAGGTTCTAGTTGTACCAA |
| | | | | | | 1 | CGCCTTGGCTTTGTGTTAGCATTTC |
| | | | | | | 1 | TCCTGAAGTGTCTGTTGGCAATA |
| | | | | | | 1 | AGAGATTTTCTATTGCTGGGAAGGTG |
| | | | | | | 1 | TGTTTCTCCACAATTTGTTTGTG |

Table 8

| | | | | | | | |
|-----|----------|-----------|----------|----------|---|---|-----------------------------|
| 475 | Table 3A | Hs.6727 | AB014560 | 3327133 | mRNA for KIAA0660 protein, complete cds /cds=(120,1568) | 1 | TGCAACCAAATTGGCTTTACCATCTT |
| 476 | Table 3A | Hs.52526 | AB014569 | 3327151 | KIAA0669 gene product (KIAA0669), mRNA /cds=(1016,3358) | 1 | GGCTTTAGTAGGTATAGAAGACAA |
| 477 | Table 3A | Hs.5734 | AB014579 | 3327171 | meningioma expressed antigen 5 (hyaluronidase) (MGEA5), mRNA /cds=(395,3145) | 1 | TGTCAAATAAAAGAGAACGAACAGGT |
| 478 | Table 3A | Hs.153293 | AB014601 | 3327215 | mRNA for KIAA0701 protein, partial cds /cds=(0,1892) | 1 | AGTTTGGTGAGCTGAGCTAGTGT |
| 479 | Table 3A | Hs.192705 | AB015798 | 11067366 | PRO0457 protein (PRO0457), mRNA /cds=(985,1431) | 1 | TCCTGTAGAAAACGAACTGTAAAGA |
| 480 | Table 3A | Hs.247433 | AB015856 | 3953530 | activating transcription factor 6 (ATF6), mRNA /cds=(42,2054) | 1 | CCATGCAAGAGGCAAAATAAACT |
| 481 | Table 3A | Hs.288031 | AB016247 | 3721881 | sterol-C5-desaturase (fungal ERG3, delta-5-desaturase)-like (SC5DL), mRNA /cds=(48,947) | 1 | ACAGTAGCTTTGTAGTGGGTTTTCTG |
| 482 | Table 3A | Hs.179729 | AB016811 | 4514625 | collagen, type X, alpha 1 (Schmid metaphyseal chondrodysplasia) (COL10A1), mRNA /cds=(0,2042) | 1 | TGCTGTGCTTTTTAATTCATGTA |
| 483 | Table 3A | Hs.10458 | AB018249 | 4033626 | gene for CC chemokine LEC, complete cds | 1 | GATTCCTGTCATGAAGGAAAGCAAGA |
| 484 | Table 3A | Hs.19822 | AB018298 | 3882230 | SEC24 (S. cerevisiae) related gene family, member D (SEC24D), mRNA /cds=(200,3298) | 1 | CAGCTCACAGACACGCGCATCTG |
| 485 | Table 3A | Hs.5378 | AB018305 | 3882244 | mRNA for KIAA0762 protein, partial cds /cds=(0,1874) | 1 | TTTTCTGTACCTTTCTAAACCTCTCTT |
| 486 | Table 3A | Hs.21264 | AB018325 | 3882284 | mRNA for KIAA0782 protein, partial cds /cds=(0,3540) | 1 | CCCTCTGTGATGGTTTTGTGTTT |
| 487 | Table 3A | Hs.8182 | AB018339 | 3882312 | mRNA for KIAA0796 protein, partial cds /cds=(0,3243) | 1 | AAATCTTATTCTCTCTCTTCCCTC |
| 488 | Table 3A | Hs.55947 | AB018348 | 3882330 | mRNA for KIAA0805 protein, partial cds /cds=(0,3985) | 1 | ACTTTTCCCTACTTCTCTGCAA |
| 489 | Table 3A | Hs.181300 | AB020335 | 6518494 | Pancreas-specific TSA305 mRNA, complete cds /cds=(45,2429) | 1 | TGGAATCAGACATCTCCAGATGGTT |
| 490 | Table 3A | Hs.22960 | AB020623 | 3985929 | breast carcinoma amplified sequence 2 (BCAS2), mRNA /cds=(48,725) | 1 | TGGACCCTGCCATGTGTAGGTCA |
| 491 | Table 3A | Hs.45719 | AB020630 | 4240131 | CAAX box protein TIMAP mRNA, complete cds /cds=(52,1755) | 1 | AATTTAGCACCTCAGGAATAACTTATT |
| 492 | Table 3A | Hs.123654 | AB020631 | 4240136 | mRNA for KIAA0824 protein, partial cds /cds=(0,4936) | 1 | GGTTTAGGTGAGTTCTTGGCGGG |
| 493 | Table 3A | Hs.334700 | AB020640 | 14133218 | mRNA for KIAA0833 protein, partial cds /cds=(0,5017) | 1 | AACCATGTAACCTCATTGAACATTTT |
| 494 | Table 3A | Hs.14945 | AB020644 | 4240162 | mRNA for KIAA0837 protein, partial cds /cds=(0,2237) | 1 | CAACTTAAGGTCTGCATAGCAGA |
| 495 | Table 3A | Hs.197298 | AB020657 | 4240188 | NS1-binding protein-like protein mRNA, complete cds /cds=(555,2483) | 1 | AAACCAGGTTAATGGCTAAGAATGGG |
| 496 | Table 3A | Hs.13264 | AB020663 | 4240200 | mRNA for KIAA0856 protein, partial cds /cds=(0,3212) | 1 | TAACATGACTCTTGTGGATTGTT |
| 497 | Table 3A | Hs.104315 | AB020669 | 4240212 | suppressor of clear, C. elegans, homolog of (SHOC2), mRNA /cds=(277,2025) | 1 | CTCTTGGCTGAGCTTCTACAGGGCTG |
| 498 | Table 3A | Hs.18166 | AB020677 | 6635136 | mRNA for KIAA0870 protein, partial cds /cds=(0,3061) | 1 | AGAGCTGCGCTTTGGGGACTTCAG |
| 499 | Table 3A | Hs.27973 | AB020681 | 4240236 | KIAA0874 protein (KIAA0874), mRNA /cds=(0,6188) | 1 | TTTCCTTTGGGGCATGATGTTTTAAC |
| 500 | Table 3A | Hs.75415 | AB021288 | 4038732 | cDNA: FLJ22810 fis, clone KIAA2933, highly similar to AB021288 mRNA for beta 2-microglobulin /cds=UNKNOWN | 1 | CTTTGCTTTAGAAGCACAAAGCTGT |
| 501 | Table 3A | Hs.215857 | AB022663 | 5019617 | HFB30 mRNA, complete cds /cds=(236,1660) | 1 | ATAGAATGAGCTTGGTTAAGCACCTC |
| 502 | Table 3A | Hs.104305 | AB023143 | 4589483 | death effector filament-forming Ced-4-like apoptosis protein (DEFCAP), transcript variant B, mRNA /cds=(522,4811) | 1 | TCCTTTGCCCTTCACCTGACTCC |
| 503 | Table 3A | Hs.154296 | AB023149 | 4589507 | mRNA for KIAA0932 protein, partial cds /cds=(0,2782) | 1 | TTGAGTAGAACTCGATTTTCCCTAG |
| 504 | Table 3A | Hs.4014 | AB023163 | 4589535 | mRNA for KIAA0946 protein, partial cds /cds=(0,2005) | 1 | AGGCCAAATTCCTTTTATCTGGGT |
| 505 | Table 3A | Hs.75478 | AB023173 | 4589555 | mRNA for KIAA0956 protein, partial cds /cds=(0,2020) | 1 | TTCTAAACACATTCCTGATCACCAAAC |
| 506 | Table 3A | Hs.184523 | AB023182 | 4589573 | mRNA for KIAA0965 protein, partial cds /cds=(0,1392) | 1 | AACCTCAGAAAGAGAGTGAAGATAAAA |
| 507 | Table 3A | Hs.103329 | AB023187 | 14133226 | KIAA0970 protein (KIAA0970), mRNA /cds=(334,2667) | 1 | CCCTAGAATGCTTAAATGTGCTGT |
| 508 | Table 3A | Hs.158135 | AB023198 | 4589605 | mRNA for KIAA0981 protein, partial cds /cds=(0,1737) | 1 | TTAATGCCAGTCCTCATGTAACCTCA |
| 509 | Table 3A | Hs.75361 | AB023200 | 4589609 | mRNA for KIAA0983 protein, complete cds /cds=(55,2106) | 1 | GGTATCTTCAGCTTGTGGAGAATA |

Table 8

| | | | | | | | |
|-----|-----------|-----------|----------|----------|---|---|---|
| 510 | Table 3A | Hs.343557 | AB023216 | 14133228 | 601500320F1 cDNA, 5' end /clone=IMAGE:3902237 /clone_end=5' | 1 | TTTGGTTCATCCGTGTGCTGTTCTTTT GGGTTCAGAGAGGTTTGGCCAT |
| 511 | Table 3A | Hs.23860 | AB023227 | 4589669 | mRNA for KIAA1010 protein, partial cds /cds=(0,3949) | 1 | GGCAGTAATGCAAGAGTCCTTTGTG AAGAGTGTTCCTATGTAGAGATGT |
| 512 | Table 3A | Hs.90093 | AB023420 | 4579903 | mRNA for heat shock protein apg-2, complete cds /cds=(278,2800) | 1 | AAATGCAGAGCAGAAATGGACCAGTG GATGGACAAGGAGACACCCAGGCC |
| 513 | Table 3A | Hs.6790 | AB026908 | 5931603 | microvascular endothelial differentiation gene 1 (MDG1), mRNA /cds=(202,873) | 1 | AGTGTTCCTGCTGCCAGTTCCTTCCT CTTAGGCGTGGTTGAGAAAAGC |
| 514 | Table 3A | Hs.21542 | AB028958 | 5689405 | KIAA1035 protein (KIAA1035), mRNA /cds=(88,3648) | 1 | CAGTCTCTGCCACTTGTGCTAGTTTT TGTGTGGTGTTTAGAAACATGGGC |
| 515 | Table 3A | Hs.9846 | AB028963 | 5689416 | mRNA for KIAA1040 protein, partial cds /cds=(0,1636) | 1 | TCCCACTTAGGTTTGGCATTTTGGCA GATAAGCTAATCTTGTATAAAGCA |
| 516 | Table 3A | Hs.89519 | AB028969 | 5689428 | KIAA1046 protein (KIAA1046), mRNA /cds=(577,1782) | 1 | GTAATAGCCCTACATGGTGTAGTCT GCATTATATATAAACTGTGTGCA |
| 517 | Table 3A | Hs.126084 | AB028978 | 5689446 | mRNA for KIAA1055 protein, partial cds /cds=(0,2607) | 1 | AGCTCCTGTGCTGACCTTCAAGTTAC GTTTTGGAAGCTGAATACTAAAGG |
| 518 | Table 3A | Hs.7243 | AB028980 | 5689450 | mRNA for KIAA1057 protein, partial cds /cds=(0,2934) | 1 | ACACTAGGGAAGAACCTTAATTCTAA ATTTGGTTCATGTGTGGCAAGTG |
| 519 | Table 3A | Hs.8021 | AB028981 | 5689452 | mRNA for KIAA1058 protein, partial cds /cds=(0,4604) | 1 | TAAGTGAATCACTGCCCTGCTGTAA TTAAACATTCTGTACCACATCTGT |
| 520 | Table 3A | Hs.76118 | AB028986 | 5689462 | ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) (UCHL1), mRNA /cds=(31,669) | 1 | CCCCAGTGCCTTGTAGTCTTCTCCTA TGTCATAATAAAGCTACATTTTCT |
| 521 | Table 3A | Hs.325530 | AB028990 | 5689470 | mRNA for KIAA1067 protein, partial cds /cds=(0,2072) | 1 | GACAGACTTGGACACAAAACCGATCC ATAGAAGGGCTTCCCAAACCTTGT |
| 522 | Table 3A | Hs.154525 | AB028999 | 5689488 | mRNA for KIAA1076 protein, partial cds /cds=(0,2415) | 1 | CCATATGTAACCTGTTTGAAGAGAA GTGTTTCGCTTGTGTGCTCTTGATG |
| 523 | Table 3A | Hs.155546 | AB029003 | 5689496 | mRNA for KIAA1080 protein, partial cds /cds=(0,1554) | 1 | GTATCATCTGCCAAGACCAGGGCCT GCTTCACCAAGCCACAATAAAGTC |
| 524 | Table 3A | Hs.26334 | AB029006 | 5689502 | mRNA for KIAA1083 protein, complete cds /cds=(221,1975) | 1 | AATGAACCACTTACAGTTCGGTTTTG GACTCTGAGTCAAAGGATTTTCCT |
| 525 | Table 3A | Hs.54886 | AB029015 | 5689520 | mRNA for KIAA1092 protein, partial cds /cds=(0,3464) | 1 | GCCGAGTCAGCACATGGGTAGAGAT GATGTAAAGCAGCCCAATCTGGAAA |
| 526 | Table 3A | Hs.117333 | AB029016 | 14133234 | mRNA for KIAA1093 protein, partial cds /cds=(179,5362) | 1 | ACCTTCTGGGAGGAGGGTCCGATTTC AATCTGAACCTTGAACCTTCAACTC |
| 527 | Table 3A | Hs.279039 | AB029027 | 5689544 | KIAA1104 protein (KIAA1104), mRNA /cds=(494,2281) | 1 | GCACCATGTAGAAATTTTCACTTTGTA CTGGCAGGCTCGTTTTACCTCATT |
| 528 | Table 3A | Hs.278586 | AB029031 | 5689552 | mRNA for KIAA1108 protein, partial cds /cds=(0,2291) | 1 | TCTCCAGTCTGATTAAGTGTACACAG TAGCTTTAGATGCCGTGGACGTGA |
| 529 | Table 3A | Hs.7910 | AB029551 | 6714542 | YEAF1 mRNA for YY1 and E4TF1 associated factor 1, complete cds /cds=(198,878) | 1 | TTCTGTACTGGCATGTGCACGACT ATGTTATTAGAAGCCACTTTATCA |
| 530 | Table 3A | Hs.14805 | AB031050 | 7684246 | solute carrier family 21 (organic anion transporter), member 11 (SLC21A11), mRNA /cds=(193,2325) | 1 | GCCAGCTTGGAGGATGGACATTTCTG GATACACATACACATACAAAACAG |
| 531 | db mining | Hs.91600 | AB031479 | 6539431 | SEEK1 protein (SEEK1), mRNA /cds=(274,732) | 1 | TCAGCTCCTTGATCTAAGCCTCCCAG AGAGACCCCTAGAATGTTCCCTC |
| 532 | db mining | Hs.146824 | AB031480 | 6539433 | SPR1 protein (SPR1), mRNA /cds=(315,725) | 1 | CCGGCGGCAGGAACATCAGTAGAC AGCTGCTGCTTCCATGAACCGGAAA |
| 533 | Table 3A | Hs.99872 | AB032251 | 6683491 | BPTF mRNA for bromodomain PHD finger transcription factor, complete cds /cds=(471,8816) | 1 | TGTTGCCTTGAATATAACAGTACAATT TGCAATTACTCTGCACAGGCT |
| 534 | Table 3A | Hs.8858 | AB032252 | 6683493 | bromodomain adjacent to zinc finger domain, 1A (BAZ1A), mRNA /cds=(115,5139) | 1 | AAAAGTAACACCCCTCCCTTTTCTCTG ACAGTCTTTACAGCTTTAGAGAAC |
| 535 | Table 3A | Hs.286430 | AB032948 | 6329727 | 601655926R1 cDNA, 3' end /clone=IMAGE:3855679 /clone_end=3' | 1 | AATGAAATGTAGTTGGGTTCTTCTCTG TAATGCGCTATTATGTCTTGGGCT |
| 536 | Table 3A | Hs.44087 | AB032952 | 6329754 | mRNA for KIAA1126 protein, partial cds /cds=(0,1857) | 1 | AACCTCCTTGTGTCTGTTTCTCTGTTT CTCTGTGGCTGACTCAATAAACT |
| 537 | Table 3A | Hs.153489 | AB032972 | 6330026 | mRNA for KIAA1146 protein, partial cds /cds=(0,815) | 1 | GTGGAGGGTGAGATGTGAAGATGT GGGATGAACCTGGAATGAACGAATT |
| 538 | Table 3A | Hs.12461 | AB032973 | 6330032 | mRNA for KIAA1147 protein, partial cds /cds=(0,569) | 1 | GGCCTAAAGAAAGCTGGGGTTAATCC TGAAGCTAAAGTAAATGTTTCTT |
| 539 | Table 3A | Hs.343199 | AB032976 | 6330050 | EST374106 cDNA | 1 | TCCATCCCTTTCCATCAAGACCTTCA TTAGCTTATGATATTGCTGCCGA |
| 540 | Table 3A | Hs.6298 | AB032977 | 6382017 | mRNA for KIAA1151 protein, partial cds /cds=(0,689) | 1 | GGAGGTCTCTTCCAGATTGCTCTTCT GCCGAATTATTGTTATCTATCCG |
| 541 | Table 3A | Hs.290398 | BF341403 | 11287894 | 602013369F1 cDNA, 5' end /clone=IMAGE:4149209 /clone_end=5' | 1 | GCACACCTGCTCAGAGGACCATAAC CGTGTGGGGACAATAACCCGAGGGG |
| 542 | Table 3A | Hs.7041 | AB033034 | 6382021 | mRNA for KIAA1208 protein, partial cds /cds=(24,2015) | 1 | ACAAATGGATTTGTGAAGAGCAGATTC CATGAGTAACTCTGACAGGTATT |
| 543 | Table 3A | Hs.29679 | AB033042 | 6330568 | cofactor required for Sp1 transcriptional activation, subunit 3 (130kD) (CRSP3), mRNA /cds=(119,4225) | 1 | TGAGAGACATTGTTAATTTTGGGGGA ATTGGCATTGCGAAAGACTTGAAA |
| 544 | Table 3A | Hs.7252 | AB033050 | 6330623 | mRNA for KIAA1224 protein, partial cds /cds=(0,1908) | 1 | TGCTAGACATTTCTATACTCTGTTGTA ACACTGAGGTATCTCATTTGCC |

Table 8

| | | | | | | | |
|-----|-----------|-----------|-----------|----------|---|---|-----------------------------|
| 545 | Table 3A | Hs.267690 | AB033054 | 6330689 | mRNA for KIAA1228 protein, partial cds /cds=(0,2176) | 1 | GTGGGGGATGGGGGTTAAAAAGTAG |
| 546 | Table 3A | Hs.9873 | AB033076 | 14133246 | mRNA for KIAA1250 protein, partial cds /cds=(139,5472) | 1 | AGAACCTCCTTCTGTCTCAACTAAT |
| 547 | Table 3A | Hs.146668 | AB033079 | 6382025 | mRNA for KIAA1253 protein, partial cds /cds=(0,1418) | 1 | CAGGTGAGTAGTGGCCGCGTAATATC |
| 548 | Table 3A | Hs.301721 | AB033081 | 6330899 | mRNA for KIAA1255 protein, partial cds /cds=(0,2866) | 1 | ATTGGAGTACATTCTTTATACTGT |
| 549 | Table 3A | Hs.40193 | AB033085 | 6330932 | mRNA for KIAA1259 protein | 1 | CCCCAACCTTATTCTGTGTGTAGACA |
| 550 | Table 3A | Hs.43141 | AB033093 | 6331205 | mRNA for KIAA1267 protein, partial cds /cds=(94,3411) | 1 | TTGTATTCCACAATTTTGAATGGC |
| 551 | Table 3A | Hs.42179 | AB033112 | 6331388 | mRNA for KIAA1286 protein, partial cds /cds=(197,3841) | 1 | CGAATGGCTTAAACTAATTTGCTATG |
| 552 | Table 3A | Hs.63128 | AB033118 | 6331442 | mRNA for KIAA1292 protein, partial cds /cds=(0,1788) | 1 | ATCCTCTAACACCGAAATTTCCCA |
| 553 | Table 3A | Hs.278670 | AB034205 | 6899845 | acid-inducible phosphoprotein (OA48-18), mRNA /cds=(275,445) | 1 | AGAGGGAATCAGAAAAATGCCAAGC |
| 554 | Table 3A | Hs.76507 | AB034747 | 12862475 | LPS-induced TNF-alpha factor (PIG7), mRNA /cds=(233,919) | 1 | CTTTTCTCTTGAATGTGCTATTTT |
| 555 | db mining | Hs.184 | AB036432 | 6691625 | advanced glycosylation end product-specific receptor (AGER), mRNA /cds=(0,1214) | 1 | CACCTTCTCTGTGTTAACCTTGTGCCT |
| 556 | Table 3A | Hs.194369 | AB036737 | 8096339 | mRNA for RERE, complete cds /cds=(636,5336) | 1 | GTCTCCTGTATGATCACATCACC |
| 557 | Table 3A | Hs.125037 | AB037752 | 7243042 | hypothetical protein FLJ20548 (FLJ20548), mRNA /cds=(167,1432) | 1 | TGTGTCTCTGTGCGCTCTGCTGTGAA |
| 558 | Table 3A | Hs.22941 | AB037784 | 7243106 | mRNA for KIAA1363 protein, partial cds /cds=(0,1293) | 1 | GCACATGATGCTCTATTATTGTA |
| 559 | Table 3A | Hs.258730 | AB037790 | 7243118 | mRNA for KIAA1369 protein, partial cds /cds=(0,1963) | 1 | TGAGAGTAAGCACATGACAGCGCTG |
| 560 | Table 3A | Hs.29716 | AB037791 | 7243120 | mRNA for KIAA1370 protein, partial cds /cds=(49,3372) | 1 | CTTGCGTGTGTCTGTTTTATGTT |
| 561 | Table 3A | Hs.9663 | AB037796 | 7243130 | mRNA for KIAA1375 protein, partial cds /cds=(0,1640) | 1 | TCGTGTGAATCAGACTAAGTGGGATT |
| 562 | Table 3A | Hs.24684 | AB037797 | 7243132 | mRNA for KIAA1376 protein, partial cds /cds=(143,1456) | 1 | TCATTTTTACAACCTCTGCTCTACT |
| 563 | Table 3A | Hs.6685 | AB037801 | 7243140 | mRNA for KIAA1380 protein, partial cds /cds=(0,3798) | 1 | TGCAACGAATATGGATACCACATAGT |
| 564 | Table 3A | Hs.334878 | NM_032837 | 14249549 | hypothetical protein FLJ14775 (FLJ14775), mRNA /cds=(171,533) | 1 | ACTTTGGTGTACCTGCTTTTGAA |
| 565 | Table 3A | Hs.301434 | AB037808 | 7243154 | mRNA for KIAA1387 protein, partial cds /cds=(0,2852) | 1 | GAGGACGGCAGAGTAGTACTGGAG |
| 566 | Table 3A | Hs.301434 | AB037808 | 7243154 | mRNA for KIAA1387 protein, partial cds /cds=(0,2852) | 1 | TTGCCATGAGATAACACAGTGTAAAC |
| 567 | Table 3A | Hs.15370 | AB037828 | 7243194 | mRNA for KIAA1407 protein, partial cds /cds=(0,2235) | 1 | AGTAGACACCCAGAAATCGTGACT |
| 568 | Table 3A | Hs.274396 | AB037844 | 7243226 | mRNA for KIAA1423 protein, partial cds /cds=(0,1851) | 1 | GCTGTAGGCTAAGAGGGTGCAGGG |
| 569 | Table 3A | Hs.149918 | AB037901 | 10567163 | GASC-1 mRNA, complete cds /cds=(150,3320) | 1 | CTAGACACGAAGCTTAAACTATTCA |
| 570 | Table 3A | Hs.284205 | AB040120 | 12657580 | up-regulated by BCG-CWS (LOC64116), mRNA /cds=(477,1859) | 1 | CCAGTGTGGAGGTAGCAAAGCATCTA |
| 571 | Table 3A | Hs.6682 | AB040875 | 13516845 | solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA /cds=(235,1740) | 1 | TCTATTCTGATGTTTGGAAA |
| 572 | Table 3A | Hs.109694 | AB040884 | 7959160 | mRNA for KIAA1451 protein, partial cds /cds=(0,1467) | 1 | GCCAGTATGCCACAGAATGCTCTAAA |
| 573 | Table 3A | Hs.210958 | AB040919 | 7959232 | mRNA for KIAA1486 protein, partial cds /cds=(11,2044) | 1 | CCCTTGCTGCTTATCAAAAACC |
| 574 | Table 3A | Hs.20237 | AB040922 | 7959238 | mRNA for KIAA1489 protein, partial cds /cds=(1619,3154) | 1 | TGTGTAGTGTGACGCGGCACCTTTTA |
| 575 | Table 3A | Hs.35089 | AB040929 | 7959252 | mRNA for KIAA1496 protein, partial cds /cds=(0,2763) | 1 | CACCTTCTAGTAGCTCAAGCTAGT |
| 576 | Table 3A | Hs.201500 | AB040942 | 7959278 | mRNA for KIAA1509 protein, partial cds /cds=(0,3982) | 1 | TCCTGGAATCGTTAATCTAAAGCAG |
| 577 | Table 3A | Hs.93836 | AB040959 | 7959318 | mRNA for KIAA1526 protein, partial cds /cds=(0,2892) | 1 | TTTCCCCTGTTTTGGAGATTTTTGT |
| 578 | Table 3A | Hs.89135 | AB040961 | 7959322 | mRNA for KIAA1528 protein, partial cds /cds=(4,2226) | 1 | TCCTGGAATCGTTAATCTAAAGCAG |
| 579 | Table 3A | Hs.85752 | AB040974 | 7959348 | mRNA for KIAA1541 protein, partial cds /cds=(908,2341) | 1 | TTGAGAAAGTCCTGTGCAGTCGTGAGA |
| 580 | Table 3A | Hs.18259 | AB044661 | 11094140 | XPA binding protein 1; putative ATP(GTP)-binding protein (NTPBP), mRNA /cds=(24,1148) | 1 | TGATTACTCTTATTTGGTGTGCTG |
| 581 | Table 3A | Hs.142838 | AB044971 | 13699901 | nucleolar protein interacting with the FHA domain of pKi-67 (NIFK), mRNA /cds=(54,935) | 1 | TCGTCTTTGCGAATGGCTTAATTCT |
| 582 | Table 3A | Hs.140720 | AB045118 | 13365650 | FRAT2 mRNA, complete cds /cds=(129,830) | 1 | GACACTACCTTTCTGGGAAATGTT |
| | | | | | | 1 | TTTGTAGTGTGCTGATGGGAAGCTAG |
| | | | | | | 1 | TTGTTGGCCTTTGTGAAATGAAAT |
| | | | | | | 1 | TTGACAAAGCCCAACATGATCTCAG |
| | | | | | | 1 | GAATTACATTTTCCACAGACACCA |
| | | | | | | 1 | ACCTGTACCGCTTCTAGTTGCTTCAA |
| | | | | | | 1 | CCATTTTATAACCATTTTGTACA |
| | | | | | | 1 | TCCTTAAGGTGCACAGTAAATGTACA |
| | | | | | | 1 | GATAGTTATAGGCCACTGTTTTGT |
| | | | | | | 1 | AGCTCATATGAACACTGCTCTGAACT |
| | | | | | | 1 | CCTCTGACTATGACATTCAACTTAA |
| | | | | | | 1 | CATGACAAACATTACTAGCATGTTCA |
| | | | | | | 1 | ACTGCACCATTGTTCTGGCACTGTA |
| | | | | | | 1 | ACCTCTTTCTACCAATTTTCACTTTT |
| | | | | | | 1 | GCAGAAACTGTTTACATTTTCCA |
| | | | | | | 1 | GGGTTGTGTATTAAATAGCCATTAT |
| | | | | | | 1 | TCTGGAACCTAAGGACAGGACTGT |
| | | | | | | 1 | GCCTTGCAGGTTGACGACAGCTGTCA |
| | | | | | | 1 | TTGATTTATATACAGAGCTTATGA |
| | | | | | | 1 | CTGGACGGGCGTGGGTTCTGGGTCA |
| | | | | | | 1 | GCTTCTTTTACCTCAATTTTGTG |
| | | | | | | 1 | AAAGTCTGAGGTGTGGAACAGTTATT |
| | | | | | | 1 | TAAGCATTAGTCAACCTGGTCCT |
| | | | | | | 1 | TGGGCAAGACATGATTAATGAATCAG |
| | | | | | | 1 | AATCCTGTTCATTGGTGACTGG |
| | | | | | | 1 | CCTGTGTAAAGAAGAAATACAAGAG |
| | | | | | | 1 | ACTCAAACACCTACACATTCACGG |
| | | | | | | 1 | TGGCTTGTTCATCTCCAGATGTAGC |
| | | | | | | 1 | TATTGATGTACACTTCGCAACGGA |

Table 8

| | | | | | | | |
|-----|----------|-----------|----------|----------|---|---|--|
| 583 | Table 3A | Hs.136414 | AB045278 | 13568433 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 (B3GNT5), mRNA /cds=(129,1265) | 1 | AACATCAGCTTGGATGGTCACTTGA ATAGAAGATGGTTATACACAGTGT |
| 584 | Table 3A | Hs.127270 | AB046765 | 10047154 | mRNA for KIAA1545 protein, partial cds /cds=(0,2445) | 1 | CCACGGTGGACCCTGTTTGTGTTTAAA TATTCTGTTCCCATGTCAATCAGT |
| 585 | Table 3A | Hs.65641 | AB046766 | 10047156 | hypothetical protein FLJ20073 (FLJ20073), mRNA /cds=(16,1908) | 1 | TTGTGTAGGAACTTTTGCAGTTTGA CACTAAGATAACTTCTGTGTGCAT |
| 586 | Table 3A | Hs.323822 | AB046771 | 10047166 | mRNA for KIAA1551 protein, partial cds /cds=(0,3750) | 1 | ACTCAAATCAGTTAGCTTCAAACAAA AACGAAAGTTAGACCAAGGGAACG |
| 587 | Table 3A | Hs.323822 | AB046771 | 10047166 | mRNA for KIAA1551 protein, partial cds /cds=(0,3750) | 1 | ACTCAAATCAGTTAGCTTCAAACAAA AACGAAAGTTAGACCAAGGGAACG |
| 588 | Table 3A | Hs.17767 | AB046774 | 10047172 | mRNA for KIAA1554 protein, partial cds /cds=(0,3963) | 1 | TTGTGTGCTGTGCTTCAAAGCCTTAA CTGTCAAATCTTGCATTATCTTGT |
| 589 | Table 3A | Hs.44054 | AB046785 | 10047194 | ninein (GSK3B interacting protein) (NIN), mRNA /cds=(202,6345) | 1 | ACATTATCATGGCATGACTTAAAGGGA ACATTGGTTTGTGAAGGAAAAACA |
| 590 | Table 3A | Hs.168640 | AB046801 | 10047236 | mRNA for KIAA1581 protein, partial cds /cds=(0,1639) | 1 | TGTGTGACTTTTCATGCTTCTGGGGTT GGAGCTTAAAGATCCAACTGAGA |
| 591 | Table 3A | Hs.129750 | AB046805 | 10047244 | mRNA for KIAA1585 protein, partial cds /cds=(27,1814) | 1 | TGCTGGTATTCTGACATGCCAATTTTT GGAAACCTGTATTACACCTTAA |
| 592 | Table 3A | Hs.18587 | AB046808 | 10047250 | Homo sapiens, clone MGC:15071 IMAGE:4110510, mRNA, complete cds /cds=(977,2212) | 1 | TTGAGTGTCTGCAGCAGCCCTGGACT TCCAGACTTCTATCACATGAGAAA |
| 593 | Table 3A | Hs.11123 | AB046813 | 10047260 | mRNA for KIAA1593 protein, partial cds /cds=(477,3338) | 1 | TGGTGCTGATGCTTAGTTGTCTCATG CCATTAAATTGAAAAAGTAGTTG |
| 594 | Table 3A | Hs.343582 | AB046825 | 10047284 | RC6-HT0592-270300-Q11-D11 cDNA | 1 | GGAGGTCAGTTGATTTCCCGAGGTAC ATTTCATGGTGTGACAGACACATGG |
| 595 | Table 3A | Hs.222746 | AB046830 | 10047294 | mRNA for KIAA1610 protein, partial cds /cds=(0,1456) | 1 | AGATCCTTTCAGTCCCTAGACCTCCA TTCACCTGTTTCTCTCTGCTGCTGG |
| 596 | Table 3A | Hs.6639 | AB046844 | 10047324 | mRNA for KIAA1624 protein, partial cds /cds=(0,1800) | 1 | GATCCGATCATGGTGATGTACGGGG TGAATTCTCTTCCCGTGTGCAAAAT |
| 597 | Table 3A | Hs.288140 | AB046857 | 10047350 | mRNA for KIAA1637 protein, partial cds /cds=(0,1441) | 1 | ATGGTTTCAAAATTCAGGTCCCAAA ATGGCAGCATTTTATGTTCTGAC |
| 598 | Table 3A | Hs.44566 | AB046861 | 10047358 | KIAA1641 protein (KIAA1641), mRNA /cds=(40,453) | 1 | CAAGTATGTATGCAACTTTCACACC AACAACTGTAATCTGTAGCTAGT |
| 599 | Table 3A | Hs.82113 | AB049113 | 10257384 | dUTP pyrophosphatase (DUT), mRNA /cds=(29,523) | 1 | TGGTGATTCTCCAGGCCATTTAATAC CCTGCAATGTAATTGTCCCTCTGT |
| 600 | Table 3A | Hs.323463 | AB051480 | 12697930 | mRNA for KIAA1693 protein, partial cds /cds=(0,2707) | 1 | TTCTGCCTCAATGTTTACTGTGCCCTT GTTTTGCTAGTTTGTGTTTGTG |
| 601 | Table 3A | Hs.19597 | AB051481 | 12697932 | mRNA for KIAA1694 protein, partial cds /cds=(0,2274) | 1 | ACTACTGTACGTCAGCTGTGTACAAA GAGATGTGAAATACTTTCAGGCAA |
| 602 | Table 3A | Hs.20281 | AB051487 | 12697944 | mRNA for KIAA1700 protein, partial cds /cds=(108,2180) | 1 | TGTTGAACGGTTAAACTGTGCATTTT TCATTTTGTATGTGTCTGATGTT |
| 603 | Table 3A | Hs.7076 | AB051492 | 12697954 | mRNA for KIAA1705 protein, partial cds /cds=(1713,3209) | 1 | AATGGTCAAGGTTTGCATATTCTAT ATGAAGATCACAAGGTGGTATCGT |
| 604 | Table 3A | Hs.25127 | AB051512 | 12697994 | mRNA for KIAA1725 protein, partial cds /cds=(0,3129) | 1 | TGTGAACCTTGTGCGCAAAATGTGCAGA TTCAATGTTCTTGTGATGATTTGA |
| 605 | Table 3A | Hs.66053 | AB051540 | 12698050 | mRNA for KIAA1753 protein, partial cds /cds=(0,2457) | 1 | CCCCTTGGGCTCAGCACGAAAGGGC TTTCAATGAATTAAGTGAAACATTT |
| 606 | Table 3A | Hs.7187 | AB051544 | 12698058 | mRNA for KIAA1757 protein, partial cds /cds=(347,4576) | 1 | AATGAGTTGTGTGAAGCCTCCGTCT CCCCTCTTGCTTAGCCCGTAG |
| 607 | Table 3A | Hs.248367 | AB058677 | 14017778 | MEGF11 protein (MEGF11), mRNA /cds=(159,3068) | 1 | AGCCTAAACATGTATCTGTGCATTTT ATGGGTGACTTTGAAAGATCTGT |
| 608 | Table 3A | Hs.227400 | AF000145 | 3095031 | mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA /cds=(360,3014) | 1 | ACCAGGTTTGTGACAAAATGCACACTT TTGGCTCTTTTGGTATATGTTCT |
| 609 | Table 3A | Hs.8180 | AF000652 | 2795862 | syndecan binding protein (syntenin) (SDCBP), mRNA /cds=(148,1044) | 1 | CCTGACTCCTCTTGCAACAAAATG ATAGTTGACACTTTATCTGATTT |
| 610 | Table 3A | Hs.147916 | AF000982 | 2580549 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3 (DDX3), transcript variant 2, mRNA /cds=(856,2844) | 1 | TTGTATTGTCATATCAGTGACTTGT ACATTGACCAATAGCATTTGAGCA |
| 611 | Table 3A | Hs.13980 | AF000993 | 2580571 | ubiquitously transcribed tetratricopeptide repeat gene, X chromosome (UTX), mRNA /cds=(26,4231) | 1 | TTGTAAAGTTGCAATTACTGCAATGA CAGACCAATAAACAATTGCTGCCA |
| 612 | Table 3A | Hs.159523 | AF001622 | 3930162 | class-I MHC-restricted T cell associated molecule (CRTAM), mRNA /cds=(0,1181) | 1 | ACAGCAAACCTTGGCATTATGTGGA GCATTTCTCATTGTTGGAATCTGA |
| 613 | Table 3A | Hs.58435 | AF001862 | 2232149 | FYN-binding protein (FYB-120/130) (FYB), mRNA /cds=(30,2381) | 1 | TGGTCATTCTGCTGTGTTTCATTAGGT GCCAATGTGAAGTCTGGATTTTAA |
| 614 | Table 3A | Hs.76918 | AF002020 | 2276462 | Niemann-Pick disease, type C1 (NPC1), mRNA /cds=(123,3959) | 1 | GGCATGAAATGAGGGACAAAGAAAG CATCTCGTAGGTGTGTCTACTGGGT |
| 615 | Table 3A | Hs.18792 | AF003938 | 2897941 | thioredoxin-like, 32kD (TXNL), mRNA /cds=(205,1074) | 1 | AATCTTGACACATGCAATTGTAAATAA AAGTCACCACCTTTGCCAAGCTT |
| 616 | Table 3A | Hs.337778 | AF004230 | 2343108 | hypothetical protein FLJ11068 (FLJ11068), mRNA /cds=(163,1188) | 1 | TGATGCCCTTCATCTGTTCACTCATCT CCAAAAACAGTAAAAATAACCACT |
| 617 | Table 3A | Hs.183805 | AF005213 | 2843115 | ankyrin 1, erythrocytic (ANK1), transcript variant 3, mRNA /cds=(84,5726) | 1 | GGCCAAAGCTGAATGCCATGAATATCA GTGAGACGCGTTATAAGGAATCCT |
| 618 | Table 3A | Hs.42915 | AF006082 | 2282029 | ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA /cds=(74,1258) | 1 | CCTGCCAGTGTCAGAAAATCCTATTT ATGAATCCTGTGCGTATTCTTGG |

Table 8

| | | | | | | | |
|-----|-----------|-----------|----------|---------|---|---|---|
| 619 | Table 3A | Hs.6895 | AF006086 | 2282037 | actin related protein 2/3 complex, subunit 3 (21 kD) (ARPC3), mRNA /cds=(25,581) | 1 | TCAAGAAATTTGGGTGGGAGAAAAGAA AGTGGGTATCAAGGGTGATTGA |
| 620 | Table 3A | Hs.82425 | AF006088 | 2282041 | actin related protein 2/3 complex, subunit 5 (16 kD) (ARPC5), mRNA /cds=(24,479) | 1 | CAAACCTGGTGCAGAAATCTATAAAC TCTTTGCTGTTTTGATACCTGCT |
| 621 | Table 3A | Hs.22670 | AF006513 | 2645428 | chromodomain helicase DNA binding protein 1 (CHD1), mRNA /cds=(163,5292) | 1 | GCTACTTGTTTACATTGTACACTGCG ACCACCTTGCCGCTTTTCATCACA |
| 622 | Table 3A | Hs.24752 | AF006516 | 2245670 | spectrin SH3 domain binding protein 1 (SSH3BP1), mRNA /cds=(81,1607) | 1 | ACTGGATGCTACAGACTTATAACAGC ATAGTGAATGGTAAGACTAGTGCA |
| 623 | Table 3A | Hs.321149 | AF007155 | 2852635 | cDNA FLJ10257 fis, clone HEMBB1000887 /cds=UNKNOWN | 1 | CCTCCCCATATGCCTCAGCCCCATCTC TGCTCCTGTTGAATTTTGTATT |
| 624 | Table 3A | Hs.5409 | AF008442 | 2266928 | RNA polymerase I subunit (RPA40), mRNA /cds=(22,1050) | 1 | CCAGTGTGACTAGGGATCCTGAGTTT TCTGGGACAATTCACAGCTTAATC |
| 625 | Table 3A | Hs.225977 | AF012108 | 2331249 | nuclear receptor coactivator 3 (NCOA3), mRNA /cds=(183,4421) | 1 | TGACCCCTCTTTAAGTTATGTGTGTG GGGAGAAATAGAATGGTGCTCTTA |
| 626 | Table 3A | Hs.334874 | AF012872 | 2326226 | phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds /cds=(0,6134) | 1 | GTGTGAGTCCTCTGTTTGCACCTGGAC ATATTCCTACCTGTCTTATTCA |
| 627 | Table 3A | Hs.199291 | AF015041 | 4102706 | NUMB-R protein (NUMB-R) mRNA, complete cds /cds=(209,2038) | 1 | AGGGGAAGGGGTGCCTGGCGGGTAC TTTTCTATCTTTTATTTCCAGATT |
| 628 | Table 3A | Hs.51233 | AF016266 | 2529562 | TRAIL receptor 2 mRNA, complete cds /cds=(117,1439) | 1 | TCATGCTTCTGCCCTGTCAAAGGGTCC CTATTTGAAATGTGTATAATACA |
| 629 | Table 3A | Hs.76807 | AF016270 | 2655005 | major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA /cds=(26,790) | 1 | AGCTAGCAGATCGTAGCTAGTTTGT TTGTCTTGTCATTGTACAGACTT |
| 630 | Table 3A | Hs.104624 | AF016495 | 6560598 | aquaporin 9 (AQP9), mRNA /cds=(286,1173) | 1 | AGCCCAAGATTTCCCAAGGCATTAGG TTTCCCACTGCTTTGTGCTGATA |
| 631 | Table 3A | Hs.10958 | AF021819 | 2460317 | RNA-binding protein regulatory subunit (DJ-1), mRNA /cds=(20,589) | 1 | GTGTCTATACATTTCTAAGCCTTGTTT GCAGAAATAACAGGGCATTTAGC |
| 632 | Table 3A | Hs.125134 | AF023142 | 4102966 | pre-mRNA splicing SR protein rA4 mRNA, partial cds /cds=(0,3473) | 1 | TAGAGGTGTCAGATGCTATATTATA TCCGCTCCCGGTGTACTGCAGCCC |
| 633 | Table 3A | Hs.108809 | AF026292 | 2559009 | chaperonin containing TCP1, subunit 7 (eta) (CCT7), mRNA /cds=(68,1699) | 1 | TTTACAAAGGAAGGGGTAGTAATTGG CCCACTCTCTTCTTACTGGAGGCT |
| 634 | Table 3A | Hs.168103 | AF026402 | 2655201 | prp28, U5 snRNP 100 kd protein (U5-100K), mRNA /cds=(39,2501) | 1 | ACACGGTGAACCTGGCTGTGCCATCT TTGTCACTGAGTGAAATCTCTGTT |
| 635 | Table 3A | Hs.9573 | AF027302 | 2522533 | ATP-binding cassette, sub-family F (GCN20), member 1 (ABCF1), mRNA /cds=(94,2517) | 1 | TGAGGACTTGGGGCAGGAAGGAAT GCTGCTGAACCTTGAATTTCCCTTTA |
| 636 | Table 3A | Hs.168132 | AF031167 | 2739159 | interleukin 15 (IL15), mRNA /cds=(316,804) | 1 | TCAGACCTTGGATCAGATGAACCTCT AGAAATGAAGGCAGAAAATGTCA |
| 637 | Table 3A | Hs.170133 | AF032885 | 2895491 | forkhead box O1A (rhabdomyosarcoma) (FOXO1A), mRNA /cds=(385,2352) | 1 | CCACGTTCTTGTCCGATACCTCTGAG AAGTGCCCTGATGTTGATGTACTTA |
| 638 | Table 3A | Hs.74276 | AF034607 | 4426566 | chloride intracellular channel 1 (CLIC1), mRNA /cds=(236,961) | 1 | GCCTGGGTGAGATTTTATTGTGGGG TGGGATGAGTAGGACACATATTT |
| 639 | Table 3A | Hs.106890 | AF035306 | 2661067 | clone 23771 mRNA sequence /cds=UNKNOWN | 1 | GGGTGCCCACTGATGTGAAGGGG AGGCAGTCTCAATTTATTTCAATA |
| 640 | Table 3A | Hs.184697 | AF035307 | 2661068 | clone 23785 mRNA sequence /cds=UNKNOWN | 1 | CAGTCACTGGGTCTATATTAAACAGC AACCAGAGCAACAAATGGCAACAC |
| 641 | Table 3A | Hs.278589 | AF035737 | 2827179 | general transcription factor II, i (GTF2I), transcript variant 1, mRNA /cds=(370,3366) | 1 | TGACATGGTAGCAGAAATAGGCCCTT TTATGTGTGCTTCTATTTTACCT |
| 642 | Table 3A | Hs.8257 | AF035947 | 9695283 | cytokine-inducible inhibitor of signalling type 1b mRNA, complete cds /cds=(3131,3925) | 1 | AGCAAAGAACAGTTTGGTGGTCTTTT CTCTCCACTGATTTTCTGTAAAT |
| 643 | Table 3A | Hs.6900 | AF037204 | 2906012 | ring finger protein 13 (RNF13), mRNA /cds=(151,1296) | 1 | AGCCCTGCTAAACTATGTACAGAGGA AACTGTTCAAGTATTGGATTGAA |
| 644 | Table 3A | Hs.155489 | AF037448 | 3037012 | NS1-associated protein 1 (NSAP1), mRNA /cds=(204,1892) | 1 | TGTCAACGATGTTCCAGTAGTGTTT AGATTTGGTGTCTTCAAAGGTAGT |
| 645 | Table 3A | Hs.12311 | AF038202 | 2795923 | clone 23570 mRNA sequence /cds=UNKNOWN | 1 | GGCTTTTGGCCATCAAGAATAAAAA GAAATAAAACCAAGGGTTACCCG |
| 646 | Table 3A | Hs.76807 | AF038564 | 2708328 | major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA /cds=(26,790) | 1 | TGCCTGTTGCACATCTTGTAAATTTG GACAATGGCTCTTAGAGAGTTAT |
| 647 | Table 3A | Hs.303627 | AF039575 | 2773157 | heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA-binding protein 1, 37kD) (HNRPD), transcript variant 1, mRNA /cds=(285,1352) | 1 | TGCGGCTAGTTCAGAGAGATTTTAG AGCTGTGGTGGACTTCATAGATGA |
| 648 | Table 3A | Hs.29417 | AF039942 | 4730928 | HCF-binding transcription factor Zhangfei (ZF), mRNA /cds=(457,1275) | 1 | AATGGAAGGATTAGTATGGCCATTTT TTAAAGCTGCTTTGTTAGGTTCT |
| 649 | Table 3A | Hs.8185 | AF042284 | 5256829 | CGI-44 protein; sulfide dehydrogenase like (yeast) (CGI-44), mRNA /cds=(76,1428) | 1 | CCATGTGGGCTACTCATGATGGGCTT GATTCTTTGGGAATAATAAATGA |
| 650 | db mining | Hs.298727 | AF042838 | 2815887 | MEK kinase 1 (MEKK1) mRNA, partial cds /cds=(0,4487) | 1 | AACGAGGCCAGTGGGGAACCCCTTAC CTAAGTATGTGATTGACAAATCATG |
| 651 | Table 3A | Hs.82280 | AF045229 | 2906029 | regulator of G-protein signalling 10 (RGS10), mRNA /cds=(43,546) | 1 | CCTCTCAGGACGTGCCGGGTTTATCA TTGCTTTGTTATTGTAAGGACTG |
| 652 | Table 3A | Hs.62112 | AF046001 | 2895869 | zinc finger protein 207 (ZNF207), mRNA /cds=(202,1638) | 1 | CCACTGCCTGAAAGGTTTGTACAGAT GCATGCCACAGTAGATGCCACAT |

Table 8

| | | | | | | | |
|-----|------------|-----------|----------|----------|---|---|-----------------------------|
| 653 | Table 3A | Hs.241520 | AF047002 | 2896145 | transcriptional coactivator ALY mRNA, partial cds /cds=(0,701) | 1 | TTTTGGGATAAATTTTACTGGTTGCTG |
| 654 | Table 3A | Hs.132904 | AF047033 | 5051627 | sodium bicarbonate cotransporter 3 (SLC4A7) mRNA, complete cds /cds=(71,3715) | 1 | TTGTGGAGAGGTTGGCGTTTCCA |
| 655 | Table 3A | Hs.50785 | AF047442 | 3335139 | SEC22, vesicle trafficking protein (S. cerevisiae)-like 1 (SEC22L1), mRNA /cds=(119,766) | 1 | TGAAGTATAAGCCTCTACTGGGTCTA |
| 656 | Table 3A | Hs.40323 | AF047472 | 2921872 | BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog (BUB3), mRNA /cds=(70,1056) | 1 | TATTGTGAATCATCCTGCCTTTCA |
| 657 | Table 3A | Hs.26584 | AF051782 | 2947237 | diaphanous 1 (HDIA1) mRNA, complete cds /cds=(0,3746) | 1 | CTCGTCTATTGGCCCCGTGAGAAAGT |
| 658 | Table 3A | Hs.313 | AF052124 | 3360431 | secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) (SPP1), mRNA /cds=(87,989) | 1 | TAACCTTTGTTGTTTTCCTTTTAT |
| 659 | Table 3A | Hs.227949 | AF052155 | 3360466 | SEC13 (S. cerevisiae)-like 1 (SEC13L1), mRNA /cds=(60,1028) | 1 | TCCCCTTCTGTCCCCTAGTAAGCCCA |
| 660 | literature | Hs.115770 | AF053712 | 3057145 | tumor necrosis factor (ligand) superfamily, member 11 (TNFSF11), transcript variant 1, mRNA /cds=(156,1109) | 1 | GTTGCTGTATCTGAACAGTTTGAG |
| 661 | Table 3A | Hs.178710 | AF054174 | 3341991 | clathrin, heavy polypeptide (Hc) (CLTC), mRNA /cds=(172,5199) | 1 | AAACCTATTTCCCTTGCCCTCATAGGC |
| 662 | Table 3A | Hs.233952 | AF054185 | 4092057 | proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7), mRNA /cds=(24,770) | 1 | TTCTGGGATGTCATCACCTCCAGT |
| 663 | Table 3A | Hs.158164 | AF054187 | 4092059 | transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) (TAP1), mRNA /cds=(30,2456) | 1 | GAATTTGGTGGTGTCAATTGCTTATTT |
| 664 | Table 3A | Hs.334826 | AF054284 | 4033734 | splicing factor 3b, subunit 1, 155kD (SF3B1), mRNA /cds=(0,3914) | 1 | GTTTCCCACGGTGTGCCAGCAA |
| 665 | Table 3A | Hs.13131 | AF055581 | 3845720 | lymphocyte adaptor protein (LNK), mRNA /cds=(357,2084) | 1 | CTATTTTGGGTCATTTTATGTACCTT |
| 666 | Table 3A | Hs.278501 | AF056322 | 3252910 | SPG-100 (SP100) gene, partial cds; and high mobility group 1-like protein L3 (HMG1L3) retropseudogene sequence /cds=(0,617) | 1 | TGGGTTTCAGGCATTATTTGGGGG |
| 667 | Table 3A | Hs.6856 | AF056717 | 3046994 | ash2 (absent, small, or homeotic, Drosophila, homolog)-like (ASH2L), mRNA /cds=(4,1890) | 1 | TAATTGTTGAACAGGTGTTTTCACACA |
| 668 | Table 3A | Hs.169895 | AF061736 | 4335936 | ubiquitin-conjugating enzyme E2L 6 (UBE2L6), mRNA /cds=(47,508) | 1 | AGTGCCGCAAAATGTACCTTTTT |
| 669 | Table 3A | Hs.182579 | AF061738 | 4335940 | leucine aminopeptidase (LOC51058), mRNA /cds=(186,1745) | 1 | CCCCCTCAGAAGAATCATGAATTTGC |
| 670 | Table 3A | Hs.184592 | AF061944 | 6933863 | protein kinase, lysine deficient 1 (PRKWKN1), mRNA /cds=(0,7148) | 1 | AACAGACCTAATTTTGGTTACTT |
| 671 | Table 3A | Hs.79015 | AF063591 | 12002013 | antigen identified by monoclonal antibody MRC OX-2 (MOX2), mRNA /cds=(57,868) | 1 | GGCCTTTCCATTCCATTATTCACACT |
| 672 | Table 3A | Hs.11000 | AF063605 | 4071360 | MY047 protein (MY047), mRNA /cds=(84,479) | 1 | GAGTGTCTACAATAAACTCCG |
| 673 | Table 3A | Hs.129708 | AF064090 | 3283355 | tumor necrosis factor (ligand) superfamily, member 14 (TNFSF14), mRNA /cds=(48,770) | 1 | TGGTGTCTCAAAGGAGTAAGTCGAGC |
| 674 | Table 3A | Hs.83530 | AF064839 | 4206051 | map 3p21; 3.15 cR from WI-9324 repeat region, complete sequence /cds=UNKNOWN | 1 | TTGGTTTGAAATTTGTACTGTTTC |
| 675 | Table 3A | Hs.4747 | AF067008 | 3873220 | dyskeratosis congenita 1, dyskerin (DKC1), mRNA /cds=(92,1636) | 1 | TGCCAGTAGTACCAAGAACACAGTG |
| 676 | Table 3A | Hs.307357 | AF067519 | 3850317 | PITSLRE protein kinase beta SV1 isoform (CDC2L2) mRNA, complete cds /cds=(79,2412) | 1 | ATTATATACACTATACTGGAGGGA |
| 677 | Table 3A | Hs.307357 | AF067529 | 3850337 | PITSLRE protein kinase beta SV1 isoform (CDC2L2) mRNA, complete cds /cds=(79,2412) | 1 | AGGACACATCTGACATCCTGTGTTTG |
| 678 | Table 3A | Hs.268763 | AF068235 | 4321975 | Breakpoint cluster region protein, uterine leiomyoma, 1; barrier to autointegration factor (BCRP1), mRNA /cds=(507,776) | 1 | GTTAAATATACAGCACATTGTGA |
| 679 | Table 3A | Hs.341182 | AF068836 | 3192908 | 602417256F1 cDNA, 5' end /clone=IMAGE:4536829 /clone_end=5' | 1 | TGGGTTGTGAAATTTGGCATGGAAAT |
| 680 | Table 3A | Hs.92384 | AF070523 | 3764088 | vitamin A responsive; cytoskeleton related (JWA), mRNA /cds=(89,655) | 1 | TTAAAGCAGGTTCTTGTAGTGCA |
| 681 | Table 3A | Hs.151903 | AF070525 | 3387880 | clone 24708 mRNA sequence /cds=UNKNOWN | 1 | TGTGAAAGAACTTGCTTGACGCTTT |
| 682 | Table 3A | Hs.26118 | AF070582 | 3387954 | hypothetical protein MGC13033 (MGC13033), mRNA /cds=(200,304) | 1 | AACAAAATGAGAAACTTCCCAAT |
| 683 | Table 3A | Hs.106823 | AF070635 | 3283905 | mRNA for KIAA1823 protein, partial cds /cds=(52,1185) | 1 | GTATATATCCTCCAGCATTAGTCCA |

Table 8

| | | | | | | | |
|-----|-----------|-----------|----------|---------|---|---|---|
| 684 | Table 3A | Hs.108112 | AF070640 | 3283913 | Homo sapiens, histone fold protein CHRA17; DNA polymerase epsilon p17 subunit, clone MGC:2725 IMAGE:2822216, mRNA, complete cds /cds=(80,523) | 1 | CAGTGAAGATTTGTGAGTGAAGAAT GCTGAGAAGATTGTAATGCTTTGT |
| 685 | Table 3A | Hs.76691 | AF070673 | 3978241 | stannin mRNA, complete cds /cds=(175,441) | 1 | TTGTCTCAAAGCTACCAAGTTTGTGC AATAAGTGAAGGGATGTCATCCT |
| 686 | Table 3A | Hs.223615 | AF070674 | 3978243 | RC2-BN0074-150400-018-c08 cDNA | 1 | ACATCGAAGGTGTGCATATATGTTGA ATGACATTTTAGGGACATGGTGT |
| 687 | Table 3A | Hs.112255 | AF071076 | 4545098 | nucleoporin 98kD (NUP98), mRNA /cds=(124,5262) | 1 | GGCTATCTCAGGCAATATGGCCAGCA CCTGGGTCTTTATGCATGAAGATA |
| 688 | Table 3A | Hs.76095 | AF071596 | 3851531 | immediate early response 3 (IER3), mRNA /cds=(11,481) | 1 | GCTGTACCGGAGCGCATGTCGAGAT CGCCTAGTATGTTCTGTGAACACAA |
| 689 | Table 3A | Hs.18571 | AF072860 | 3290197 | protein kinase, interferon-inducible double stranded RNA dependent activator (PRKRA), mRNA /cds=(96,1037) | 1 | AGCTGCTGACTGTGACTGTCATCCTGT TCTTGTAGCCATTGTGAATAAGA |
| 690 | Table 3A | Hs.79877 | AF072928 | 3916215 | myotubularin related protein 6 mRNA, partial cds /cds=(0,1398) | 1 | CTCACAGGTGGACTGAGAAATCAGTT ACATCTTAAGTGACCTACAGGGTA |
| 691 | Table 3A | Hs.143648 | AF073310 | 4511968 | insulin receptor substrate-2 (IRS2) mRNA, complete cds /cds=(516,4532) | 1 | GTGCATTGTATTAGTCTGTATTGATC ATGGATGCCCTCCTTAATAGCCA |
| 692 | Table 3A | Hs.151411 | AF075587 | 3319325 | KIAA0916 protein (KIAA0916), mRNA /cds=(146,14071) | 1 | CCTGTACAATTGCATCACGGGTGGG GATAAAAAGAGGAATATTCGGTTT |
| 693 | Table 3A | Hs.550 | AF076465 | 5430704 | phosducin (PDC), transcript variant PhLOP2, mRNA /cds=(5,358) | 1 | AAACAGAGCTGTCTTCAGCAACATTA TTAGTAGACAAAGAGGATGTGGAT |
| 694 | Table 3A | Hs.4311 | AF079586 | 4574148 | SUMO-1 activating enzyme subunit 2 (UBA2), mRNA /cds=(25,1947) | 1 | ACTCAAGTTTTCAGTTTGTACCGCCT GGTATGCTGTGTGAAGAGGCAAT |
| 695 | db mining | Hs.159376 | AF080577 | 3551871 | RAG2 mRNA, partial cds /cds=(0,324) | 1 | TGACTCCTGCCAAGAAATCCTTTCTT AGAAGGTTGTTTGATTAGTTTTC |
| 696 | Table 3A | Hs.107979 | AF081282 | 4336324 | small membrane protein 1 (SMP1), mRNA /cds=(99,572) | 1 | TTGTATTATCTGCTTTGCTGATGTAGA CAAGAGTTAACTGAGTAGCATGC |
| 697 | Table 3A | Hs.36794 | AF082569 | 4206702 | cyclin D-type binding-protein 1 (CCNDBP1), mRNA /cds=(87,1172) | 1 | AAAGATTGTTGGTTAGGCCAGATTGA CACCTATTTATAACCATATGCGT |
| 698 | Table 3A | Hs.8765 | AF083255 | 3435311 | RNA helicase-related protein (RNAHP), mRNA /cds=(17,2146) | 1 | TGGTAAGTGTTCAGGATTGCTCCAG GTTTGAGATGGTATTGCTAAATTT |
| 699 | Table 3A | Hs.168913 | AF083420 | 5326765 | serine/threonine kinase 24 (Ste20, yeast homolog) (STK24), mRNA /cds=(78,1373) | 1 | TGCACCTTGTAGTGGATTCTGCATAT CATCTTTCCACCTAAAAATGTCT |
| 700 | Table 3A | Hs.327546 | AF084555 | 5813858 | hypothetical protein MGC10786 (MGC10786), mRNA /cds=(36,169) | 1 | CACCTAGCACTTGTGATGCAATAGAAC ACTTCGCTGTACTGAAAGGGCCA |
| 701 | Table 3A | Hs.211610 | AF090693 | 4249665 | apoptosis-related RNA binding protein (NAPOR-3) mRNA, complete cds /cds=(67,1593) | 1 | ACCGAGGCTTTCCTATTTCTACAAC GATTGTACTTATGCATTTGTACC |
| 702 | Table 3A | Hs.5437 | AF090891 | 6690159 | Tax1 (T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA /cds=(83,2326) | 1 | CAGGAGCTACTTTGAGTTTGGTGTTA CTAGGATCAGGGTCAGTCTTTGGC |
| 703 | Table 3A | Hs.192705 | AF090927 | 6690220 | PRO0457 protein (PRO0457), mRNA /cds=(985,1431) | 1 | TAGAGAGAGGCCCGTGGCCTGAGGT AGTGACAGAGGAGATAGTAGAGCAG |
| 704 | Table 3A | Hs.201675 | AF091263 | 4140646 | RNA binding motif protein 5 (RBM5), mRNA /cds=(148,2595) | 1 | TTTTGGAAGATTTTCAGTCTAGTTGC CAAATCTGGCTCCTTACAAAAGA |
| 705 | Table 3A | Hs.241558 | AF099149 | 3930775 | ariadne (Drosophila) homolog 2 (ARIH2), mRNA /cds=(144,1625) | 1 | AAGTTAATTGAGCAATGTCTATCTGC TCAAAGTTGAGTGGTTTATTCACA |
| 706 | Table 3A | Hs.306357 | AF103458 | 4378245 | isolate donor N clone N168K immunoglobulin kappa light chain variable region mRNA, partial cds /cds=(0,303) | 1 | TTGCAGTGTATTACTGTCAGCAGTAT GGTAGCTCACCGTGGACGTTCCGGC |
| 707 | Table 3A | Hs.184601 | AF104032 | 4426639 | L-type amino acid transporter subunit LAT1 mRNA, complete cds /cds=(66,1589) | 1 | TATTCTGTGTTAATGGCTAACCTGTTA CACTGGGCTGGGTTGGGTAGGGT |
| 708 | Table 3A | Hs.294603 | AF104398 | 4063708 | 601657573R1 cDNA, 3' end /clone=IMAGE:3875611 /clone_end=3' | 1 | AAACTGAATGAGAGAAAATTGTATAA CCATCCTGCTGTTCCCTTTAGTGCA |
| 709 | Table 3A | Hs.7043 | AF104921 | 9409793 | succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA /cds=(31,1032) | 1 | TGACACTGGTCTTGACAGTACAACGG AAGCCAAAACAAGGTGGAAGATGT |
| 710 | Table 3A | Hs.4876 | AF105366 | 5108522 | solute carrier family 12 (potassium/chloride transporters), member 6 (SLC12A6), mRNA /cds=(51,3350) | 1 | GGTCAAGTATATTTGGACCTATTATC CTCGGCAAGCCAAGATGCAACAT |
| 711 | Table 3A | Hs.167460 | AF107405 | 5531903 | pre-mRNA splicing factor (SFRS3) mRNA, complete cds /cds=(95,589) | 1 | AGTTCACAAATATGGTTCAAATGTAAC AGTGCAAGATTGAATATGGAGGCA |
| 712 | Table 3A | Hs.79335 | AF109733 | 4566529 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1 (SMARCD1), mRNA /cds=(265,1572) | 1 | TTGCATCTTTCCAGGAGAGCCTCACA TTCTTCTCCAGGTTGTATCACCC |
| 713 | Table 3A | Hs.274472 | AF113008 | 6642739 | high-mobility group (nonhistone chromosomal) protein 1 (HMG1), mRNA /cds=(52,699) | 1 | GTGAGTCAGGAGCAGGAGCGTGCGG ACCAAAAATCCTCAGCCCTTACGAC |

Table 8

| | | | | | | | |
|-----|-----------|-----------|-----------|----------|---|---|---|
| 714 | Table 3A | Hs.180946 | U66589 | 1575566 | ribosomal protein L5 pseudogene mRNA, complete cds /cds=UNKNOWN | 1 | TCACCTTATGCAATGTGAATTATCACT ACAGAACTCCATCTTACTCCAGA |
| 715 | Table 3A | Hs.109441 | AF113213 | 11640573 | cDNA FLJ14235 fis, clone NT2RP4000167 /cds=(82,2172) | 1 | TTTGATGTAATATAACCTAACGTTGTG CTGGTACCTGTTTTACCATGTGT |
| 716 | Table 3A | Hs.297681 | AF113676 | 6855600 | clone FLB2803 PRO0684 mRNA, complete cds /cds=(1108,2364) | 1 | CTCCATCCCTGGCCCCCTCCCTGGAT GACATTAAAGAAAGGGTTGAGCTGG |
| 717 | Table 3A | Hs.297681 | AF113676 | 6855600 | clone FLB2803 PRO0684 mRNA, complete cds /cds=(1108,2364) | 1 | CTCCATCCCTGGCCCCCTCCCTGGAT GACATTAAAGAAAGGGTTGAGCTGG |
| 718 | Table 3A | Hs.75117 | AF113702 | 6855636 | interleukin enhancer binding factor 2, 45kD (ILF2), mRNA /cds=(39,1259) | 1 | GGCTTAGCTGCCAGTCTCCCATTTGT GACCTATGCCATCCATCTATAATG |
| 719 | Table 3A | Hs.177415 | AF116606 | 7959715 | PRO0890 mRNA, complete cds /cds=(1020,1265) | 1 | GGCCCCAATGCCAATCTTAAGTCTT TTGTAATCTGGCTTTCTCTAATA |
| 720 | Table 3A | Hs.321158 | AF116620 | 8924006 | hypothetical protein PRO1068 (PRO1068), mRNA /cds=(1442,1750) | 1 | TGTCAGGTTTGGGCTTGGGTTCAAG TGTATATATTCCTGTAAGTTTCTT |
| 721 | Table 3A | Hs.288036 | AF116679 | 7959856 | tRNA isopentenylpyrophosphate transferase (IPT), mRNA /cds=(60,1040) | 1 | TGCATCGTAAAACCTTCAGAAGGAAA GGAGAATGTTTTGTGGACCACTTT |
| 722 | Table 3A | Hs.238205 | AF116682 | 7959862 | PRO2013 mRNA, complete cds /cds=(135,380) | 1 | TTGACATTCTGCGAAAGCAACAAGCA AACTGAAGACCAACTCCTATGAGA |
| 723 | Table 3A | Hs.83583 | NM_005731 | 5031598 | actin related protein 2/3 complex, subunit 2 (34 kD) (ARPC2), mRNA /cds=(84,986) | 1 | CGCCTCTTCAGGTTCTTAAGGGATTCT TCCGTTTTGGTTCATTTTGTACA |
| 724 | Table 3A | Hs.128740 | AF118274 | 4680228 | DNb-5 mRNA, partial cds /cds=(0,1601) | 1 | CCTTGTTGGACAGGGGACAGGCTG CCTACTGGAATGTAAATATGTGATA |
| 725 | Table 3A | Hs.225939 | AF119417 | 7670074 | sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) (SIAT9), mRNA /cds=(277,1365) | 1 | TTTCTGAATGCCTACCTGGCGGTGTA TACCAGGCAGTGTCACGTTTAAA |
| 726 | Table 3A | Hs.184011 | AF119665 | 6563255 | pyrophosphatase (inorganic) (PP), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,946) | 1 | TGTGCAAGGGGAGCACATATTGGAT GTATATGTTACCATATGTTAGGAAA |
| 727 | Table 3A | Hs.2186 | AF119850 | 7770136 | Homo sapiens, eukaryotic translation elongation factor 1 gamma, clone MGC:4501 IMAGE:2964623, mRNA, complete cds /cds=(2278,3231) | 1 | TCAAGTGAACATCTCTTGCCATCACC TAGCTGCCTGCACCTGCCCTTCAG |
| 728 | Table 3A | Hs.111334 | AF119897 | 7770230 | PRO2760 mRNA, complete cds /cds=UNKNOWN | 1 | CCGAGGAGAAAGCGCGAGGGCTACGA GCGTCTCCTGAAGATGCAAAACCAG |
| 729 | Table 3A | Hs.9851 | AF123073 | 12698331 | C/EBP-induced protein (LOC81558), mRNA /cds=(30,1391) | 1 | GCAGCTGTTTGAAGTTTGTATATTTTC CGTACTGCAGAGCTTACACAAAA |
| 730 | Table 3A | Hs.180566 | AF123094 | 5669089 | mucosa associated lymphoid tissue lymphoma translocation gene 1 (MALT1), mRNA /cds=(164,2638) | 1 | GCCTGTGAAATAGTACTGCATTTACA TAAAGTGAGACATTGTGAAAAGGC |
| 731 | Table 3A | Hs.7540 | AF126028 | 7158285 | unknown mRNA /cds=(0,1261) | 1 | GCTCTGATTGTACAAGAATTACCTGT GCTAGTCAAGTTGTTGTTTTCTCT |
| 732 | Table 3A | Hs.15259 | AF127139 | 6724085 | BCL2-associated athanogene 3 (BAG3), mRNA /cds=(306,2033) | 1 | CTGTCTTTTGTAGCTCTGGACTGGAG GGGTAGATGGGGAGTCAATTACCC |
| 733 | Table 3A | Hs.304177 | AF130085 | 11493474 | clone FLB8503 PRO2286 mRNA, complete cds /cds=UNKNOWN | 1 | GGTACAACCTTCCAATTTCTTCCAT GCGGACCCCTCCTGCCAAAAGA |
| 734 | Table 3A | Hs.279789 | AF130094 | 11493492 | histone deacetylase 3 (HDAC3), mRNA /cds=(55,1341) | 1 | GCAATTCTCCCTGCGTCATGGATTTC AAGGCTTTTTAATCACCTTCGGTT |
| 735 | Table 3A | Hs.6456 | AF130110 | 11493523 | clone FLB6303 PRO1633 mRNA, complete cds /cds=(2546,3097) | 1 | CCTTCGCTTTAATCATAGTCTAATTTA TTTGCCGTGCCATTTTCCATACA |
| 736 | Table 3A | Hs.333555 | AF131753 | 4406571 | cytoplasmic protein mRNA, complete cds /cds=(236,3181) | 1 | TGGTTGGAAGTGGGTGGGTTATGA AATTGATAGTGTTTTAGAAAAACT |
| 737 | Table 3A | Hs.64001 | AF131762 | 4406584 | clone 25218 mRNA sequence /cds=UNKNOWN | 1 | ACCTTCCTCCAGGAAAAGCCATTCAA GCCTGATTATTTTCTAAGTAACT |
| 738 | Table 3A | Hs.8148 | AF131856 | 4406702 | selenoprotein T (LOC51714), mRNA /cds=(138,629) | 1 | CTGTATAGCTTTCCACCTCCACACA AAATCACCCAGTTAATGTGTGTGT |
| 739 | Table 3A | Hs.301824 | AF132197 | 11493539 | hypothetical protein PRO1331 (PRO1331), mRNA /cds=(422,616) | 1 | GGGGTACCTGTGTTGAGTTGATAAAC ATTTCATCTTCATTAACCTGCT |
| 740 | Table 3A | Hs.79933 | AF135162 | 7259481 | cyclin I (CCNI), mRNA /cds=(0,1133) | 1 | TGTCCACCTTTCAGCCTGTTTCTGT CATGTAGTTTCAACAAGTGCTACC |
| 741 | Table 3A | Hs.160417 | AF137030 | 6649056 | transmembrane protein 2 (TMEM2), mRNA /cds=(148,4299) | 1 | ATGCTACCTCAAAGTGCTACCGATAA ACCTTTCTAATTGTAAGTGCCCTT |
| 742 | Table 3A | Hs.70337 | AF138903 | 7767238 | nectin-like protein 2 (NECL2) mRNA, complete cds /cds=(3,1331) | 1 | AGCACCCATTCCGACCATGATATAAT CATATCAAAGGGTGAGAATCATTT |
| 743 | Table 3A | Hs.65450 | AF148537 | 10039550 | reticulin 4a mRNA, complete cds /cds=(141,3719) | 1 | TGTGGTTTAAGCTGTACTGAACTAAA TCTGTGGAATGCATTGTGAACCTGT |
| 744 | Table 3A | Hs.334466 | AF151049 | 7106819 | hypothetical protein (LOC51245), mRNA /cds=(0,359) | 1 | ATTACGAACAGTAAACGAGGAG GACATGGAGTGACTATCGGGGCGG |
| 745 | Table 3A | Hs.278429 | AF151054 | 7106829 | hepatocellular carcinoma-associated antigen 59 (LOC51759), mRNA /cds=(27,896) | 1 | TCCTCCAGCTGACAGAAAAATCCAGG ATGAGATCAGAAGGATACTGGTGT |
| 746 | db mining | Hs.274509 | AF151103 | 5758136 | T-cell receptor aberrantly rearranged gamma-chain mRNA from cell line HPB-MLT /cds=UNKNOWN | 1 | TTTACACGCCCTGAAGCAGTCTTCTT TGCTAGTTGAATTATGGTGTGT |
| 747 | Table 3A | Hs.279918 | AF151875 | 4929702 | hypothetical protein (HSPC111), mRNA /cds=(62,598) | 1 | GTTTCACGGAAAAGCCAGAACCTGCT GTTTTCAGGGTGGGTGATGTAATA |

Table 8

| | | | | | | | |
|-----|------------|-----------|----------|----------|--|---|---|
| 748 | Table 3A | Hs.31323 | AF153419 | 13133509 | IkappaBkinase complex-associated protein (IKBKAP) mRNA, complete cds /cds=(310,4308) | 1 | AGTGCTCTTGCTTTGGATAACTGTAA AGGGACCCATGCTGATAGACTGGA |
| 749 | Table 3A | Hs.296323 | AF153609 | 5231142 | serum/glucocorticoid regulated kinase (SGK), mRNA /cds=(42,1337) | 1 | TGCCCCAGTTGTGTCAGTCAGAGCCGTT GGTGTTTTTTCATTGTTTAAAATGT |
| 750 | Table 3A | Hs.22350 | AF157116 | 8571911 | cDNA: FLJ23595 fis, clone LNG15262 /cds=UNKNOWN | 1 | AAACCAATGGACAAACTCTTGTCTTC AAGGAACAAACTCTTAGGTTGGCA |
| 751 | Table 3A | Hs.5548 | AF157323 | 7688696 | p45SKP2-like protein mRNA, complete cds /cds=(37,2081) | 1 | AAACATCATGAGAGTGAGGAGGCTGTC CACCCAGAAAGGCACATACCTAGTGC |
| 752 | Table 3A | Hs.19807 | AF161339 | 6841091 | rho-gtpase activating protein ARHGAP9 (ARHGAP9), mRNA /cds=(406,2658) | 1 | AGTGGATTAACCCCTGCTTCTCTTCT TGTTCCCTGTTATCATCTCTCCCT |
| 753 | Table 3A | Hs.259683 | AF161364 | 6841141 | HSPC101 mRNA, partial cds /cds=(0,556) | 1 | GTCTGCTTATTGCTGTCTCTTACTAG GTTCAATTTCTTGGAGGCCGTGAT |
| 754 | Table 3A | Hs.180145 | AF161415 | 6841243 | HSPC297 mRNA, partial cds /cds=(0,438) | 1 | TGGCTGACTGACATGACGTCCATA AATGCAGATGTTTGTCTCATTACG |
| 755 | Table 3A | Hs.339814 | AF161430 | 6841273 | nt85d12.s1 cDNA /clone=IMAGE:1205303 | 1 | GCCAGACTTGAAAGAGGCGCTCAGA AAAAGTAGATGCGTATCTGTACAAA |
| 756 | Table 3A | Hs.284295 | AF161451 | 6841315 | HSPC333 mRNA, partial cds /cds=(0,443) | 1 | CGCTTAAATGTTACCGTCCACAGCT TTGGAATAAACCATCTCTGGGAAGT |
| 757 | Table 3A | Hs.284295 | AF161455 | 6841323 | HSPC333 mRNA, partial cds /cds=(0,443) | 1 | TTAATGTTTACCGTCCACAGCTTTGG AATAAACCATCTCTGGGAAGTTGCT |
| 758 | Table 3A | Hs.284162 | AF165521 | 9294748 | 60S ribosomal protein L30 isolog (LOC51187), mRNA /cds=(143,634) | 1 | TCTAGCCAGCATTTGATCTAGAAGCA GAGGAATCCAGCGCCTTTTAAAA |
| 759 | Table 3A | Hs.283740 | AF173296 | 9622516 | DC6 protein (DC6), mRNA /cds=(161,466) | 1 | TTGCTCAGCATGCCAGCCTTTAAGAT TGAATTAGATTGTGTTGTGTGCT |
| 760 | Table 3A | NA | AF173954 | 6002958 | Cloning vector pGEM-URA3 | 1 | AAAAGGTATAGAAATGCTGGTTGGAA TGCTTATTTGAAAAGACTGGCCA |
| 761 | Table 3A | Hs.81001 | AF174605 | 6164752 | F-box protein Fbx25 (FBX25) mRNA, partial cds /cds=(0,818) | 1 | CTGCTTCACGCGCTGTCTCCGCGAGC ACTTCATCGAGCTCTTCAAGTTT |
| 762 | Table 3A | Hs.288836 | AF176706 | 6573265 | hypothetical protein FLJ12673 (FLJ12673), mRNA /cds=(2,1687) | 1 | AGAGCAGCTTGTGTATGTAACGCTT CAGTGAACCTGCTAATGATCCAAAT |
| 763 | Table 3A | Hs.250619 | AF182420 | 10197639 | phorbol-like protein MDS019 (MDS019), mRNA /cds=(231,1385) | 1 | TCAAACCTACTAATCCAGCGACAATT TGATCGGTTTTGTAGGTAGAGGA |
| 764 | Table 3A | Hs.279789 | AF187554 | 6653225 | histone deacetylase 3 (HDAC3), mRNA /cds=(55,1341) | 1 | TCAACCTCCGTCATGTTTAAAGAACCC TTTTATCTTTTCTCTGCTATGCT |
| 765 | Table 3A | Hs.49163 | AF189011 | 8886721 | ribonuclease III (RN3) mRNA, complete cds /cds=(245,4369) | 1 | TTTCCATCTGTGTCCAGATTGTGAC CCTAGACTTTCAATTGACAGGTAA |
| 766 | Table 3A | Hs.106778 | AF189723 | 6826913 | calcium transport ATPase ATP2C1 (ATP2C1A) mRNA, complete cds /cds=(202,2913) | 1 | CATGTCGTTAGATGGAACATGGAAGC CATTGTCTAATCAACTCTATCATT |
| 767 | Table 3A | Hs.102506 | AF193339 | 7341090 | eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), mRNA /cds=(72,3419) | 1 | ATGTAATCCTGTAGGTTGGTACTTCC CCCCAACTGATTATAGGTAACAGT |
| 768 | Table 3A | Hs.179573 | AF193556 | 6907041 | collagen, type I, alpha 2 (COL1A2), mRNA /cds=(139,4239) | 1 | TGAATGATCAGAACTGACATTTAATTC ATGTTTGTCTCGCCATGCTTCTT |
| 769 | Table 3A | Hs.126550 | AF195514 | 11225484 | VPS4-2 ATPase (VPS42) mRNA, complete cds /cds=(201,1535) | 1 | TTTGACATTTTACATATGCTATGTGG TTGCCTTTGGGTTTCTGTACAG |
| 770 | Table 3A | Hs.56542 | AF195530 | 9739016 | Homo sapiens, X-prolyl aminopeptidase (aminopeptidase P) 1, soluble, clone MGC:15561 IMAGE:3139868, mRNA, complete cds /cds=(140,2011) | 1 | TGGTCATGTTCCAGGTGCTAGTACAT CATTGATGATCACCTTAATGCTCA |
| 771 | Table 3A | Hs.44143 | AF197569 | 11385353 | BAF180 (BAF180) mRNA, complete cds /cds=(96,4844) | 1 | AGCATAAAGAGTTGTGGATCAGTAGC CATTTTAGTTACTGGGGTGGGGG |
| 772 | Table 3A | Hs.160999 | AF198614 | 7582270 | AV648418 cDNA, 3' end /clone=GLCBJC04 /clone_end=3' | 1 | TCAACACTTGTCTTTATTGACACAAC CAGACTTTCTCAGTTCTCTGTTCT |
| 773 | Table 3A | Hs.26367 | AF202092 | 11493699 | PC3-96 protein (PC3-96), mRNA /cds=(119,586) | 1 | ATGAAGAAAAATCAATGAGACTGTTGC AGAAGGAGGGGAGAACTTGGAGT |
| 774 | Table 3A | Hs.182982 | AF204231 | 6808610 | 88-kDa Golgi protein (GM88) mRNA, complete cds /cds=(342,2237) | 1 | ACTGAAAGACTTTTGCTTAAAGTGGC ATTATTGACTGCTGATGTGATGCT |
| 775 | Table 3A | Hs.197298 | AF205218 | 12003206 | NS1-binding protein-like protein mRNA, complete cds /cds=(555,2483) | 1 | TTGGTTGGTAACCTCTGTAATCTCTAA CTATCACTGTTTGGTCTGGACT |
| 776 | Table 3A | Hs.155530 | AF208043 | 6644296 | IFI16b (IFI16b) mRNA, complete cds /cds=(264,2312) | 1 | CCACCATATATACTAGCTGTTAATCCT ATGGAATGGGGTATTGGGAGTGC |
| 777 | literature | Hs.185708 | AF208502 | 6630993 | early B-cell transcription factor (EBF) mRNA, partial cds /cds=(0,1761) | 1 | AGAGGAATCTGAAAGTGACGGGTGTT GGTTAAAGTTGTACCTCCCAAGTA |
| 778 | Table 3A | Hs.5862 | AF208844 | 7582275 | hypothetical protein (BM-002), mRNA /cds=(39,296) | 1 | TTTTTCTCCATCCTGTTTCTAGCACAA AAATTTGCCTGCTGTGTACAA |
| 779 | Table 3A | Hs.82911 | AF208850 | 7582287 | BM-008 mRNA, complete cds /cds=(341,844) | 1 | CAGATTGATTGAAAGGTGTGTCAGCC TGATTTAAACCAAAACCCTGAACC |
| 780 | Table 3A | Hs.12830 | AF208855 | 7582297 | hypothetical protein (LOC51320), mRNA /cds=(67,459) | 1 | GCAACTAATAAGCCAAGGAATCGACA TATATTAGGTGCGTGTACTGTTTCT |
| 781 | Table 3A | Hs.295231 | AF212224 | 9437514 | CLK4 mRNA, complete cds /cds=(153,1514) | 1 | TGTCAGTGATAAATGTGATTGATCT TGCTTTTGTACATGGAGGTCAAC |
| 782 | Table 3A | Hs.284162 | AF212226 | 13445483 | 60S ribosomal protein L30 isolog (LOC51187), mRNA /cds=(143,634) | 1 | TCTAGCCAGCATTTGATCTAGAAGCA GAGGAATCCAGCGCCTTTTAAAA |
| 783 | Table 3A | Hs.68644 | AF212233 | 13182746 | microsomal signal peptidase subunit mRNA, complete cds /cds=(57,635) | 1 | AGGGAACAGTGTGGAGATGTTTTTGT CTTGTCCAAATAAAAGATTACCA |
| 784 | Table 3A | Hs.332404 | AF212241 | 13182760 | CDA02 protein (CDA02), mRNA /cds=(2,1831) | 1 | ACCCATTGGTATACAGAAATATTC TGTGCCACACTTAATGTCAATCT |

Table 8

| | | | | | | | |
|-----|----------|-----------|----------|----------|--|---|-----------------------------|
| 785 | Table 3A | Hs.9414 | AF217190 | 11526792 | MLEL1 protein (MLEL1) mRNA, complete cds /cds=(73,3099) | 1 | TTGATGATACCACCAGTAAAAATAGG |
| 786 | Table 3A | Hs.288850 | AF220656 | 7107358 | cDNA: FLJ22528 fis, clone HRC12825 /cds=UNKNOWN | 1 | TTTCAACCGAAAGGGGAGATCCAATA |
| 787 | Table 3A | Hs.46847 | AF223489 | 7578788 | TRAF and TNF receptor-associated protein (AD022), mRNA /cds=(16,1104) | 1 | GAAGACCCGCTCCTTAAATAAACA |
| 788 | Table 3A | Hs.79025 | AF226044 | 9295326 | HSNFRK (HSNFRK) mRNA, complete cds /cds=(641,2938) | 1 | ACAGAGGGCAAAGTTAAGCTTGATGAT |
| 789 | Table 3A | Hs.112242 | AF228422 | 12656020 | normal mucosa of esophagus specific 1 (NMES1), mRNA /cds=(189,440) | 1 | GGTTAAAAATCGGTTTGATAGCACC |
| 790 | Table 3A | Hs.55173 | AF231023 | 7407145 | cadherin, EGF LAG seven-pass G-type receptor 3, flamingo (Drosophila) homolog (CELSR3), mRNA /cds=(281,10219) | 1 | TGTTGATTTCCCTCATTGTGTAAAC |
| 791 | Table 3A | Hs.4788 | AF240468 | 9992877 | nicastrin mRNA, complete cds /cds=(142,2271) | 1 | ATTGACAGGTATGTGACAAATGGG |
| 792 | Table 3A | Hs.196015 | AF241534 | 9502099 | hydatidiform mole associated and imprinted (HYMAI) mRNA, complete sequence /cds=UNKNOWN | 1 | CACAACTAGATTCTGGACACCAAGTG |
| 793 | Table 3A | Hs.81897 | AF241785 | 12005486 | NPD012 (NPD012) mRNA, complete cds /cds=(552,2252) | 1 | TGCGGAAATGCTTCTGCTACATTT |
| 794 | Table 3A | Hs.153042 | AF244129 | 10197716 | cell-surface molecule Ly-9 mRNA, complete cds /cds=(30,1994) | 1 | GGCCCTCTTCTGTCTGTGTAATTT |
| 795 | Table 3A | Hs.20597 | AF244137 | 7670839 | host cell factor homolog (LCP), mRNA /cds=(316,1536) | 1 | GTTCCGTGAAGCGCGCTCTGTTT |
| 796 | Table 3A | Hs.145956 | AF246126 | 8571416 | zinc finger protein mRNA, complete cds /cds=(1073,3133) | 1 | CACTGTCTTTCTCCAGGCCCTCAGA |
| 797 | Table 3A | Hs.239625 | AF246221 | 7659294 | integral membrane protein 2B (ITM2B), mRNA /cds=(170,970) | 1 | TGGCACATTAGGGTGGGCGTGCCTG |
| 798 | Table 3A | Hs.6289 | AF246238 | 12005510 | hypothetical protein FLJ20886 (FLJ20886), mRNA /cds=(0,524) | 1 | AGGAGCTATGATTAGACTTCTGTTAG |
| 799 | Table 3A | Hs.81248 | AF248648 | 9246972 | CUG triplet repeat, RNA-binding protein 1 (CUGBP1), mRNA /cds=(137,1585) | 1 | ACTTCTCACTCTATCACCACAT |
| 800 | Table 3A | Hs.81248 | AF248648 | 9246972 | CUG triplet repeat, RNA-binding protein 1 (CUGBP1), mRNA /cds=(137,1585) | 1 | ACCCACTTTCTCCTTGGTAAAGCGTT |
| 801 | Table 3A | Hs.183434 | AF248966 | 12005668 | ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M8-9 (APT6M8-9), mRNA /cds=(102,1154) | 1 | TACTTAACAAAATAATACCCGAGA |
| 802 | Table 3A | Hs.24125 | AF251039 | 7547030 | putative zinc finger protein (LOC51780), mRNA /cds=(744,4997) | 1 | GTACACATGACACAGATGTACATA |
| 803 | Table 3A | Hs.103521 | AF254411 | 9438032 | ser/arg-rich pre-mRNA splicing factor SR-A1 (SR-A1) gene | 1 | ATATCATGCTCACGCTTGGAGTGT |
| 804 | Table 3A | Hs.42949 | AF260237 | 14009497 | hypothetical protein HES6 (HES6), mRNA /cds=(0,674) | 1 | ATGTGCATGTGAATGGCCTAGAGAAC |
| 805 | Table 3A | Hs.174131 | AF261087 | 9802305 | ribosomal protein L6 (RPL6), mRNA /cds=(26,892) | 1 | CTATTTTGTGTCTAAAGTTTACA |
| 806 | Table 3A | Hs.153612 | AF261091 | 10179833 | iron inhibited ABC transporter 2 mRNA, complete cds /cds=(111,1982) | 1 | AGATCCTGTCTCCTTTAGCCTCACT |
| 807 | Table 3A | Hs.44198 | AF263613 | 8453173 | membrane-associated calcium-independent phospholipase A2 gamma mRNA, complete cds /cds=(225,2573) | 1 | AATCAAGTTGGGTCCTATCTTCCC |
| 808 | Table 3A | Hs.107707 | AF265439 | 12005981 | mitochondrial ribosomal protein S15 (MRPS15), mRNA /cds=(0,851) | 1 | AGTTGTAGTTGCCCTGTACCTAGT |
| 809 | Table 3A | Hs.8084 | AF267856 | 12006038 | HT033 mRNA, complete cds /cds=(203,931) | 1 | TTGTTAGTGCTTTCGATACACAT |
| 810 | Table 3A | Hs.8084 | AF267856 | 12006038 | HT033 mRNA, complete cds /cds=(203,931) | 1 | AATCCTTTAACTCTGCGGATAGCATT |
| 811 | Table 3A | Hs.77690 | AF267863 | 12006052 | RAB5B, member RAS oncogene family (RAB5B), mRNA /cds=(20,667) | 1 | TGGTAGGTAGTGATTAACTGTGAA |
| 812 | Table 3A | Hs.8203 | AF269150 | 9755050 | endomembrane protein emp70 precursor isolog (LOC56889), mRNA /cds=(19,1779) | 1 | GGAGGAGGAGCTTATTTCTTGGTGTA |
| 813 | Table 3A | Hs.267288 | AF271994 | 8515856 | dopamine responsive protein DRG-1 mRNA, complete cds /cds=(15,938) | 1 | CTTGAATCAGAAGGTCCTGCAAG |
| 814 | Table 3A | Hs.147644 | AF272148 | 8575774 | zinc finger protein 331; zinc finger protein 463 (ZNF361), mRNA /cds=(376,1767) | 1 | AAGTGAAGTGGGTGAATTTCTACTTT |
| 815 | Table 3A | Hs.339912 | AF277292 | 9664852 | qh07h06.x1 cDNA, 3' end /clone=IMAGE:1844027 /clone_end=3' | 1 | TTATGTTGGAGTGGACCAATGTCT |
| 816 | Table 3A | Hs.287369 | AF279437 | 10719561 | Interleukin 22 (IL22), mRNA /cds=(71,610) | 1 | TGGGATTGATTGGCCCATAGGTACAT |
| 817 | Table 3A | Hs.196270 | AF283645 | 11545416 | folate transporter/carrier (LOC81034), mRNA /cds=(128,1075) | 1 | TGGAATGTATATCTCTCCAGCT |

Table 8

| | | | | | | | |
|-----|----------|-----------|----------|----------|--|---|---|
| 818 | Table 3A | Hs.324278 | L08048.1 | 184250 | mRNA; cDNA DKFZp566M063 (from clone DKFZp566M063) /cds=UNKNOWN | 1 | TGGGGGTTGTAAATGGCATGGAAAT TTAAAGCAGGTTCTTGTGGTGCA |
| 819 | Table 3A | Hs.116481 | AF283777 | 10281735 | CD72 antigen (CD72), mRNA /cds=(108,1187) | 1 | GATAGGGGCGGCCCGGAGCCAGCCA GGCAGTTTTATTGAAATCTTTTTAA |
| 820 | Table 3A | Hs.283022 | AF287008 | 9624485 | triggering receptor expressed on myeloid cells 1 (TREM1), mRNA /cds=(47,751) | 1 | CATTTGTACCTAGGCCACGAAACCC ACGAGAATGTCTCTGACTTCCAG |
| 821 | Table 3A | Hs.44865 | AF288571 | 9858157 | lymphoid enhancer factor-1 (LEF1) mRNA, complete cds /cds=(654,1853) | 1 | AGTGGGATTTTATGCCAGTTGTTAAA ATGAGCATTGATGTACCCATTTT |
| 822 | Table 3A | Hs.212172 | AF294900 | 10242315 | beta-carotene 15,15'-dioxygenase (BCDO), mRNA /cds=(218,1861) | 1 | CTTTCCTTTGCTCCCTCCCATGTTTCT GGTGGACTAAATTGTGTATCTGG |
| 823 | Table 3A | Hs.7886 | AF302505 | 10242358 | pellino (Drosophila) homolog 1 (PEL1), mRNA /cds=(4038,5294) | 1 | AGTTTTCTAGATTGTGCATGCTTTGT GACTAATGCAAGAAAGCAAGTCC |
| 824 | Table 3A | Hs.47783 | AF307339 | 12751140 | B aggressive lymphoma gene (BAL), mRNA /cds=(228,2792) | 1 | GAAACACTTTCAGGACCTTCTTCTCT CTTGCACTTGTCTTTTAATCTCT |
| 825 | Table 3A | Hs.250528 | AF308285 | 12060321 | Homo sapiens, clone IMAGE:4098694, mRNA, partial cds /cds=(0,2501) | 1 | CTCGAGGGGCCAATTACAGGAGCAC AGGAAGGTTCTGATTACACACCTCT |
| 826 | Table 3A | Hs.153057 | AF311312 | 10863767 | infertility-related sperm protein mRNA, complete cds /cds=(198,2978) | 1 | TTGAGTTAAGTTGCATTTCTTTGGGC TATGAAGGAGTCTCTTAAAGTTTG |
| 827 | Table 3A | Hs.6151 | AF315591 | 11139703 | pumilio (Drosophila) homolog 2 (PUM2), mRNA /cds=(23,3217) | 1 | AGGGATTGTTTCTGGACCAGTTTGTG TAAGTCTGCTCTTATTGGTTCA |
| 828 | Table 3A | Hs.194976 | AF319438 | 12667351 | SH2 domain-containing phosphatase anchor protein 1 (SPAP1), mRNA /cds=(303,1070) | 1 | TGAAGTCTGCTACATCCAGACACTG TGCAAATAAATTATTCTGTCTACC |
| 829 | Table 3A | Hs.36752 | AF319476 | 11762083 | protein kinase anchoring protein GKAP42 (GKAP42), mRNA /cds=(174,1274) | 1 | ACTATGCAGTTTTCTTGAAGGAACT AAAAGCAACTAGCTCCCTAATGGT |
| 830 | Table 3A | Hs.114309 | AF323540 | 12408012 | apolipoprotein L-1 mRNA, splice variant B, complete cds /cds=(273,1517) | 1 | GTCTTTCCAGCATCCACTCTCCCTTG TCCTCTGGGGGCATATCTCAGTC |
| 831 | Table 3A | Hs.27721 | AF332469 | 12642816 | Wolf-Hirschhorn syndrome candidate 1-like 1 (WHSC1L1), transcript variant long, mRNA /cds=(518,4831) | 1 | GCAGTAGGTAGGCTCACTTCTCTTTTC CCTTCAAAATGCTTTTCATAGGCT |
| 832 | Table 3A | Hs.203181 | AF333025 | 13936737 | Bv8 protein (BV8) mRNA, partial cds /cds=(0,356) | 1 | TCTGCTGTTGGGCTGGTGTGGGAC AGAAGGAATGGAAAGCCAAATTAAT |
| 833 | Table 3A | NA | AI904802 | 6495189 | 1q12-21.2 Contains a cyclophilin-like gene, a novel gene, ESTs, GSSs and STS | 1 | CCACTTGGAATAGGAATATCACCCCT ATCTTGGAAGACCAGGTGGAGGCT |
| 834 | Table 3A | Hs.5122 | AJ001235 | 12418001 | 602293015F1 cDNA, 5' end /clone=IMAGE:4387778 /clone_end=5' | 1 | GCCCTATGGCGTTGTTAAACACGAGC GTATGCTAGTAAGTATCATTCATA |
| 835 | Table 3A | Hs.9071 | AJ002030 | 2570006 | progesterone receptor membrane component 2 (PGRMC2), mRNA /cds=(6,677) | 1 | GTGGGTGCATGGGGCTGTGGAGTGG GTGTACAGTATGGATGTGTCTGAATG |
| 836 | Table 3A | Hs.196769 | AJ006835 | 3236105 | RNA transcript from U17 small nucleolar RNA host gene, variant U17HG-AB /cds=UNKNOWN | 1 | CATTGCTGTATGCCAGTCCCATC CGTGTCTGCTGTAACATACATAGA |
| 837 | Table 3A | Hs.181461 | AJ009771 | 3646273 | ariadne (Drosophila) homolog, ubiquitin-conjugating enzyme E2-binding protein, 1 (ARIH1), mRNA /cds=(314,1987) | 1 | TGTCTGCTCTTCCATTTTCTCGTCTC TCTCCCTCTTCCCCATTATCC |
| 838 | Table 3A | Hs.18259 | AJ010842 | 3646129 | XPA binding protein 1; putative ATP(GTP)-binding protein (NTPBP), mRNA /cds=(24,1148) | 1 | TGGGCAAGACATGATTAATGAATCAG AATCCTGTTTCATTGGTGACTTGG |
| 839 | Table 3A | Hs.109281 | AJ011895 | 3758818 | Nef-associated factor 1 (NAF1), mRNA /cds=(110,2017) | 1 | CCAGATTAGGGTGGCTGTCCATCCCT GGATAGCTATTTGCACGAATCATG |
| 840 | Table 3A | Hs.306328 | AJ012504 | 5441364 | mRNA activated in tumor suppression, clone TSAP13 extended /cds=UNKNOWN | 1 | CGGAGCTCTGCTCTGCTGTAGGAA GCCCGGTACGCTTCATGACAGCA |
| 841 | Table 3A | Hs.118958 | AJ012506 | 5441365 | syntaxin 11 (STX11), mRNA /cds=(183,1046) | 1 | GCACTGAATATCGAACAAGCACTCAA ATTGAAGTATCAGTCATGTTTTGT |
| 842 | Table 3A | Hs.58103 | AJ131693 | 4584422 | mRNA for AKAP450 protein /cds=(222,11948) | 1 | AGCTCGAGGTGCTCCTGCACCTTTTCT ATAAGGCTACTGAAGTTACATGTT |
| 843 | Table 3A | Hs.59757 | AJ132592 | 6822171 | zinc finger protein 281 (ZNF281), mRNA /cds=(23,2710) | 1 | TGCCATTGGAATGTTTCTACACGATC CTATTAAGAAATATGTGATGCCCT |
| 844 | Table 3A | Hs.326159 | AJ223075 | 3355596 | leucine rich repeat (in FLII) interacting protein 1 (LRRFIP1), mRNA /cds=(178,2532) | 1 | GGATAACAAGTAATGTCTGAAGCA TGAGGGGCTTATTGCTTTACC |
| 845 | Table 3A | Hs.137548 | AJ223324 | 3392916 | CD84 antigen (leukocyte antigen) (CD84), mRNA /cds=(44,1030) | 1 | TGTTTTCTCACTACATTGTACATGTG GGAATTACAGATAAACGGAAGCC |
| 846 | Table 3A | Hs.333140 | AJ225093 | 3090427 | mRNA for single-chain antibody, complete cds (scFv2) /cds=(0,806) | 1 | AAAACCTCATCTCAGAAGAGGATCTGA ATGGGGCCGCACATCACCATCATC |
| 847 | Table 3A | Hs.27182 | AJ238243 | 4826530 | mRNA for phospholipase A2 activating protein /cds=(28,2244) | 1 | AAACCCCTTTAAATGAGGGCCAGTAT TATCTCTGCTTTCAGAAATAGACA |
| 848 | Table 3A | Hs.6947 | AJ238403 | 12697195 | mRNA for huntingtin interacting protein 1 | 1 | GACCTGACTCCACTCTTAAACCTGGG TCTTCTCTTGGGGTGTCTGTCTAG |
| 849 | Table 3A | Hs.54642 | AJ243721 | 6006497 | methionine adenosyltransferase II, beta (MAT2B), mRNA /cds=(0,1004) | 1 | CTTTTATAGCAGTTTATGGGGAGCAC TTGAAAGAGCGTGTGATCATGTAT |

Table 8

| | | | | | | | |
|-----|----------|-----------|-----------|----------|---|---|------------------------------|
| 850 | Table 3A | Hs.55968 | AJ245539 | 6688166 | partial mRNA for GalNAc-T5 (GALNT5 gene) /cds=(0,2006) | 1 | AGATCCTGAAAGTAGCTGCCTGTGAC |
| 851 | Table 3A | Hs.18827 | AJ250014 | 8250235 | cylindromatosis (turban tumor syndrome) (CYLD), mRNA /cds=(391,3261) | 1 | CCAGTGAAGCCATATCAAAAGTGG |
| 852 | Table 3A | Hs.250905 | AJ250865 | 6688221 | hypothetical protein (LOC51234), mRNA /cds=(0,551) | 1 | TACTGCTAAGTGTCTGGTTGGGGTGG |
| 853 | Table 3A | Hs.169610 | AJ251595 | 6491738 | mRNA for transmembrane glycoprotein (CD44 gene) /cds=(178,2406) | 1 | TGAGATGATGATTAGATCAGGGGT |
| 854 | Table 3A | Hs.107393 | AJ270952 | 7687995 | chromosome 3 open reading frame 4 (C3orf4), mRNA /cds=(880,1641) | 1 | TTGTACCCAGAGACTATGATTTATATT |
| 855 | Table 3A | Hs.135187 | AJ271326 | 12043566 | unc93 (C.elegans) homolog B (UNC93B), mRNA /cds=(41,1834) | 1 | GATTGCACCTTGCTGCCCATGATT |
| 856 | Table 3A | Hs.126355 | AJ271684 | 6900101 | C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5 (CLECSF5), mRNA /cds=(197,763) | 1 | TTTCAGATGCTTCTGGGAGACACCAA |
| 857 | Table 3A | Hs.334647 | AJ271747 | 9714271 | hypothetical protein FLJ20011 (FLJ20011), mRNA /cds=(380,856) | 1 | AGGGTGAAGCTATTTATCTGTAGT |
| 858 | Table 3A | Hs.88414 | AJ271878 | 12666977 | BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA /cds=(708,3233) | 1 | TTGTGGTAATATGATGTGCCCTTCCCTT |
| 859 | Table 3A | Hs.150601 | AJ272212 | 7981276 | mRNA for protein serine kinase (PSKH1 gene) /cds=(130,1404) | 1 | GCCTAAATCCCTTCCCTGGTGTGT |
| 860 | Table 3A | Hs.287369 | AJ277247 | 9968293 | interleukin 22 (IL22), mRNA /cds=(71,610) | 1 | CACAAGGTGCGCGGTTACCGCTACTT |
| 861 | Table 3A | Hs.56247 | AJ277832 | 9968295 | mRNA for inducible T-cell co-stimulator (ICOS gene) /cds=(67,666) | 1 | GGAGGAGGACCACTGGACGAGAG |
| 862 | Table 3A | Hs.14512 | AJ278191 | 8745180 | DIPB protein (HSA249128), mRNA /cds=(177,1211) | 1 | TAGACTCAGCAACAATCCACCTGAG |
| 863 | Table 3A | Hs.134342 | AJ278245 | 12227251 | mRNA for LanC-like protein 2 (lanc2 gene) /cds=(186,1538) | 1 | ATCAGCAGAGCCACCCTAGATCAG |
| 864 | Table 3A | Hs.279860 | AJ400717 | 7573518 | tumor protein, translationally-controlled 1 (TPT1), mRNA /cds=(94,612) | 1 | CCTCAGAGGCTTACTCTAACCCATCC |
| 865 | Table 3A | Hs.130881 | AJ404611 | 11558481 | B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), mRNA /cds=(228,2735) | 1 | CAGAATAATGGAGACTTCATGTG |
| 866 | Table 3A | Hs.10647 | AK000005 | 7209310 | mRNA for FLJ00005 protein, partial cds /cds=(0,337) | 1 | AGGCTGTTGATGCTTATTCTCTGTAA |
| 867 | Table 3A | Hs.29052 | AK000196 | 7020122 | hypothetical protein FLJ20189 (FLJ20189), mRNA /cds=(122,841) | 1 | CTAAGAATTTTACCTTTTGGGGGA |
| 868 | Table 3A | Hs.79110 | AK000221 | 7020163 | nucleolin (NCL), mRNA /cds=(111,2234) | 1 | GTAACGTCATCCTCTGTATTAGTAA |
| 869 | Table 3A | Hs.20157 | NM_025197 | 13376787 | hypothetical protein FLJ13660 similar to CDK5 activator-binding protein C53 (FLJ13660), mRNA /cds=(993,2252) | 1 | ACAGGCTGCCTCTCCAGGGAGGGC |
| 870 | Table 3A | Hs.180804 | AK000271 | 7020240 | cDNA FLJ20264 fis, clone COLF7912 /cds=UNKNOWN | 1 | AACTAACCCCTTTCCCTGCTAGAAA |
| 871 | Table 3A | Hs.180952 | AK000299 | 7020288 | cDNA FLJ20292 fis, clone HEP05374 /cds=(21,1403) | 1 | TAACAATTAGATGCCCAAAGCGA |
| 872 | Table 3A | Hs.272793 | AK000316 | 7020318 | hypothetical protein FLJ20309 (FLJ20309), mRNA /cds=(41,1279) | 1 | GCCTCGACACATCCTCATCCCAGCA |
| 873 | Table 3A | Hs.102669 | AK000354 | 7020383 | cDNA FLJ20347 fis, clone HEP13790 /cds=(708,1481) | 1 | TGGGACACCTCAAGATGAATAATA |
| 874 | Table 3A | Hs.26434 | AK000367 | 7020405 | hypothetical protein FLJ20360 (FLJ20360), mRNA /cds=(79,2304) | 1 | GCACAGTCACATTCCCTCCTTAGGAA |
| 875 | Table 3A | Hs.120769 | AK000470 | 7020580 | cDNA FLJ20463 fis, clone KAT06143 /cds=UNKNOWN | 1 | TCTTCCCTTCCACCCCTTTACA |
| 876 | Table 3A | Hs.5811 | AK000474 | 7020586 | chromosome 21 open reading frame 59 (C21ORF59), mRNA /cds=(360,776) | 1 | TTTGAGGTTCTTTGGTTTITGTAGTAA |
| 877 | Table 3A | Hs.279581 | AK000575 | 7020763 | hypothetical protein FLJ20568 (FLJ20568), mRNA /cds=(6,422) | 1 | AAGCCAGTTCTGTGGTGATGACC |
| 878 | Table 3A | Hs.75884 | AK000639 | 7020863 | DKFZP586A011 protein (DKFZP586A011), mRNA /cds=(330,632) | 1 | CATCTGAAGTGTGGAGCCTTACCCAT |
| 879 | Table 3A | Hs.234149 | AK000654 | 7020886 | hypothetical protein FLJ20647 (FLJ20647), mRNA /cds=(90,836) | 1 | TTTCATCACCACCTTACCGGAGTAGT |
| 880 | Table 3A | Hs.266175 | AK000680 | 7020924 | cDNA FLJ20673 fis, clone KIAA4464 /cds=(104,1402) | 1 | TTTTGGCAGTTGTCTGCATTAACTCG |
| 881 | Table 3A | Hs.30882 | AK000689 | 7020935 | cDNA FLJ20682 fis, clone KIAA3543, highly similar to AF131826 clone 24945 mRNA sequence /cds=UNKNOWN | 1 | TTTCATCACCACCTTACCGGAGTAGT |
| 882 | Table 3A | Hs.243901 | AK000745 | 7021025 | cDNA FLJ20738 fis, clone HEP08257 /cds=UNKNOWN | 1 | TTTGGCAGTTGTCTGCATTAACTCG |
| 883 | Table 3A | Hs.274248 | AK000765 | 7021058 | hypothetical protein FLJ20758 (FLJ20758), mRNA /cds=(464,1306) | 1 | TTTCATCACCACCTTACCGGAGTAGT |

Table 8

| | | | | | | | |
|-----|----------|-----------|----------|---------|---|---|------------------------------|
| 884 | Table 3A | Hs.93872 | AK000967 | 7021958 | mRNA for KIAA1682 protein, partial cds /cds=(19,2346) | 1 | TGAGAGCTGAAATGAGACCATTTACT |
| 885 | Table 3A | Hs.321245 | AK001111 | 7022169 | cDNA FLJ10249 fis, clone HEMBB1000725, highly similar to Rattus norvegicus GTPase Rab8b mRNA /cds=UNKNOWN | 1 | TTGAGCTAAGACCTTAGGAAATTCAC |
| 886 | Table 3A | Hs.117950 | AK001163 | 7022244 | multifunctional polypeptide similar to SAICAR synthetase and AIR carboxylase (ADE2H1), mRNA /cds=(24,1301) | 1 | TGTCATTGTACACTTTATTTCCCTCAC |
| 887 | Table 3A | Hs.194676 | AK001313 | 7022490 | tumor necrosis factor receptor superfamily, member 6b, decoy (TNFRSF6B), transcript variant 2, mRNA /cds=(827,4486) | 1 | GGTCTCTTTGACTAATCACCAAAAAAG |
| 888 | Table 3A | Hs.7837 | AK001319 | 7022500 | phosphoprotein regulated by mitogenic pathways (C8FW), mRNA /cds=(273,1391) | 1 | AGGTTCTTCTGTACATACGTGTATA |
| 889 | Table 3A | Hs.44672 | AK001332 | 7022524 | hypothetical protein FLJ10470 (FLJ10470), mRNA /cds=(6,2054) | 1 | ACTTGGATGCTGCCGCTACTGAATGT |
| 890 | Table 3A | Hs.76556 | AK001361 | 7022572 | protein phosphatase 1, regulatory (inhibitor) subunit 15A (PPP1R15A), mRNA /cds=(240,2264) | 1 | GGGAGGCGTGGCTGAGACCACTGG |
| 891 | Table 3A | Hs.173374 | AK001362 | 7022574 | cDNA FLJ10500 fis, clone NT2RP2000369 /cds=UNKNOWN | 1 | TCTCCAGAAATGTACTTATCTTACCTC |
| 892 | Table 3A | Hs.808 | AK001364 | 7022577 | heterogeneous nuclear ribonucleoprotein F (HNRPF), mRNA /cds=(323,1570) | 1 | GGCATGTACTGTAGTCACTCAGT |
| 893 | Table 3A | Hs.279521 | AK001403 | 7022638 | hypothetical protein FLJ20530 (FLJ20530), mRNA /cds=(10,1683) | 1 | TGTGCACTGTTGTAACCACTTCAGAA |
| 894 | Table 3A | Hs.108332 | AK001428 | 7022679 | cDNA FLJ10566 fis, clone NT2RP2002959, highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) /cds=UNKNOWN | 1 | TTTCTGCTAGGCCCTTGATGCT |
| 895 | Table 3A | Hs.183297 | AK001433 | 7022686 | enhancer of polycomb 1 (EPC1) mRNA, complete cds /cds=(151,2442) | 1 | CATCGGCCAGACAGAGTTGAATGCAA |
| 896 | Table 3A | Hs.7943 | AK001437 | 7022693 | RPB5-mediating protein (RMP), mRNA /cds=(465,1991) | 1 | GCAATCCAGAAGAAGTGTACAGC |
| 897 | Table 3A | Hs.343211 | AK001451 | 7022717 | 602321909F1 cDNA, 5' end /clone=IMAGE:4425098 /clone_end=5' | 1 | TGCTTAACTATTTATTTTGGC |
| 898 | Table 3A | Hs.268012 | AK001471 | 7022749 | fatty-acid-Coenzyme A ligase, long-chain 3 (FACL3), mRNA /cds=(142,2304) | 1 | TTTGGCGCTAGTTGGCTATTCAAGAA |
| 899 | Table 3A | Hs.236844 | AK001514 | 7022816 | hypothetical protein FLJ10652 (FLJ10652), mRNA /cds=(50,1141) | 1 | ACCTCGCCCTCTGAATGTCATAC |
| 900 | Table 3A | Hs.215766 | AK001548 | 7022868 | GTP-binding protein (NGB), mRNA /cds=(23,1924) | 1 | GTTTACGTGGAAGAAACGCTAAGGGT |
| 901 | Table 3A | Hs.18063 | AK001630 | 7023001 | cDNA FLJ10768 fis, clone NT2RP4000150 /cds=UNKNOWN | 1 | TTGCTCCAGGAAAGGAGAGGAAG |
| 902 | Table 3A | Hs.14347 | AK001665 | 7023081 | cDNA FLJ12877 fis, clone NT2RP2003825 /cds=(313,738) | 1 | TGCTCAAATCAGGACTTAAATCATAG |
| 903 | Table 3A | Hs.12457 | AK001676 | 7023081 | hypothetical protein FLJ10814 (FLJ10814), mRNA /cds=(92,3562) | 1 | GCACCACATTTTTCATGTCAGACT |
| 904 | Table 3A | Hs.169407 | AK001725 | 7023165 | SAC2 (suppressor of actin mutations 2, yeast, homolog)-like (SACM2L), mRNA /cds=(0,2165) | 1 | TGAAATCTACCCATCTTGAGGGAGG |
| 905 | Table 3A | Hs.267604 | AK001749 | 7023205 | hypothetical protein FLJ10450 (FLJ10450), mRNA /cds=(66,1622) | 1 | ACCGTTCCTCAGTTAAGGACTTGT |
| 906 | Table 3A | Hs.110445 | AK001779 | 7023263 | CGI-97 protein (LOC51119), mRNA /cds=(170,922) | 1 | ATGAGTGTGTCGGAATCCCGTGCTTA |
| 907 | Table 3A | Hs.12999 | AK001822 | 7023330 | cDNA FLJ10960 fis, clone PLACE1000564 /cds=UNKNOWN | 1 | AAATACGCTCTTAAATATTTTCT |
| 908 | Table 3A | Hs.296323 | AK001838 | 7023355 | serum/glucocorticoid regulated kinase (SGK), mRNA /cds=(42,1337) | 1 | AAATCAGAACTGAGGTAGCTTAGAGA |
| 909 | Table 3A | Hs.81648 | AK001883 | 7023426 | hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4 (FLJ11021), mRNA /cds=(446,1054) | 1 | TGTAGCCGATGTAAGTGTCCGATTT |
| 910 | Table 3A | Hs.181112 | AK001934 | 7023506 | HSPC126 protein (HSPC126), mRNA /cds=(25,837) | 1 | AGGCTTTAGCAAAGATGGATATATTG |
| 911 | Table 3A | Hs.4863 | AK001942 | 7023519 | cDNA FLJ11080 fis, clone PLACE1005181 /cds=UNKNOWN | 1 | GTGACTGAGACAGAAGAACTGGCA |
| 912 | Table 3A | Hs.30822 | AK001972 | 7023569 | hypothetical protein FLJ11110 (FLJ11110), mRNA /cds=(44,1033) | 1 | AGTGGGCCCTAACTCATGTGAGCTTGA |
| 913 | Table 3A | Hs.173203 | AK002009 | 7023629 | beta-1,3-N-acetylglucosaminyltransferase (BETA3GNT), mRNA /cds=(235,1428) | 1 | TAAGTATGAACTCATTGGGAGCA |
| 914 | Table 3A | Hs.8033 | AK002026 | 7023658 | hypothetical protein FLJ11164 (FLJ11164), mRNA /cds=(56,1384) | 1 | AACACTAACCTCTCCCTCCTGGCTC |
| 915 | Table 3A | Hs.92918 | AK002059 | 7023711 | hypothetical protein (BM-009), mRNA /cds=(385,1047) | 1 | AAGAACTACTCCGAAGTCAGTCTG |
| | | | | | | 1 | TCTGTCAGGAAATGTAACCTTTGGTTT |
| | | | | | | 1 | ATTTTGGCTTATTTCCAGGGGT |
| | | | | | | 1 | AAATTGTGCCCGGACTTACCTTTTCATT |
| | | | | | | 1 | GAACATGCTGCCATAACTTAGATT |
| | | | | | | 1 | TGGCAGGGAGCTGGGACCTGGAGAG |
| | | | | | | 1 | ACAACCTCTGTAATAAAACACTTT |
| | | | | | | 1 | AGGGAGATAATGGAGTCCACTTTAAT |
| | | | | | | 1 | TTGGAATTCTGTGTGAGCTATGAT |
| | | | | | | 1 | AGATCAGTGATTACTGGTGTAGTGTT |
| | | | | | | 1 | GTAAATCAGGTTAAACCCACTTCCA |
| | | | | | | 1 | CCATTTGACAGTAAAGGCTCTTGGCT |
| | | | | | | 1 | TCTGTTGGAGGATGGGAAATTGT |
| | | | | | | 1 | TTTAACAGCCTGTCTCCCGGCATCA |
| | | | | | | 1 | GGAGTCATTGAACAATCATGGAAT |
| | | | | | | 1 | AATACTATTGTTTGGCAGGTCAATCC |
| | | | | | | 1 | ACACACTTCTGCCCCCACTGCATT |
| | | | | | | 1 | TTATCAGATGGGATAAGCTGGGACTAT |
| | | | | | | 1 | AAACAATGGAAATAAGCCACTGT |
| | | | | | | 1 | CCCTGTGCCTTTCTTTGAGAGTGAA |
| | | | | | | 1 | GGTGGGTGGAGTTGACCAAGAGAAA |
| | | | | | | 1 | TGTGTGCGTAGAATATTACGTATGCA |
| | | | | | | 1 | TGTTTCATGCTAAAGAATGGCTGT |

Table 8

| | | | | | | | |
|-----|----------|-----------|----------|----------|--|---|---|
| 916 | Table 3A | Hs.155313 | AK002127 | 7023814 | DNA sequence from clone RP5-885L7 on chromosome 20q13.2-13.33. Contains ESTs, STSs, GSSs and eight CpG islands. Contains the 3' end of the NTSR1 gene for high affinity neurotensin receptor 1, a putative novel gene, a novel gene similar to a fly gene, the gene for opioid growth factor receptor (7-60 protein), the COL9A3 gene for collagen IX alpha 3, a putative novel gene similar to a fly gene, the TCFL5 gene for basic helix-loop-helix transcription factor-like 5, an ARF4 (ADP-ribosylation factor 4) pseudogene, a novel gene and the 3' end of the gene for a novel protein similar to mouse death inducer obliterato 1 (DIO-1) (contains KIAA0333) /cds=(0,3129) | 1 | TCTACATGTGACTGGCTTTCTTGCCC TCGTCTCTTGAATGTTTAGACTCT |
| 917 | Table 3A | Hs.5518 | AK002173 | 7023889 | cDNA FLJ11311 fis, clone PLACE1010102 /cds=UNKNOWN | 1 | TGGTACCCAAACTCACCATTGGTCC TCTTTAATCTTTGAGGGTTTCAAT |
| 918 | Table 3A | Hs.270557 | AK021517 | 10432713 | cDNA FLJ11455 fis, clone HEMBA1001497 /cds=UNKNOWN | 1 | TTCCATTTATTCATGTACATTGGCCAG TTCTGCTCCTTGTCTGACTTCT |
| 919 | Table 3A | Hs.126707 | AK021519 | 10432715 | hypothetical protein FLJ11457 (FLJ11457), mRNA /cds=(103,867) | 1 | AACCATCTGGAGTCAGTACAGATCAT CAATCCTTCCACATATACAAGTTC |
| 920 | Table 3A | Hs.77558 | AK021563 | 10432767 | cDNA FLJ11501 fis, clone HEMBA1002100 /cds=UNKNOWN | 1 | GGCCACCTGCTGACTATTGTGGTTT AAAAATAAAGGTTTACTTGTCTGC |
| 921 | Table 3A | Hs.11571 | AK021632 | 10432852 | cDNA FLJ11570 fis, clone HEMBA1003309 /cds=UNKNOWN | 1 | TCTTTGTAAAGCAGCATGATACAAT CTGGTGCCAGTGTATATTTTGCA |
| 922 | Table 3A | Hs.12315 | AK021670 | 10432901 | hypothetical protein FLJ11608 (FLJ11608), mRNA /cds=(561,1184) | 1 | CATGGATATCATGTATCCTTCTCGGT GCTCACACACCTGTCACCTTGTAA |
| 923 | Table 3A | Hs.241567 | AK021704 | 10432943 | RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant M5SP-2, mRNA /cds=(265,1434) | 1 | ATAAGGTGCATAAAACCCCTTAAATTC ATCTAGTAGCTGTCCCCCGAACA |
| 924 | Table 3A | Hs.271541 | AK021715 | 10432954 | cDNA FLJ11653 fis, clone HEMBA1004538 /cds=UNKNOWN | 1 | TGGACCCGAGTCTGCTGAGTTTATAA GGTTCAAAAATATGGTAAATCT |
| 925 | Table 3A | Hs.5019 | AK021776 | 10433029 | cDNA FLJ11714 fis, clone HEMBA1005219, weakly similar to NUCLEAR PROTEIN SNF7 /cds=UNKNOWN | 1 | ACTCGACCTTGGTAAACGGAAATGTT GGGGGTGAAGAGAAACATCACTA |
| 926 | Table 3A | Hs.286212 | AK021791 | 10433048 | hypothetical protein FLJ11729 (FLJ11729), mRNA /cds=(311,1150) | 1 | TTCAAGTTCTGCGAAATTAATTGGG CAGGTTAATGTGTACCTGAAACT |
| 927 | Table 3A | Hs.9096 | AK021925 | 10433223 | hypothetical protein FLJ20473 (FLJ20473), mRNA /cds=(57,1472) | 1 | TCCCAGGATGGGGCTCATACAAC CCTTCATCTGCATCAACATTTAAT |
| 928 | Table 3A | Hs.288178 | AK022030 | 10433346 | cDNA FLJ11968 fis, clone HEMBB1001133 /cds=UNKNOWN | 1 | TTTTAGACATGGAGTGCAGGTGGACA CTGTGTGAACGTGTTTTTGGTCACT |
| 929 | Table 3A | Hs.22265 | AK022057 | 10433376 | pyruvate dehydrogenase phosphatase (PDP), mRNA /cds=(131,1855) | 1 | CAAGAACTTGGTCTGCAGTCTGGAA GCTTGCTGCTCTATAGAAATGAA |
| 930 | Table 3A | Hs.22265 | AK022057 | 10433376 | pyruvate dehydrogenase phosphatase (PDP), mRNA /cds=(131,1855) | 1 | CAAGAACTTGGTCTGCAGTCTGGAA GCTTGCTGCTCTATAGAAATGAA |
| 931 | Table 3A | Hs.20281 | AK022103 | 10433424 | mRNA for KIAA1700 protein, partial cds /cds=(108,2180) | 1 | TGTTGAACGGTTAACTGTGCATTTT TCATTTTGATGTGTCATGTATGTT |
| 932 | Table 3A | Hs.9043 | AK022215 | 10433563 | cDNA FLJ12153 fis, clone MAMMA1000458 /cds=UNKNOWN | 1 | CCGCTTCAACTGAGGGTCATTTTACC AGAGTCAATAAAGGCCAACCCCTTC |
| 933 | Table 3A | Hs.94576 | AK022267 | 10433626 | cDNA FLJ12205 fis, clone MAMMA1000931 /cds=UNKNOWN | 1 | ATTCTGAGGGTGACTGAGGCTACAG CTGCTATCACATGCCGAACCTTCTT |
| 934 | Table 3A | Hs.318725 | AK022280 | 10433640 | CGI-72 protein (LOC51105), mRNA /cds=(69,1400) | 1 | TGGTATCAGGAGTGTGGGATTTCTCAG CACTGCTAATGAAGATCCCCTCTT |
| 935 | Table 3A | Hs.132221 | AK022463 | 10433867 | hypothetical protein FLJ12401 (FLJ12401), mRNA /cds=(3,1526) | 1 | CGCAGAGAGGAGAAAAGGAGACAGC AAGACGCCAATAAGAAACACAACCT |
| 936 | Table 3A | Hs.105779 | AK022481 | 10433892 | cDNA FLJ12419 fis, clone MAMMA1003047, highly similar to protein inhibitor of activated STAT protein PIASy mRNA /cds=UNKNOWN | 1 | CCCGCACGGGCAGCTGAAGGCCGCT GTTTTCTAATATTTGATTCTAATT |
| 937 | Table 3A | Hs.8068 | AK022497 | 10433916 | hematopoietic PBX-interacting protein (HPIP), mRNA /cds=(80,2275) | 1 | CCCTGAGGAGATGTAGCAAATTGAGT GTGGGTTTTGGAGTCTGAGCCCTCA |
| 938 | Table 3A | Hs.179882 | AK022499 | 10433920 | hypothetical protein FLJ12443 (FLJ12443), mRNA /cds=(187,900) | 1 | CCAGAGGGAGGGTTGCCATGAAGGA ACTTGGGATTTTCAATGGAATAAAT |
| 939 | Table 3A | Hs.267863 | AK022537 | 10433983 | hypothetical protein FLJ12475 (FLJ12475), mRNA /cds=(16,1065) | 1 | CCTTTCAGCTCTGGACGAATTACCAA AGGCCATGAATTGGCACTGTGTGT |
| 940 | Table 3A | Hs.332541 | AK022546 | 10433997 | Homo sapiens, Similar to RIKEN cDNA 2700083B06 gene, clone MGC:4669 IMAGE:3531883, mRNA, complete cds /cds=(67,1050) | 1 | AGGAAGATGGCGCTGTTATCAGCGG GGAAATGTACTATTTAAGATCAGCT |
| 941 | Table 3A | Hs.21938 | AK022654 | 10434010 | hypothetical protein FLJ12492 (FLJ12492), mRNA /cds=(172,1848) | 1 | ATCCAAGTCTGAAACTCTGCGCTCTA GTACTGCTGTTAAGATACACAACCT |

Table 8

| | | | | | | | |
|-----|----------|-----------|----------|----------|--|---|---|
| 942 | Table 3A | Hs.7010 | AK022568 | 10434032 | Homo sapiens, clone MGC:14452 IMAGE:4304209, mRNA, complete cds /cds=(88,1953) | 1 | TGGATAGCCATTCTGCTCAACCACA CATTCTCTAAGAAACAGCTTGAAA |
| 943 | Table 3A | Hs.11556 | AK022628 | 10434128 | cDNA FLJ12566 fis, clone NT2RM4000852 /cds=UNKNOWN | 1 | TGTTGTATGTGGATGGGGAAGTTTGT TTTCTCCTCTTAGCATTTGTTTCT |
| 944 | Table 3A | Hs.173885 | AK022681 | 10434216 | hypothetical protein FLJ12619 (FLJ12619), mRNA /cds=(391,1080) | 1 | TCTGAATGATCCTACTCCTTTGGAGT AAAAATCAGTCTTACCAGTTTCCA |
| 945 | Table 3A | Hs.288836 | AK022735 | 10434309 | hypothetical protein FLJ12673 (FLJ12673), mRNA /cds=(2,1687) | 1 | TCCTTTTGTAGCCACTTTGAGTCTGC AGTTGTCAAGTAAAGCCTTTTAAAG |
| 946 | Table 3A | Hs.9908 | AK022758 | 10434350 | cDNA FLJ12696 fis, clone NT2RP1000513, highly similar to NifU-like protein (hNifU) mRNA /cds=UNKNOWN | 1 | GGGGGAAATTACCAAGTAGAATGCCCTT GGTCTGAATATTTGATAGAACCAA |
| 947 | Table 3A | Hs.77573 | AK022790 | 10434395 | uridine phosphorylase (UP), mRNA /cds=(352,1284) | 1 | CTGGTACTTTACAGTTTGCACCAAC TCTGCCAAGCCACTGGATCTTACA |
| 948 | Table 3A | Hs.27475 | AK022811 | 10434426 | cDNA FLJ12749 fis, clone NT2RP2001149 /cds=UNKNOWN | 1 | ATCCAGTCACTCATCAAGTGTAATCT GTCTCCTAAATATCTCTGGAACCT |
| 949 | Table 3A | Hs.58488 | AK022834 | 10434461 | catenin (cadherin-associated protein), alpha-like 1 (CTNNA1), mRNA /cds=(43,2247) | 1 | AGCTTTTGGGGTCAGATCTCTGGAAC ATCATGTGATGAAGCTGACATTTT |
| 950 | Table 3A | Hs.108779 | AK022874 | 10434520 | cDNA FLJ12812 fis, clone NT2RP2002498 /cds=(3,2360) | 1 | AGCAGTTAGGCTTGACTTTGAGGAGA GGCTGTGATGTTTATGATCCCTGA |
| 951 | Table 3A | Hs.56847 | AK022936 | 10434613 | cDNA FLJ12874 fis, clone NT2RP2003769 /cds=UNKNOWN | 1 | GCTGTCCACAGAAACGCCCTTAAGT AGCCCTACCTTACTCCTTAGAGCT |
| 952 | Table 3A | Hs.14347 | AK022939 | 10434618 | cDNA FLJ12877 fis, clone NT2RP2003825 /cds=(313,738) | 1 | CATGGGTATTAACTGCTTTGCTGCT GGTAACTACTGAAAGAACCTGCTT |
| 953 | Table 3A | Hs.4859 | AK022974 | 10434675 | cyclin L ania-6a (LOC57018), mRNA /cds=(54,1634) | 1 | AGGATTTGATTTCTTGAACCCCTCTA GGTCTCTAGAACACTGAGGACAGT |
| 954 | Table 3A | Hs.193313 | AK023013 | 10434731 | Homo sapiens, NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b), clone MGC:1432 IMAGE:2990086, mRNA, complete cds /cds=(150,509) | 1 | GGACTCAGGAGCTAATACTGTCTACA GTGGAGCTTGGTCAATTAGAAGC |
| 955 | Table 3A | Hs.288141 | AK023078 | 10434831 | hypothetical protein MGC3156 (MGC3156), mRNA /cds=(156,2501) | 1 | ACCAGGAGGACAGAGTTTGCTTTCAT ATTTTCCTGTAAAGTAAGAGGGCT |
| 956 | Table 3A | Hs.17279 | AK023088 | 10434845 | tyrosylprotein sulfotransferase 1 (TPST1), mRNA /cds=(81,1193) | 1 | CCATGAAGAAGCAAGACGAAACACA CAGGAGGGGAAATCCTGGGATTCT |
| 957 | Table 3A | Hs.142442 | AK023129 | 10434909 | cDNA FLJ13067 fis, clone NT2RP3001712, highly similar to HP1-BP74 protein mRNA /cds=UNKNOWN | 1 | TTGGAATTTGTGTTGCATGTAAGGCA ATCTTTCCTGTTGAAATCTTCT |
| 958 | Table 3A | Hs.180638 | AK023143 | 10434930 | hypothetical protein FLJ13081 (FLJ13081), mRNA /cds=(170,2098) | 1 | AGGAACTGAGTAGACTCCTGTGTAA CCCTGTTTGGAACTTTGCCTTCTT |
| 959 | Table 3A | Hs.172035 | AK023154 | 10434948 | cDNA FLJ13092 fis, clone NT2RP3002147 /cds=(34,606) | 1 | TTTACAAGGCAGAAATGGGGTGTAACA GTTGAATTAACATAGCAATCACGT |
| 960 | Table 3A | Hs.7797 | AK023166 | 10434966 | TERF1 (TRF1)-interacting nuclear factor 2 (TINF2), mRNA /cds=(262,1326) | 1 | TAGTAGGAATGAAGTGGAAAGTCCAG GCTTGGATTGCCTAACTACACTGCT |
| 961 | Table 3A | Hs.72782 | AK023183 | 10434995 | hypothetical protein FLJ11171 (FLJ11171), mRNA /cds=(134,2446) | 1 | AGTGTTTAGTCTCATGTTGGGAACAC ATGAATGTGATGAACATAGTGAAT |
| 962 | Table 3A | Hs.234265 | AK023204 | 10435025 | cDNA FLJ13142 fis, clone NT2RP3003212, moderately similar to Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA /cds=(55,1443) | 1 | ACCCTTTGAGAGTTCCACAGTGGTA GTAGAGTGGTTAACGCTTTTCT |
| 963 | Table 3A | Hs.236494 | AK023223 | 10435057 | RAB10, member RAS oncogene family (RAB10), mRNA /cds=(90,692) | 1 | TTGCCCCCTTTTCTGTAAGTCTCTTGG GATCCTGTGTAGAAGCTGTTCTCA |
| 964 | Table 3A | Hs.288932 | AK023256 | 10435106 | hypothetical protein FLJ13194 (FLJ13194), mRNA /cds=(300,809) | 1 | ACTCATCAATTGAAAGTCCCTCCAAA AAGAGAATATTGGGAAACCATGG |
| 965 | Table 3A | Hs.126925 | AK023275 | 10435137 | hypothetical protein FLJ13213 (FLJ13213), mRNA /cds=(233,1669) | 1 | AGATGGGTGAATCAGTTGGGTTTGT AAATACTTGTATGTGGGGAAGACA |
| 966 | Table 3A | Hs.75748 | AK023290 | 10435162 | cDNA FLJ13228 fis, clone OVARC1000085, highly similar to mRNA for proteasome subunit HC5 /cds=UNKNOWN | 1 | TCAGACCTGGTTGATTTGTACTTTG GAACTGTACCTTGGATGGTTTGT |
| 967 | Table 3A | Hs.285017 | AK023291 | 10435163 | hypothetical protein FLJ21799 (FLJ21799), mRNA /cds=(159,923) | 1 | GTATCTCATGGCTCTTGATGTGGAA AGAAGTTGACAGAGGGTTGCAGGG |
| 968 | Table 3A | Hs.288929 | AK023320 | 10435204 | hypothetical protein FLJ13258 similar to fused toes (FLJ13258), mRNA /cds=(163,1041) | 1 | AGTTCAAGTGAAGAAACCAAGAACAC TTGTTCTAGTGTGTTGTTT |
| 969 | Table 3A | Hs.227400 | AK023362 | 10435266 | mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA /cds=(360,3014) | 1 | GCAGATGGCTATGTGCTAGAGGGCA AAGAGTTGGAGTTCTATCTTAGGAA |
| 970 | Table 3A | Hs.155160 | AK023379 | 10435291 | Homo sapiens, Similar to splicing factor, arginine/serine-rich 2 (SC-35), clone MGC:2622 IMAGE:3501687, mRNA, complete cds /cds=(30,878) | 1 | TTGGTGTCAATGATCTGGTGACAATA GGATTACATTGGAGCCAATTGAAT |
| 971 | Table 3A | Hs.125034 | AK023402 | 10435324 | mRNA for putative N-acetyltransferase /cds=(208,2808) | 1 | AACTAGAAGATGTACTTCGACAGCAT CCATTTTACTTCAAGGCAGCAAGA |
| 972 | Table 3A | Hs.285107 | AK023459 | 10435401 | hypothetical protein FLJ13397 (FLJ13397), mRNA /cds=(221,1558) | 1 | ATACACTTTTCCAAATTTGTCCCAACA GCCCTGTAAGCCAGCTTTCTTCT |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|--|---|--|
| 973 | Table 3A | Hs.172028 | AK023460 | 10435403 | a disintegrin and metalloproteinase domain 10 (ADAM10), mRNA /cds=(469,2715) | 1 | GCATTTTCTTCACTTGCAGGCAAACCT TGGCTCTCAATAAACTTTTACCAC |
| 974 | Table 3A | Hs.315054 | AK023470 | 10435414 | hypothetical protein MGC15875 (MGC15875), mRNA /cds=(651,1178) | 1 | ATTAGACCAGACAGGTGATTCTTCTAA AGAAAACTCCTGACATGCACACCCA |
| 975 | Table 3A | Hs.164005 | AK023494 | 10435442 | cDNA FLJ13432 fis, clone PLACE1002537 /cds=UNKNOWN | 1 | AGCCAAATGTGTACATCAAACTCT TCAGCAGCTTTTGCATAATCCAGG |
| 976 | Table 3A | Hs.129872 | AK023512 | 10435467 | sperm associated antigen 9 (SPAG9), mRNA /cds=(110,2410) | 1 | TCCTCAAAGGGGAAACTATGAAGGG GAAGAAGACAAACCTAAGATACCA |
| 977 | Table 3A | Hs.63525 | AK023529 | 10435489 | cDNA FLJ13467 fis, clone PLACE1003519, highly similar to hnRNP-E2 mRNA /cds=UNKNOWN | 1 | AGATGGACTGGAGCTTTTCTTTGTG AATAGAACTGGATGCCACAGTGA |
| 978 | Table 3A | Hs.116278 | AK023633 | 10435617 | cDNA FLJ13571 fis, clone PLACE1008405 /cds=UNKNOWN | 1 | AGTTGTCAGAAGACTCCTGGGTGTAC AGAGCAAATCAAGCTGCATCAGTA |
| 979 | Table 3A | Hs.43047 | AK023647 | 10435632 | cDNA FLJ13585 fis, clone PLACE1009160 /cds=UNKNOWN | 1 | AGTGGCTTCATAGCTACTGACAAATG TCTGAATATTGTGCTGCCCTTCA |
| 980 | Table 3A | Hs.163495 | AK023670 | 10435662 | cDNA FLJ13608 fis, clone PLACE1010628 /cds=UNKNOWN | 1 | GCCTGTACAAACATTCAGGTTAGTTG GCAGTCTATAATGTGAGTTGGGT |
| 981 | Table 3A | Hs.17448 | AK023680 | 10435673 | cDNA FLJ13618 fis, clone PLACE1010925 /cds=UNKNOWN | 1 | AAGGAAGGTAAAGTTAGGGGACTAG AAGACTCTAAATTTGGCTTCTCAGTA |
| 982 | Table 3A | Hs.178357 | AK023719 | 10435734 | hypothetical protein FLJ13657 (FLJ13657), mRNA /cds=(87,1172) | 1 | AGAATAATTGCCCATGTTTAATTATA GCAGACACGCCATTCTAACAGGT |
| 983 | Table 3A | Hs.30818 | AK023743 | 10435768 | cDNA FLJ13681 fis, clone PLACE2000014, weakly similar to HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III /cds=UNKNOWN | 1 | AACTTGGTATTGTTGTAGTTTATGTAG TAAGTGACTTGGCACCACATCAGA |
| 984 | Table 3A | Hs.157777 | AK023779 | 10435815 | cDNA FLJ13717 fis, clone PLACE2000425 /cds=UNKNOWN | 1 | AGTTTAACTTTTCTCACCCCTGTATA GAAAATGCCTTGGCTCTCAAGAG |
| 985 | Table 3A | Hs.7871 | AK023813 | 10435861 | cDNA FLJ13751 fis, clone PLACE3000339, weakly similar to GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) /cds=(436,2805) | 1 | GTCTTGGGCTGGATGGGTTATAGAG CTGAGCGGCTGTGATGTTCTGTTT |
| 986 | Table 3A | Hs.49391 | AK023825 | 10435876 | cDNA FLJ13763 fis, clone PLACE4000089 /cds=(56,547) | 1 | GACACATCTAGAATGTTTTCTTTTAC CGTACCTCCAAAAGAGGCAATTT |
| 987 | Table 3A | Hs.119908 | AK023975 | 10436193 | nucleolar protein NOP5/NOP58 (NOP5/NOP58), mRNA /cds=(0,1589) | 1 | ACCAGGGATGCTCTCTAACGTAATCA AGGGAAGGTTGAGTAAGACAAAGT |
| 988 | Table 3A | Hs.26039 | AK023999 | 10436234 | cDNA FLJ13937 fis, clone Y79AA1000805 /cds=UNKNOWN | 1 | ACACAGTTTCAGTTTTTGGGGAACTA GTTTTGTCAATACTACACCCCT |
| 989 | Table 3A | Hs.23170 | AK024023 | 10436276 | homolog of yeast SPB1 (JM23), mRNA /cds=(300,1289) | 1 | TGCACTGGGAATTTCTGAGTGAGGTC TTACCTCTCTTTAAACCTCTTCA |
| 990 | Table 3A | Hs.24719 | AK024029 | 10436287 | cDNA FLJ13967 fis, clone Y79AA1001402, weakly similar to paraneoplastic cancer-testis-brain antigen (MA4) mRNA /cds=(684,1397) | 1 | AAGGCAGAAATAGATGCTGAGATTGG TTAAGTTTGCATGACCATCTTGA |
| 991 | Table 3A | Hs.168232 | AK024030 | 10436289 | hypothetical protein FLJ13855 (FLJ13855), mRNA /cds=(314,1054) | 1 | TGCCCTAATCTTGAGTTGAGGAAATA TATGCACAGGAGTCAAAGAGATGT |
| 992 | Table 3A | Hs.129872 | AK024068 | 10436350 | sperm associated antigen 9 (SPAG9), mRNA /cds=(110,2410) | 1 | GCTAGATTGTGAAGTACATGGGATTT CATGAGCCAGAGGAGGCATTGGGA |
| 993 | Table 3A | Hs.333300 | AK024088 | 10436379 | hypothetical protein FLJ14026 (FLJ14026), mRNA /cds=(57,1826) | 1 | GCCTCAAAGAAACACAGAGTGCCTT GTTCTAAACGTAAGTTCTGAATCC |
| 994 | Table 3A | Hs.281434 | AK024090 | 10436383 | cDNA FLJ14028 fis, clone HEMBA1003838 /cds=UNKNOWN | 1 | AATCCCAGGGGCTGGTTAAGTGCTGT GTGATAACTGTTTGGATGAGACT |
| 995 | Table 3A | Hs.287864 | AK024092 | 10436385 | cDNA FLJ14030 fis, clone HEMBA1004086 /cds=UNKNOWN | 1 | AGGTTTCTTACCAACACAAATGGAC AGTGGATTGACTTTCTAAAGACT |
| 996 | Table 3A | Hs.288856 | AK024094 | 10436388 | prefoldin 5 (PFDN5), mRNA /cds=(423,926) | 1 | CCTGGTGATGGGAAGGCTCTGTGTT TTAATGCCAATAAATGTGCCAGCT |
| 997 | Table 3A | Hs.206868 | AK024118 | 10436421 | cDNA FLJ14056 fis, clone HEMBB1000335 /cds=UNKNOWN | 1 | AAAATATTGAGCCAGGCCCTGGGGA AGTGGGAAGTGAGAGCCAGAGCGGC |
| 998 | Table 3A | Hs.118990 | AK024119 | 10436422 | cDNA FLJ14057 fis, clone HEMBB1000337 /cds=UNKNOWN | 1 | AGCACACAAGGAATCCCAGAAAATGT TGGCTGAAGGAATAAATGGATGGA |
| 999 | Table 3A | Hs.235498 | AK024137 | 10436443 | hypothetical protein FLJ14075 (FLJ14075), mRNA /cds=(111,2027) | 1 | CACCTGCCTACCGCCATTCATGATTAA ACCATCCAGAAATACCATCCCTGT |
| 1000 | Table 3A | Hs.289037 | AK024197 | 10436518 | cDNA FLJ14135 fis, clone MAMMA1002728 /cds=UNKNOWN | 1 | AAATGAGATGGCCTCTGCGGACACAT GAAAGGGTACTTTCAGCTTACCAA |
| 1001 | Table 3A | Hs.289088 | AK024202 | 10436523 | heat shock 90kD protein 1, alpha (HSPCA), mRNA /cds=(60,2258) | 1 | TGGACTAGGAGAGACTTCAATTTGGT GCTAAAGTTCCCAAGTTCATATGT |
| 1002 | Table 3A | Hs.14070 | AK024228 | 10436554 | hypothetical protein FLJ14166 (FLJ14166), mRNA /cds=(203,568) | 1 | CTCACAGCCAGCAGCAGCCCTGAGAA AGAGGCGTCCACAAATAACACGTC |
| 1003 | Table 3A | Hs.24115 | AK024240 | 10436567 | cDNA FLJ14178 fis, clone NT2RP2003339 /cds=UNKNOWN | 1 | ACAGAACATTGAGATGTGCCTAGTTC CGTATTTACAGTTTGGTCTGGCTG |
| 1004 | Table 3A | Hs.193063 | AK024263 | 10436597 | cDNA FLJ14201 fis, clone NT2RP3002955 /cds=UNKNOWN | 1 | TGAATTTTCAATGGGTGATTTAAGTG AGTCACAAGTCACAAAACCTTGTCT |
| 1005 | Table 3A | Hs.183506 | AK024275 | 10436615 | hypothetical protein FLJ14213 (FLJ14213), mRNA /cds=(119,841) | 1 | TGTACTTAAGTGCTGATGACTGTAG CCAGTTTACAACCTTTTACCATCG |
| 1006 | Table 3A | Hs.109441 | AK024297 | 10436644 | cDNA FLJ14235 fis, clone NT2RP4000167 /cds=(82,2172) | 1 | TTCTGAACATTTTGTCAAGCTCAAC AGGTTTGGAAAACCTCTGTGGGG |
| 1007 | Table 3A | Hs.9343 | AK024327 | 10436684 | cDNA FLJ14265 fis, clone PLACE1002256 /cds=UNKNOWN | 1 | TGTCAAGGGCATTAAAGCCTCTGTA AGCATAATCTTATCAAGGGGATAC |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|--|---|-----------------------------|
| 1008 | Table 3A | Hs.287631 | AK024331 | 10436690 | cDNA FLJ14269 fis, clone PLACE1003864 /cds=UNKNOWN | 1 | TCAGTCCATCTCAAGACCTGTGCCTG |
| 1009 | Table 3A | Hs.287634 | AK024372 | 10436742 | hypothetical protein FLJ14310 (FLJ14310), mRNA /cds=(406,768) | 1 | GGTAGGAGTGAAATCTCTCTCTCAAA |
| 1010 | Table 3A | Hs.246112 | AK024391 | 10436767 | cDNA FLJ14329 fis, clone PLACE4000259, highly similar to gene for U5 snRNP-specific 200kD protein /cds=(188,5623) | 1 | CTCTAGGAAAGCCCGAGTCATACT |
| 1011 | Table 3A | Hs.246112 | AK024391 | 10436767 | cDNA FLJ14329 fis, clone PLACE4000259, highly similar to gene for U5 snRNP-specific 200kD protein /cds=(188,5623) | 1 | ACAGCAGGTGTCATGGGTCAAGCATA |
| 1012 | Table 3A | Hs.137354 | AK024426 | 10440360 | mRNA for FLJ00015 protein, partial cds /cds=(373,1296) | 1 | AATCATATATAGCATTTTCAGGCA |
| 1013 | Table 3A | Hs.171118 | AK024436 | 10440380 | DNA sequence from clone RP11-165F24 on chromosome 9. Contains the 3' end of the gene for a novel protein (similar to Drosophila CG6630 and CG11376, KIAA1058, rat TRG), an RPL12 (60S ribosomal protein L12) pseudogene, ESTs, STSs, GSSs and a CpG island /cds=(0,4617) | 1 | TGTGGGTCCCTATGAGTGTAGAGCC |
| 1014 | Table 3A | Hs.43616 | AK024439 | 14020950 | mRNA for FLJ00029 protein, partial cds /cds=(0,723) | 1 | CATATCCCATAGAGTCTACCTAGA |
| 1015 | Table 3A | Hs.132569 | AK024449 | 10440411 | mRNA for FLJ00041 protein, partial cds /cds=(0,994) | 1 | TGTTTTCAATTCAGAACATTTGTCTGT |
| 1016 | Table 3A | Hs.289034 | AK024456 | 10440425 | mRNA for FLJ00048 protein, partial cds /cds=(2940,3380) | 1 | CTGTCAGCATATGTATATCAGCT |
| 1017 | Table 3A | Hs.273230 | AK024471 | 10440455 | mRNA for FLJ00064 protein, partial cds /cds=(0,830) | 1 | TGGCTACTGCAAAACCAGTTTTGACA |
| 1018 | Table 3A | Hs.41045 | AK024474 | 10440461 | mRNA for FLJ00067 protein, partial cds /cds=(1209,2933) | 1 | GGTCAGATTTTCATATGTATAGGT |
| 1019 | Table 3A | Hs.7049 | AK024478 | 10440469 | mRNA for FLJ00071 protein, partial cds /cds=(3020,3772) | 1 | AGAGGTTCTGAAAGGTCTGTGCTTG |
| 1020 | Table 3A | Hs.6289 | AK024539 | 10436843 | hypothetical protein FLJ20886 (FLJ20886), mRNA /cds=(0,524) | 1 | ATGCGTCTGGTTTTCAATCGCTGCT |
| 1021 | Table 3A | Hs.108854 | AK024569 | 10436879 | cDNA: FLJ20916 fis, clone ADSE00738, highly similar to AF161512 HSPC163 mRNA /cds=UNKNOWN | 1 | GAACAAACCTATCAAAAATGTAGC |
| 1022 | Table 3A | Hs.10362 | AK024597 | 10436910 | cDNA: FLJ20944 fis, clone ADSE01780 /cds=UNKNOWN | 1 | AGTATGATCCCTCAAAACCTCACTAA |
| 1023 | Table 3A | Hs.289069 | AK024669 | 10437005 | hypothetical protein FLJ21016 (FLJ21016), mRNA /cds=(90,1193) | 1 | CTGGAAGGATGATTTTGTCTCAGT |
| 1024 | Table 3A | Hs.10600 | AK024740 | 10437104 | DNA sequence from clone RP11-353C18 on chromosome 20 Contains ESTs, STSs, GSSs and CpG islands. Contains the NIFS gene for cysteine desulfurase, two genes for novel proteins and the gene for the splicing factor CC1.3 with a second isoform (CC1.4) /cds=(66,839) | 1 | GAGGTTTCTCACTGAGGTTGAGAG |
| 1025 | Table 3A | Hs.12293 | AK024756 | 10437124 | hypothetical protein FLJ21103 (FLJ21103), mRNA /cds=(88,1143) | 1 | GTGTTTGGATAGGACTGATCCAC |
| 1026 | Table 3A | Hs.23410 | AK024764 | 10437139 | translocase of inner mitochondrial membrane 13 (yeast) homolog B (TIMM13B), mRNA /cds=(46,333) | 1 | AAGTGTGGTTCCTGAAGGCTGTCTTT |
| 1027 | Table 3A | Hs.180139 | AK024823 | 10437226 | SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA /cds=(90,377) | 1 | GTAACCTTTTGTAGTCTTTGTGT |
| 1028 | Table 3A | Hs.159557 | AK024833 | 10437239 | karyopherin alpha 2 (RAG cohort 1, importin alpha 1) (KPNA2), mRNA /cds=(132,1721) | 1 | AATCCTTTAACTCTGCGGATAGCATT |
| 1029 | Table 3A | Hs.325093 | AK024863 | 10437271 | cDNA: FLJ21210 fis, clone COL00479 /cds=UNKNOWN | 1 | TGGTAGGTAAGTATTAAGTACAGGGC |
| 1030 | Table 3A | Hs.306720 | AK024890 | 10437303 | cDNA: FLJ21237 fis, clone COL01114 /cds=UNKNOWN | 1 | TTGATAGGTAAGTATTAAGTACAGGGC |
| 1031 | Table 3A | Hs.135570 | AK024921 | 10437337 | cDNA: FLJ21268 fis, clone COL01718 /cds=UNKNOWN | 1 | CTTCATCTGGATCAGGCGAAATTT |
| 1032 | Table 3A | Hs.6019 | AK024941 | 10437362 | cDNA: FLJ21288 fis, clone COL01927 /cds=UNKNOWN | 1 | GTTCTCTTCGCGGAAGCTTTTGATAA |
| 1033 | Table 3A | Hs.1279 | AK024951 | 10437374 | cDNA: FLJ21298 fis, clone COL02040, highly similar to HSC1R mRNA for complement component C1r /cds=UNKNOWN | 1 | GGAATTCTCAGACCGATAGGGTGT |
| 1034 | Table 3A | Hs.29977 | AK024961 | 10437386 | hypothetical protein FLJ21308 (FLJ21308), mRNA /cds=(287,1792) | 1 | AGTTTTGTACTTTTCACATAGCTTGT |
| 1035 | Table 3A | Hs.166254 | AK024969 | 10437396 | hypothetical protein DKFZp566l133 (DKFZP566l133), mRNA /cds=(133,1353) | 1 | GCCCCGTAAAAGGGTTAACAGCA |
| | | | | | | 1 | TTGGATCTGGTCTGAGGAGGACACA |
| | | | | | | 1 | CCTGGCATCGGATGACCTTTATAA |
| | | | | | | 1 | TAGACATGCTTGTGTCCACACAGCAC |
| | | | | | | 1 | ACCAATGTGATACTTCCACTGACC |
| | | | | | | 1 | ATGGGATGCGGTGGGTTGCCCAATA |
| | | | | | | 1 | AACGGCTGTGGAGTGAAATTCCTC |
| | | | | | | 1 | TTTGTACGTAGCTGTTACATGTAGGG |
| | | | | | | 1 | CAATCTGTCTTAAAGTAGGGATAA |
| | | | | | | 1 | GGAATTTCTATCTTGCAGCATCCTG |
| | | | | | | 1 | TAAATAACATTTCAAGTCCACCT |
| | | | | | | 1 | GAGATGAGTTTTGTATTTTGGGGTT |
| | | | | | | 1 | TTCAAGCATTGGAACCAAGGCCA |
| | | | | | | 1 | TCACCTAGACCCCTGTAACAGGTTAA |
| | | | | | | 1 | ATCTTCATGGGTGTTCTGTTTCTTA |
| | | | | | | 1 | GCTCTCCAGACTGTTACAGTGCATGA |
| | | | | | | 1 | GTGATAATAAAATGAGTCAGTCA |
| | | | | | | 1 | GGAGGTAACATTGGAGATGTTTGTG |
| | | | | | | 1 | AAAATATTACTCTGTGCTGTGAGGT |
| | | | | | | 1 | GGCCCTTTCTTTCTTCTGAGGATTG |
| | | | | | | 1 | CAGAGGATATAGTTATCAATCTCT |
| | | | | | | 1 | TCAACAGCACTTAACTGAAGTTTGG |
| | | | | | | 1 | GTTGCTCATACAATAACAGATTG |
| | | | | | | 1 | GGGCCATTTTATGATGCTTGCACAC |
| | | | | | | 1 | CCTCTGGGAAATTGATCTTTAAA |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|--|---|---|
| 1036 | Table 3A | Hs.156110 | AK024974 | 10437403 | cDNA: FLJ21321 fis, clone COL02335, highly similar to HSA010442 mRNA for immunoglobulin kappa light chain /cds=UNKNOWN | 1 | TTTCCACAGGGGACCTACCCCTATT GCGGTCCTCCAGCTCATCTTTAC |
| 1037 | Table 3A | Hs.323378 | AK024976 | 10437405 | coated vesicle membrane protein (RNP24), mRNA /cds=(27,632) | 1 | GGGTGAGAACACTTGCAACAGTTTAT TAATGAGGTGACTTTACCTTAGG |
| 1038 | Table 3A | Hs.21056 | AK025019 | 10437453 | cDNA: FLJ21366 fis, clone COL03012, highly similar to AB002445 mRNA from chromosome 5q21-22 /cds=UNKNOWN | 1 | AATGTACCATCAATAAATTTGGCTGC TTGGGCAGTTTTAGTTACCACTT |
| 1039 | Table 3A | Hs.337266 | AK025021 | 10437455 | RC-BT163-140599-023 cDNA | 1 | TTTTCAGAGGCTTCCTAATTAATCTTG CCCTCCTCCATTTGAGTCCATTT |
| 1040 | Table 3A | Hs.120170 | AK025068 | 10437507 | hypothetical protein FLJ21415 (FLJ21415), mRNA /cds=(138,755) | 1 | AGCTCCAACTTACGATGGAGAATTA AACTTGCTTGATTTCCACTTTGT |
| 1041 | Table 3A | Hs.288872 | AK025092 | 10437538 | mRNA for KIAA1840 protein, partial cds /cds=(71,4384) | 1 | AGCTTCCTCTTCTCAGGACAGCTTC TACTTTAGATGATCCAATAATGAT |
| 1042 | Table 3A | Hs.14555 | AK025166 | 10437628 | cDNA: FLJ21513 fis, clone COL05778 /cds=UNKNOWN | 1 | CACTGACTTCTATTCCATGAGCTTTTT CAAGGCGCTATTTTATGGCAGC |
| 1043 | Table 3A | Hs.83623 | AK025198 | 10437662 | nuclear receptor subfamily 1, group I, member 3 (NR1I3), mRNA /cds=(272,1318) | 1 | TGTTTCGTAAATTAATAGGTCTGGC CCAGAAGACCCACTCAATTGCCCT |
| 1044 | Table 3A | Hs.322680 | AK025200 | 10437664 | cDNA: FLJ21547 fis, clone COL06206 /cds=UNKNOWN | 1 | GGAAGACCCAAAGAAATCCGGAATTT CGCACCAGAGGACCCACCACGTCC |
| 1045 | Table 3A | Hs.10888 | AK025212 | 10437679 | hypothetical protein FLJ21709 (FLJ21709), mRNA /cds=(55,2316) | 1 | TCTTGTTACTTCCAGGAGAACCAG AATGGCTCTGTCACTCGAAGCC |
| 1046 | Table 3A | Hs.288708 | AK025215 | 10437682 | hypothetical protein FLJ21562 (FLJ21562), mRNA /cds=(238,2145) | 1 | TCTTTCTCTAAAGCTTGTTTGATGAAA CTGGTTGGTCCCTTCAGTGAAACA |
| 1047 | Table 3A | Hs.337561 | AK025269 | 10437749 | hypothetical protein FLJ21616 (FLJ21616), mRNA /cds=(119,1093) | 1 | GCTGTGTGACTTAGTAGATAAAATAC TGCCCTCTGCCCTTTGGGACCATGA |
| 1048 | Table 3A | Hs.2083 | AK025306 | 10437795 | cDNA: FLJ21653 fis, clone COL08586, highly similar to HUMKINDC protein kinase mRNA /cds=UNKNOWN | 1 | TCTGTAATTGGACAGCTCTCTCGAAG AGATCTTACAGACTGTATCAGCT |
| 1049 | Table 3A | Hs.76230 | AK025353 | 10437852 | cDNA: FLJ21700 fis, clone COL09849, highly similar to HSU14972 ribosomal protein S10 mRNA /cds=UNKNOWN | 1 | GGTCGTGGACGTGGTCAGCCACCTC AGTAAATTTGAGAGGATTCTTTTG |
| 1050 | Table 3A | Hs.117268 | AK025364 | 10437866 | cDNA: FLJ21711 fis, clone COL10156 /cds=UNKNOWN | 1 | AAAGTGAACCAAGAGTACAAGAGAC AGGTGAAATTAAGAGCCCCCTTGA |
| 1051 | Table 3A | Hs.5181 | AK025367 | 10437869 | proliferation-associated 2G4, 38kD (PA2G4), mRNA /cds=(97,1281) | 1 | GTCCAGGATGCAGAGCTAAAGGCC TCCTCCAGAGTCTCAAGTCGAAA |
| 1052 | Table 3A | Hs.288061 | AK025375 | 10437878 | actin, beta (ACTB), mRNA /cds=(73,1200) | 1 | CCAACTTGAGATGTATGAAGGCTTTT GGTCTCCCTGGGAGTGGGTGGAGG |
| 1053 | Table 3A | Hs.14040 | AK025425 | 10437933 | cDNA: FLJ21772 fis, clone COLF7808 /cds=UNKNOWN | 1 | TTCTCATCCCTTTACAGTTTTCTTA ACTCCAGGGTAGTGTTTAGTGTT |
| 1054 | Table 3A | Hs.85963 | AK025446 | 10437961 | cDNA: FLJ21793 fis, clone HEP00466 /cds=UNKNOWN | 1 | CATGCCAAAGACTCAACTGCCTTCAA AGATAATGTGGGTGCTAGATGCAG |
| 1055 | Table 3A | Hs.82689 | AK025459 | 10437979 | tumor rejection antigen (gp96) 1 (TRA1), mRNA /cds=(105,2516) | 1 | TCCCTTCTCCCTCCCTGCACTGAAAT GTGGGATTATGGGTACAGGAAAA |
| 1056 | Table 3A | Hs.289008 | AK025467 | 10437988 | cDNA: FLJ21814 fis, clone HEP01068 /cds=UNKNOWN | 1 | ACCATGCATAGATCAATCAAACTCT TGTGATGTTTTGTATGGACTTTGA |
| 1057 | Table 3A | Hs.22678 | AK025485 | 10438014 | chromosome 10 open reading frame 2 (C10orf2), mRNA /cds=(32,1552) | 1 | TGTGCTGCCTCAAGACTGCTGGAGTC AGGACATTTTATAGAGCCTTTTCC |
| 1058 | Table 3A | Hs.184793 | AK025533 | 10438078 | Homo sapiens, clone IMAGE3865907, mRNA, partial cds /cds=(0,1534) | 1 | TGCGAGTCTTTAGCAGACTTCAGGC CCAACTGTATTCTTCACTCAGGC |
| 1059 | Table 3A | Hs.121849 | AK025556 | 10438106 | microtubule-associated proteins 1A/1B light chain 3 (MAP1A/1BLC3), mRNA /cds=(84,461) | 1 | GTTAGTGAAGCTGTTTACTGTAAACG GGGAAAACCAGATTCTTTCATCT |
| 1060 | Table 3A | Hs.110771 | AK025557 | 10438108 | cDNA: FLJ21904 fis, clone HEP03585 /cds=UNKNOWN | 1 | GCTTCTGTAATGCCATCCCAATGTG GTTTGGTTTTGTGAACAGAAACC |
| 1061 | Table 3A | Hs.82845 | AK025583 | 10438142 | cDNA: FLJ21930 fis, clone HEP04301, highly similar to HSU90916 clone 23815 mRNA sequence /cds=UNKNOWN | 1 | TTGCCTCGATAAGTTTCCAGTCACT GAAATCTGCTGAAGGTTTACTGT |
| 1062 | Table 3A | Hs.27268 | AK025586 | 10438146 | cDNA: FLJ21933 fis, clone HEP04337 /cds=UNKNOWN | 1 | ACTTCTGAAGTGAAGAAATTTGCTGTT GACAGCCAAAGTATAGTGACAAG |
| 1063 | Table 3A | Hs.7567 | AK025615 | 10438186 | cDNA: FLJ21962 fis, clone HEP05564 /cds=UNKNOWN | 1 | AGAGCCATCTGGTGTGAAGAACTCTA TATTTGTATGTTGAGAGGGCATGG |
| 1064 | Table 3A | Hs.5985 | AK025620 | 10438193 | cDNA: FLJ21967 fis, clone HEP05652, highly similar to AF131831 clone 25186 mRNA sequence /cds=UNKNOWN | 1 | AGAACAAGTTTGGCTTTGATTTTGA AAATGACTTCTGCTAAGCACCCA |
| 1065 | Table 3A | Hs.279901 | AK025623 | 10438197 | PTD009 protein (PTD009), mRNA /cds=(257,916) | 1 | CCTGCCAAAGCAAGAAGAGGCTTG GTCCCCAGAAACAAACAGTAGTCAT |
| 1066 | Table 3A | Hs.339696 | AK025643 | 10438224 | ribosomal protein S12 (RPS12), mRNA /cds=(80,478) | 1 | GGAGTCTCAGGCCAAGGATGTCAAT GAAGAGTATTTCAATGCAAGAAAT |
| 1067 | Table 3A | Hs.339696 | AK025643 | 10438224 | ribosomal protein S12 (RPS12), mRNA /cds=(80,478) | 1 | GGAGTCTCAGGCCAAGGATGTCAAT GAAGAGTATTTCAAGTCAAGAAAT |
| 1068 | Table 3A | Hs.334489 | AK025645 | 10438227 | hypothetical protein FLJ21992 (FLJ21992), mRNA /cds=(60,845) | 1 | TTTCATCTGAATCCAGAGGTGCATCA AATTAATGACAGCTCCACTTGGC |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|--|---|---|
| 1069 | Table 3A | Hs.92414 | AK025683 | 10438280 | cDNA: FLJ22030 fis, clone HEP08669 /cds=UNKNOWN | 1 | TTGACACGTTCCACTTCCTTTGCAATT ATTGTATTAGTTGTGCACTAGT |
| 1070 | Table 3A | Hs.173705 | AK025703 | 10438305 | cDNA: FLJ22050 fis, clone HEP09454 /cds=UNKNOWN | 1 | CCAAATCAACTGTGTGAACTGTTTCT GCACTGCTTGCTAATGGTTTCATC |
| 1071 | Table 3A | Hs.13277 | AK025707 | 10438310 | hypothetical protein FLJ22054 (FLJ22054), mRNA /cds=(144,956) | 1 | ATTGAGACGGGAAAACTCGCTGTAA AATAATGCCAACCTAGATAATGCT |
| 1072 | Table 3A | Hs.5798 | AK025729 | 10438338 | pelota (Drosophila) homolog (PELO), mRNA /cds=(259,1416) | 1 | TGTTCTTGCAATTGCATTTAATGATCCC TTTTCTCCCCACCTCCACACACT |
| 1073 | Table 3A | Hs.184542 | AK025730 | 10438339 | CGI-127 protein (LOC51646), mRNA /cds=(125,490) | 1 | TGCAGATTCTAGTAGCATGCCTTAC CTACAGCACTATGTGCATTTGCTG |
| 1074 | Table 3A | Hs.75811 | AK025732 | 10438341 | N-acylsphingosine amidohydrolase (acid ceramidase) (ASAH), mRNA /cds=(17,1204) | 1 | GCAAGACCGTTTGTCACCTTCATTTT GTATAATCACAGTTGTGTTCTCTGA |
| 1075 | Table 3A | Hs.77910 | AK025736 | 10438345 | cDNA: FLJ22083 fis, clone HEP14459, highly similar to HUM3H3M 3-hydroxy-3- methylglutaryl coenzyme A synthase mRNA /cds=UNKNOWN | 1 | AATTTAACTTTTGGGTGCCAGGAAAT GGGTTTTCTCAAAGTCCATTGCCG |
| 1076 | Table 3A | Hs.170296 | AK025743 | 10438355 | cDNA: FLJ22090 fis, clone HEP16084 /cds=UNKNOWN | 1 | TCGTGGAAGGGAGAGCCATCAGCAG AAAGAGACCCGTGAGATCTTCGCCTG |
| 1077 | Table 3A | NA | AK025767 | 10438384 | FLJ22114 fis, clone HEP18441 | 1 | AAACACACCAGGGAGACACCATAAAA CAGACCAAGACTAATCTAAAAACA |
| 1078 | Table 3A | Hs.34497 | AK025769 | 10438386 | hypothetical protein FLJ22116 (FLJ22116), mRNA /cds=(270,3545) | 1 | AACCACAATCAAACATATAAATAAGC CTGGAACCACTACAACAGCA |
| 1079 | Table 3A | Hs.5822 | AK025773 | 10438391 | cDNA: FLJ22120 fis, clone HEP18874 /cds=UNKNOWN | 1 | TTTCTGATTATTTGATGCTAGCTGG AATTCAGAAATGGCATTGACCTT |
| 1080 | Table 3A | Hs.264190 | AK025774 | 10438392 | cDNA: FLJ22121 fis, clone HEP18876, highly similar to AF191298 vacuolar sorting protein 35 (VPS35) mRNA /cds=UNKNOWN | 1 | TCACCCCAAGTAGCATGATGATCTG CAATTTAAATTCCTGTGATCTGT |
| 1081 | Table 3A | Hs.12245 | AK025775 | 10438393 | cDNA: FLJ22122 fis, clone HEP19214 /cds=UNKNOWN | 1 | TGAGAAGTGCGGAATAGGTTGCTTCT ACCACCTGTTCTTAATGTAAACAGT |
| 1082 | Table 3A | Hs.26367 | AK025778 | 10438396 | PC3-96 protein (PC3-96), mRNA /cds=(119,586) | 1 | TCGAATGAGTGGTCAGGTAGTCTTAA AGAGCCTCATGTTAAATAGACACA |
| 1083 | Table 3A | Hs.285833 | AK025788 | 10438408 | cDNA: FLJ22135 fis, clone HEP20858 /cds=UNKNOWN | 1 | TGAAGTGCAAATAAAGCACTGCTAC TATAAGACATTCTGGAATGGTTGT |
| 1084 | Table 3A | Hs.90421 | AK025800 | 10438421 | cDNA: FLJ22147 fis, clone HEP22163, highly similar to AF113020 clone FLB9138 mRNA sequence /cds=UNKNOWN | 1 | GCAGTCCCAGATCCAGAACATGGGG AAGTTAGGGAAATGTGTGATTTTG |
| 1085 | Table 3A | Hs.289721 | AK025846 | 10438485 | cDNA: FLJ22193 fis, clone HRC01108 /cds=UNKNOWN | 1 | AGGTATGACAGGAACGTCTTCATGT CCTTACCCAAGCAAGTCATCCATG |
| 1086 | Table 3A | Hs.286194 | AK025886 | 10438538 | hypothetical protein FLJ22233 (FLJ22233), mRNA /cds=(35,1204) | 1 | AATTTTGAATTTCTCTTGCCACGTTA ATAAGCCAAAGCAGCGGGTGC |
| 1087 | Table 3A | Hs.279921 | AK025927 | 10438592 | HSPC035 protein (LOC51669), mRNA /cds=(16,1035) | 1 | TGACTCTGTGCTGGCAAAATGCTTG AAACCTCTATATTTCTTTTCGTTCA |
| 1088 | Table 3A | Hs.105664 | AK025947 | 10438619 | hypothetical protein FLJ22294 (FLJ22294), mRNA /cds=(240,602) | 1 | GCTCTCCACAGAAACCTTTGTCTCT GCAACTTTATCTTTGTCCCGATT |
| 1089 | Table 3A | Hs.55024 | AK026024 | 10438731 | hypothetical protein FLJ10307 (FLJ10307), mRNA /cds=(28,462) | 1 | TTGCCTTAGCCAGTGACCTCTACC TCAGTCTATGTGAGAGGAAGAGAA |
| 1090 | Table 3A | Hs.289092 | AK026033 | 10438744 | Homo sapiens, coactosin-like protein, clone MGC:19733 IMAGE:3604770, mRNA, complete cds /cds=(158,586) | 1 | ACTGTATTGGGATTGCAAGAACATC TCTGCACCTCAGACAGTTTACAGAA |
| 1091 | Table 3A | Hs.288555 | AK026078 | 10438812 | cDNA: FLJ22425 fis, clone HRC08686 | 1 | GTGTGTGTGCATGTGTGTGTTAGCAG AGGTATTTTACTCAGAAAATAGGT |
| 1092 | Table 3A | Hs.333500 | AK026091 | 10438829 | cDNA: FLJ22438 fis, clone HRC09232, highly similar to AF093250 P38IP (P38IP) mRNA /cds=UNKNOWN | 1 | GCCAGTCAAAAGTAAATGAAGAGA GGCAGCCCAACCACTCCAAAATTT |
| 1093 | Table 3A | Hs.238707 | AK026110 | 10438854 | hypothetical protein FLJ22457 (FLJ22457), mRNA /cds=(56,1462) | 1 | CACCTTTGTGGTCGAAAGGCTCAGCCT CTCTACATGAAGTCTGTGGACATG |
| 1094 | Table 3A | Hs.77385 | AK026164 | 10438926 | cDNA: FLJ22511 fis, clone HRC11837, highly similar to HUMMYLCB non- muscle myosin alkali light chain mRNA /cds=UNKNOWN | 1 | AGGCTTTCTGTCTCAGCAACTTTCC CATCTTGTCTCTTGTGATGATGT |
| 1095 | Table 3A | Hs.13179 | AK026239 | 10439028 | cDNA: FLJ22586 fis, clone HSI02774 /cds=UNKNOWN | 1 | TTTTTCTTTTGAAGCATGGAAAAACA ATCTTTTATGCCACTCCAGCCAT |
| 1096 | Table 3A | Hs.27774 | AK026264 | 10439063 | 602386841F1 cDNA, 5' end /clone=IMAGE:4515730 /clone_end=5' | 1 | CCATGATATAAGGAAGGGCCGTGCC TCATGAAAAAGCAACAGGTGGCCTC |
| 1097 | Table 3A | Hs.297666 | AK026270 | 10439073 | cDNA: FLJ22617 fis, clone HSI05379, highly similar to HSEWS EWS mRNA /cds=UNKNOWN | 1 | TAAAGGCGAGCACCGTCAGGAGCGC AGAGATCGGCCCTACTAGATGCAGA |
| 1098 | Table 3A | Hs.31137 | AK026334 | 10439167 | protein tyrosine phosphatase, receptor type, E (PTPRE), mRNA /cds=(51,2153) | 1 | TGAGCCTGACACCTGTGTTTACGAT TTGGAGACATCCCCATGTTATTCT |
| 1099 | Table 3A | Hs.236744 | AK026359 | 10439200 | cDNA: FLJ22706 fis, clone HSI13163 /cds=UNKNOWN | 1 | CTGAGCCACATCCAAGCCTGGTTTGC TGCACCTCTATTGCCAAGACTGAC |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|---|---|---|
| 1100 | Table 3A | Hs.288936 | AK026363 | 10439205 | mitochondrial ribosomal protein L9 (MRPL9), mRNA /cds=(14,817) | 1 | ACTTGCCCTCATTCTCATCATCCAACT GAACATTTGTATCCCAGCAGAA |
| 1101 | Table 3A | Hs.143631 | AK026372 | 10439218 | cDNA: FLJ22719 fis, clone HSI14307 /cds=UNKNOWN | 1 | GTATGAAGAGGAAGCCAGCAGAG CAGGAGGCAGCAGCAACAATGAGAG |
| 1102 | Table 3A | Hs.157240 | AK026394 | 10439245 | hypothetical protein MGC4737 (MGC4737), mRNA /cds=(2350,2985) | 1 | CTGTGTGTGTCCATGTCTGCAAGCAG TTCTTCAATAAATGGCCTGCCCTCC |
| 1103 | Table 3A | Hs.112497 | AK026396 | 10439247 | cDNA: FLJ22743 fis, clone HUV00901 /cds=UNKNOWN | 1 | TCAAAGCAGAGCAGACAGATTATTTGG TGTTTGCTGAAGACAGCCTTTGTG |
| 1104 | Table 3A | Hs.236449 | AK026410 | 10439266 | hypothetical protein FLJ22757 (FLJ22757), mRNA /cds=(92,2473) | 1 | ACTTCCATCTCAGCTAATGCCCCAC CAGCTCAAACACACCAATAAAGCT |
| 1105 | Table 3A | Hs.89555 | AK026432 | 10439295 | hemopoietic cell kinase (HCK), mRNA /cds=(168,1685) | 1 | TGCAATCCACAATCTGACATTCTCAG GAAGCCCCAAGTTGATATTTCTA |
| 1106 | Table 3A | Hs.343522 | AK026443 | 10439309 | ATPase, Ca++ transporting, plasma membrane 4 (ATP2B4), mRNA /cds=(397,4014) | 1 | CAGAAACCAATACTGCTGTGCACTGA GAATAAAAACCTCATGCCCCCTTGT |
| 1107 | Table 3A | Hs.32148 | AK026455 | 10439325 | AD-015 protein (LOC55829), mRNA /cds=(30,644) | 1 | CACCAGTGAGGATTACTGATGTGGAC AGTTGATGGGGTTTGTCTGTAT |
| 1108 | Table 3A | Hs.75415 | AK026463 | 10439333 | cDNA: FLJ22810 fis, clone KAI2933, highly similar to AB021288 mRNA for beta 2-microglobulin /cds=UNKNOWN | 1 | AAAGTAAGGCATGTTGTGTTAATC TGGTTATTTTGTGCCACAAGTT |
| 1109 | Table 3A | Hs.118183 | AK026486 | 10439358 | hypothetical protein FLJ22833 (FLJ22833), mRNA /cds=(479,883) | 1 | TAAGGGGTAGACAAGATCCGAATAA TCTCCACAAGTTTATTTGTGGTCT |
| 1110 | Table 3A | Hs.182979 | AK026491 | 10439364 | cDNA: FLJ22838 fis, clone KAI24494, highly similar to HUM12A ribosomal protein L12 mRNA /cds=UNKNOWN | 1 | ACATCAACAGTGGTGTGTGGAATGC CCAGCCAGTTAAGCACAAGGAAA |
| 1111 | Table 3A | Hs.2795 | AK026515 | 10439391 | lactate dehydrogenase A (LDHA), mRNA /cds=(97,1095) | 1 | ACAAACAATGCAACCAACTATCCAAG TGTTATACCAAGTAAACCCCAA |
| 1112 | Table 3A | Hs.334807 | AK026528 | 10439405 | Homo sapiens, ribosomal protein L30, clone MGC:2797, mRNA, complete cds /cds=(29,376) | 1 | TTCACCTACAAAATTCACCTGCAAAA CCTTAACCTGCAAAATTTTCTCT |
| 1113 | Table 3A | Hs.239307 | AK026535 | 10439414 | tyrosyl-tRNA synthetase (YARS), mRNA /cds=(0,1586) | 1 | GGGTACTTCTCCATAAGGCATCTCAG TCAAATCCCCTACTGTCCATAAA |
| 1114 | Table 3A | Hs.251653 | AK026594 | 10439481 | tubulin, beta, 2 (TUBB2), mRNA /cds=(0,1337) | 1 | CTTGCTGTCTTCCCTGTCCACATCCA TGCTGTACAGACACCACCATTTGAA |
| 1115 | Table 3A | Hs.277477 | AK026595 | 10439482 | major histocompatibility complex, class I, C (HLA-C), mRNA /cds=(0,1100) | 1 | AAGTCAATTCTCGAATTTGAAAGAG CAATAAAGACCTGAGAACCTTCC |
| 1116 | Table 3A | Hs.334729 | AK026603 | 10439492 | cDNA FLJ20161 fis, clone COL09252, highly similar to L33930 CD24 signal transducer mRNA /cds=UNKNOWN | 1 | AAGCTACTGTGTGTGTGAATGAACAC TCTTGCTTATTCCAGAATGCTGT |
| 1117 | Table 3A | Hs.334842 | AK026632 | 10439528 | tubulin, alpha, ubiquitous (K-ALPHA-1), mRNA /cds=(67,1422) | 1 | TGTCATGCTCCCAGAATTTAGCTTTC AGCTTAAGTACAGATGTTAAAGC |
| 1118 | Table 3A | Hs.179666 | AK026642 | 10439539 | uncharacterized hypothalamus protein HSMNP1 (HSMNP1), mRNA /cds=(231,1016) | 1 | AGGTGGTACTCAAGCCATGCTGCCCTC CTTACATCCTTTTGAACAGAGC |
| 1119 | Table 3A | Hs.288036 | AK026650 | 10439548 | tRNA isopentenylpyrophosphate transferase (IPT), mRNA /cds=(60,1040) | 1 | TGCATCGTAAACCTTCAGAAGGAAA GGAGAAATGTTTGTGGACCACTTT |
| 1120 | Table 3A | Hs.301404 | AK026664 | 10439564 | RNA binding motif protein 3 (RBM3), mRNA /cds=(276,749) | 1 | TGTGGTTAGGAAGCAATTTCCCAATG TACCTATAAGAAATGTGCATCAAG |
| 1121 | Table 3A | Hs.266940 | AK026669 | 10439570 | cDNA: FLJ23016 fis, clone LNG00874 /cds=UNKNOWN | 1 | GCTCGCTGTGCCACTTGTCTTAACCT TGAATATTTCAATTCAGAGTGCT |
| 1122 | Table 3A | Hs.288468 | JU00944 | 405046 | clone A9A2BRB6 (CAC)n/(GTG)n repeat-containing mRNA /cds=UNKNOWN | 1 | AGCTAATTTGCTGCAATGGCTGGCA GGAAACAGGTGATCAAGAGTGCA |
| 1123 | Table 3A | Hs.242868 | AK026704 | 10439618 | cDNA: FLJ23051 fis, clone LNG02642 /cds=UNKNOWN | 1 | TCGACCCAGAGGTGAATGTATTGTT ATTATTGTTTGTGTGTGTGTGA |
| 1124 | Table 3A | Hs.334861 | AK026712 | 10439629 | hypothetical protein FLJ23059 (FLJ23059), mRNA /cds=(41,1681) | 1 | TCCTTGGCAGCTGTATTCTGGAGTCT GGATGTTGCTCTCTAAAGACCTTT |
| 1125 | Table 3A | Hs.12969 | AK026747 | 10439670 | cDNA: FLJ23094 fis, clone LNG07379, highly similar to HST000007 mRNA full length insert cDNA clone EU0IMAGE 293605 /cds=UNKNOWN | 1 | TTTGCCATGTCCAGTACAGAATAATT GTACTTAGTATTGCAAGAGGGT |
| 1126 | Table 3A | Hs.90077 | AK026766 | 10439693 | TGFB-induced factor (TALE family homeobox) (TGIF), mRNA /cds=(311,1129) | 1 | TAGAGAACCTATAGCATCTTCTCATT CCCATGTGGAACAGGATGCCACAC |
| 1127 | Table 3A | Hs.287725 | AK026769 | 10439697 | cDNA: FLJ23116 fis, clone LNG07945, highly similar to HSU79240 serine/threonine kinase mRNA /cds=UNKNOWN | 1 | AACTCATGTGCAGGTTTGATAACAC CAGAACAGAGACAGTGATGCTGT |
| 1128 | Table 3A | Hs.124292 | AK026776 | 10439707 | cDNA: FLJ23123 fis, clone LNG08039 /cds=UNKNOWN | 1 | TGGCCCTGACAGTATTCATTATTTCA GATAATTCCTGTGATAGGACAAC |
| 1129 | Table 3A | Hs.20242 | AK026819 | 10439764 | hypothetical protein FLJ12788 (FLJ12788), mRNA /cds=(9,866) | 1 | ACCTGGAGAGAGAAGGTATTGAAACA TCTCCTTTATGTGTACTTTCCCA |
| 1130 | Table 3A | Hs.287995 | AK026834 | 10439781 | cDNA: FLJ23181 fis, clone LNG11094 /cds=UNKNOWN | 1 | AGAAATACCCCATCAACAAGAACAA CATTAGTTTGGCTGTCATCAACT |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|--|---|-----------------------------|
| 1131 | Table 3A | Hs.324060 | AK026836 | 10439784 | hypothetical protein FLJ23183 (FLJ23183), mRNA /cds=(226,732) | 1 | ATGGGCAAATTCCTTAGGTAAGACAAA |
| 1132 | Table 3A | Hs.6906 | AK026850 | 10439805 | cDNA: FLJ23197 fis, clone REC00917 /cds=UNKNOWN | 1 | AACACAGCCCCAAGGGCAGGTAGT |
| 1133 | Table 3A | Hs.288455 | AK026923 | 10439895 | cDNA: FLJ23270 fis, clone COL10309, highly similar to HSU33271 normal keratinocyte mRNA /cds=UNKNOWN | 1 | GCTGATGCCACTACCCGATTGTGTTA |
| 1134 | Table 3A | Hs.286236 | AK026933 | 10439907 | mRNA for KIAA1856 protein, partial cds /cds=(0,3404) | 1 | TTTGCAATTTGAGCCATTTAAAGA |
| 1135 | Table 3A | Hs.91065 | AK026954 | 10439935 | cDNA: FLJ23301 fis, clone HEP11120 /cds=(2,1888) | 1 | CCTGTTCCCTTCAGCCAACCCGTTTC |
| 1136 | Table 3A | Hs.88044 | AK026960 | 10439945 | cDNA: FLJ23307 fis, clone HEP11549, highly similar to AF041037 novel antagonist of FGF signaling (sprouty-1) mRNA /cds=UNKNOWN | 1 | TGCAGTAAATTAAGCCTGTCAAA |
| 1137 | Table 3A | Hs.298442 | AK026983 | 10439978 | adaptor-related protein complex 3, mu 1 subunit (AP3M1), mRNA /cds=(69,1325) | 1 | TGGCTTAAACCAGTGTTCAGTCTGGT |
| 1138 | Table 3A | Hs.301732 | AK027016 | 10440025 | hypothetical protein MGC5306 (MGC5306), mRNA /cds=(206,1042) | 1 | GCCAACTTCGAATGGAATACAAA |
| 1139 | Table 3A | Hs.3382 | AK027064 | 10440089 | protein phosphatase 4, regulatory subunit 1 (PPP4R1), mRNA /cds=(93,2894) | 1 | TGTGAGTTGTGACCATGTAACATGAG |
| 1140 | Table 3A | Hs.85567 | AK027067 | 10440093 | suppressor of variegation 3-9 (Drosophila) homolog 2; hypothetic (SUV39H2), mRNA /cds=(37,1089) | 1 | AGGTTTTGCTAGGGCCTATTATTT |
| 1141 | Table 3A | Hs.48320 | AK027070 | 10440098 | mRNA for ring-IBR-ring domain containing protein Dorfin, complete cds /cds=(317,2833) | 1 | AGCTGAGTAATTCTAATCTCTTCTGT |
| 1142 | Table 3A | Hs.115659 | AK027114 | 10440156 | hypothetical protein MGC5521 (MGC5521), mRNA /cds=(163,708) | 1 | GTTTTCTTGCCTTAACCACAAAT |
| 1143 | Table 3A | Hs.113205 | AK027136 | 10440188 | cDNA: FLJ23483 fis, clone KAlA04052 /cds=UNKNOWN | 1 | AATTTGCTAGAATCCAGTAAATCATTT |
| 1144 | Table 3A | Hs.289071 | AK027187 | 10440255 | cDNA: FLJ22245 fis, clone HRC02612 /cds=UNKNOWN | 1 | TGGTAGCTCTGGCTGTGCTATCA |
| 1145 | Table 3A | Hs.240443 | AK027191 | 10440260 | cDNA: FLJ23538 fis, clone LNG08010, highly similar to BETA2 MEN1 region clone epsilon/beta mRNA /cds=UNKNOWN | 1 | TGGCTCGAAGTTTCTCTAGTGTTC |
| 1146 | Table 3A | Hs.323502 | AK027192 | 10440261 | nuclear RNA export factor 1 (NXF1), mRNA /cds=(0,1679) | 1 | TGTGGAAGGAATAAAATTTGAGT |
| 1147 | Table 3A | Hs.159483 | AK027194 | 10440263 | chromosome 1 open reading frame 7 (C1orf7), mRNA /cds=(46,1590) | 1 | ACTCTTGGGAGTGCTGCAGCTTTAA |
| 1148 | Table 3A | Hs.334853 | AK027197 | 10440266 | hypothetical protein FLJ23544 (FLJ23544), mRNA /cds=(125,517) | 1 | TCATGCTGTTTAACTGTTGTGGC |
| 1149 | Table 3A | Hs.91448 | AK027210 | 10440285 | MKP-1 like protein tyrosine phosphatase (MKP-L), mRNA /cds=(233,829) | 1 | TTTACATGATTGGACCTCAGATTCT |
| 1150 | Table 3A | Hs.169854 | AK027212 | 10440288 | hypothetical protein SP192 (SP192), mRNA /cds=(179,1603) | 1 | GTTAACCAAAATTCAGAATGGGG |
| 1151 | Table 3A | Hs.57209 | AK027232 | 10440314 | hypothetical protein DKFZp566J091 (DKFZP566J091), mRNA /cds=(212,529) | 1 | TGAAATCAAGCACGGTGCGAAGCTT |
| 1152 | Table 3A | Hs.54890 | AK027243 | 10440328 | cDNA FLJ14739 fis, clone NT2RP3002402 /cds=(156,2048) | 1 | GTACCAAGTACAAAAGGTCCATGT |
| 1153 | Table 3A | Hs.279040 | AK027258 | 10440392 | HT001 protein (HT001), mRNA /cds=(241,1203) | 1 | CCTTACTCTGTCCTTGATGGAGGGGA |
| 1154 | Table 3A | Hs.279040 | AK027258 | 10440392 | HT001 protein (HT001), mRNA /cds=(241,1203) | 1 | GAAGGGAGGGCAAAGAAGTTAAAT |
| 1155 | Table 3A | Hs.152925 | AK027260 | 10440394 | mRNA for KIAA1268 protein, partial cds /cds=(0,3071) | 1 | CACCGCCATGCAACTCCATGCCTATT |
| 1156 | Table 3A | Hs.183454 | AK027789 | 14042727 | cDNA FLJ14883 fis, clone PLACE1003596, moderately similar to OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT /cds=(2,862) | 1 | TACTGGAACCTGTTATGCCAAAC |
| 1157 | Table 3A | Hs.122487 | AL040371 | 5409324 | 602365288F1 cDNA, 5' end /clone=IMAGE:4473836 /clone_end=5' | 1 | CAAGAGAATTGAAGGAGGCTAAGGAG |
| 1158 | Table 3A | Hs.79709 | AL042370 | 5421708 | phosphatidylinositol transfer protein (PITPN), mRNA /cds=(216,1028) | 1 | AAGCGCCAGGAACAAATTGCGAAGA |
| 1159 | Table 3A | Hs.252721 | AL042376 | 5421714 | 602022214F1 cDNA, 5' end /clone=IMAGE:4157715 /clone_end=5' | 1 | AGTCTCGGGTATGCTGTTGTGAAT |
| 1160 | Table 3A | Hs.182278 | AL046016 | 5434110 | Homo sapiens, calmodulin 2 (phosphorylase kinase, delta), clone MGC:1447 IMAGE:3504793, mRNA, complete cds /cds=(93,542) | 1 | GAAACTGTAAAAGTAGATGGTTGA |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|---|---|-----------------------------|
| 1161 | Table 3A | NA | AL047171 | 5936355 | (synonym: hute1) cDNA clone DKFZp586F2018 5' | 1 | TTGGTCCCACAGTTTTATGTGTCTCT |
| 1162 | Table 3A | Hs.188757 | AL049282 | 4500041 | Homo sapiens, clone MGC:5564, mRNA, complete cds /cds=(227,304) | 1 | ACTTGAAATTATGTTTCTCCCGT |
| 1163 | Table 3A | Hs.104916 | AL049305 | 4500074 | hypothetical protein FLJ21940 (FLJ21940), mRNA /cds=(92,2107) | 1 | TGGAGGATTTTTGTTAAGTCAAGTGT |
| 1164 | Table 3A | Hs.99821 | AL049319 | 4500092 | hypothetical protein FLJ14547 (FLJ14547), mRNA /cds=(25,711) | 1 | CAATCGAAGTTAAAAAGCAAGGGT |
| 1165 | Table 3A | Hs.77311 | AL049332 | 4500108 | mRNA; cDNA DKFZp564L176 (from clone DKFZp564L176) /cds=UNKNOWN | 1 | ATGGCTCTTTTCTATTAGAGCAACTT |
| 1166 | Table 3A | Hs.86405 | AL049340 | 4500124 | mRNA; cDNA DKFZp564P056 (from clone DKFZp564P056) /cds=UNKNOWN | 1 | GTGTTTCCCTGATAATGTGTACA |
| 1167 | Table 3A | Hs.42915 | AL049356 | 4500146 | ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA /cds=(74,1258) | 1 | GTCGTGACTGACTTGGTGTGTTGCTA |
| 1168 | Table 3A | Hs.184938 | AL049782 | 4902604 | Novel gene mapping to chromosome 13 /cds=UNKNOWN | 1 | TTGTGTTTCTATATACTCCGTCCA |
| 1169 | Table 3A | Hs.326248 | AK025724 | 10438333 | cDNA: FLJ22071 fis, clone HEP11691 /cds=UNKNOWN | 1 | TTTAGTCCAGTGGTTCCACAGCTGG |
| 1170 | Table 3A | Hs.139240 | AL049942 | 4884185 | mRNA; cDNA DKFZp564F1422 (from clone DKFZp564F1422) /cds=(0,1491) | 1 | CTAAGCCAGGAGTCACTTGGAGGC |
| 1171 | Table 3A | Hs.22370 | AL049951 | 4884198 | mRNA; cDNA DKFZp564O0122 (from clone DKFZp564O0122) /cds=UNKNOWN | 1 | TGGAAGACAGTAAAGAACAGCCCTCT |
| 1172 | Table 3A | Hs.150580 | AL050005 | 4884260 | mRNA; cDNA DKFZp564A153 (from clone DKFZp564A153) /cds=UNKNOWN | 1 | GTAGTCAGTAAAGTTTCACCTTCT |
| 1173 | Table 3A | Hs.14846 | AL050021 | 4884264 | mRNA; cDNA DKFZp564D016 (from clone DKFZp564D016) /cds=UNKNOWN | 1 | TGGGTGGAGTATTATGTTTAACTGGA |
| 1174 | Table 3A | Hs.133130 | AL050035 | 4884276 | mRNA; cDNA DKFZp566H0124 (from clone DKFZp566H0124) /cds=UNKNOWN | 1 | GTTGTCAAGTATGAGTCCCTCAGG |
| 1175 | Table 3A | Hs.27371 | AL050061 | 4884292 | mRNA; cDNA DKFZp566J123 (from clone DKFZp566J123) /cds=UNKNOWN | 1 | AAAGTAGTAAATCGGCTGTCTTAAT |
| 1176 | Table 3A | Hs.227429 | AL050131 | 4884338 | mRNA; cDNA DKFZp586I111 (from clone DKFZp586I111); partial cds /cds=(0,617) | 1 | AGTGCCTGTACTAATGGAATT |
| 1177 | Table 3A | Hs.323463 | AL050141 | 4884352 | mRNA for KIAA1693 protein, partial cds /cds=(0,2707) | 1 | ATGTCAAGCTTTGGGTCTCTGGAGTA |
| 1178 | Table 3A | Hs.323463 | AL050141 | 4884352 | mRNA for KIAA1693 protein, partial cds /cds=(0,2707) | 1 | TAACTTTTGTAACATTAGCCATT |
| 1179 | Table 3A | Hs.26295 | AL050166 | 4884381 | mRNA; cDNA DKFZp586D1122 (from clone DKFZp586D1122) /cds=UNKNOWN | 1 | ATCTAGGACACCTCCATCAAACTCC |
| 1180 | Table 3A | Hs.80285 | AL050192 | 4884408 | mRNA; cDNA DKFZp586C1723 (from clone DKFZp586C1723) /cds=UNKNOWN | 1 | TCTTGACATTTCCCTCTGGCTTCC |
| 1181 | Table 3A | Hs.26613 | AL050205 | 4884444 | mRNA; cDNA DKFZp586F1323 (from clone DKFZp586F1323) /cds=UNKNOWN | 1 | TGTGATGGGAACAGTGTCTTAGGGA |
| 1182 | Table 3A | Hs.15020 | AL050218 | 4884459 | DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs /cds=(0,692) | 1 | GATGCAGCTTGGACTTGAGGTAAAT |
| 1183 | Table 3A | Hs.3642 | AL050268 | 4886442 | RAB1, member RAS oncogene family (RAB1), mRNA /cds=(50,667) | 1 | AGAATGGGAGGCCAACCTTCTATCAG |
| 1184 | Table 3A | Hs.12305 | AL050272 | 4886498 | DKFZP566B183 protein (DKFZP566B183), mRNA /cds=(351,749) | 1 | AGTTAAACTTTTGACAAGGGAACA |
| 1185 | Table 3A | Hs.274170 | AL050353 | 4914574 | mRNA; cDNA DKFZp564C0482 (from clone DKFZp564C0482) /cds=UNKNOWN | 1 | AAAAATGTGAAACTGCCCTGCCCTCCC |
| 1186 | Table 3A | Hs.8128 | AL050371 | 4914606 | phosphatidylserine decarboxylase (PLSD), mRNA /cds=(223,1350) | 1 | CTTTTGCTGACAACTCCTTAGGAA |
| 1187 | Table 3A | Hs.322645 | AL050376 | 4914609 | mRNA; cDNA DKFZp586J101 (from clone DKFZp586J101) /cds=UNKNOWN | 1 | CCTCGCCTCTCTCTGCTGTAAGG |
| 1188 | Table 3A | Hs.322645 | AL050376 | 4914609 | mRNA; cDNA DKFZp586J101 (from clone DKFZp586J101) /cds=UNKNOWN | 1 | GCTGCTGTCTAGATTTATGTGTGCTC |
| 1189 | Table 3A | Hs.321247 | AL050391 | 4914591 | mRNA; cDNA DKFZp586A181 (from clone DKFZp586A181); partial cds /cds=(0,314) | 1 | TGACAAGAAATGTTTGTGTAACA |
| | | | | | | 1 | CCAGGCTGCGGTGAGAAATGCCAAGA |
| | | | | | | 1 | AGGCACTACCTCCACCCACATCAC |
| | | | | | | 1 | CCAGTTGTCTTGACAGCCTGACTCC |
| | | | | | | 1 | TGCCAGCCCTATGGAAGTTCTTT |
| | | | | | | 1 | CCAGTTGTCTTGACAGCCTGACTCC |
| | | | | | | 1 | TGCCAGCCCTATGGAAGTTCTTT |
| | | | | | | 1 | TCTTTAAGAAGACCCACATAGAAT |
| | | | | | | 1 | ACCCCTTCTCTAGCTCGCTCTG |
| | | | | | | 1 | TTTGACTTTCAGGATGTCATACTACTT |
| | | | | | | 1 | CTGTACCTAGCATTTTCAGTCCT |
| | | | | | | 1 | TGCTTAGATTTGTTCTGTTGTCAAAA |
| | | | | | | 1 | CTGTTACCCCCAAAATTGGTGTG |
| | | | | | | 1 | AACAGGTACATGCATTATGTGTACAC |
| | | | | | | 1 | ATTACTGGGCAAAGTGTCAAGTA |
| | | | | | | 1 | AGCACAAAGCAGTGTCTGTCACTTTCC |
| | | | | | | 1 | ATGCATAAAGTTTGTAGATGATGTT |
| | | | | | | 1 | AGTGACTAAATACTGGGAACCTATTT |
| | | | | | | 1 | TCTCAATCTTCTCCATGTTGTGT |
| | | | | | | 1 | CTTCAGGACTGTATGAGCCGAGCAGT |
| | | | | | | 1 | TACAAGACACAAAGAAGTAAAAA |
| | | | | | | 1 | AGGGCCAGATTTTCATGTTGACCCTGG |
| | | | | | | 1 | GGATGCTGTGAATTTCTCTGTCAG |
| | | | | | | 1 | AAATGCAGGTTTATTATCCAGCACTG |
| | | | | | | 1 | AGAGAGTTAACAAGGACTGGAAAA |
| | | | | | | 1 | AAATGCAGGTTTATTATCCAGCACTG |
| | | | | | | 1 | AGAGAGTTAACAAGGACTGGAAAA |
| | | | | | | 1 | CCCTCCTTAATCAACTTCAAGGAGCA |
| | | | | | | 1 | CCTTCATTAGTACAGCTTGCATAT |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|---------|--|---|--|
| 1190 | Table 3A | Hs.12813 | AL080156 | 5262614 | mRNA; cDNA DKFZp434J214 (from clone DKFZp434J214); partial cds /cds=(0,1081) | 1 | AAACCAGTGACTCCTAATCTTTTTCAG GTTAAGACACCTTACCATTCGCTT |
| 1191 | Table 3A | Hs.52792 | AL080213 | 5262703 | mRNA; cDNA DKFZp586I1823 (from clone DKFZp586I1823) /cds=UNKNOWN | 1 | AAGGGAACACAAAAGTGTGGTCCTGA CAATACTAATCTACCCGTTTTC |
| 1192 | Table 3A | Hs.111801 | AL096723 | 5419856 | mRNA; cDNA DKFZp564H2023 (from clone DKFZp564H2023) /cds=UNKNOWN | 1 | TTTTTGACGATCAGCCTTACTGCTAA TAAAAGCACTCCACAGGGAAAA |
| 1193 | Table 3A | Hs.306327 | AL096752 | 5419888 | mRNA; cDNA DKFZp434A012 (from clone DKFZp434A012) /cds=UNKNOWN | 1 | AAATTCTACAAAGGAGAGGTTGGGCG TTACAAAGGCATTGTGAATCTAAT |
| 1194 | Table 3A | Hs.306327 | AL096752 | 5419888 | mRNA; cDNA DKFZp434A012 (from clone DKFZp434A012) /cds=UNKNOWN | 1 | AAATTCTACAAAGGAGAGGTTGGGCG TTACAAAGGCATTGTGAATCTAAT |
| 1195 | Table 3A | Hs.172803 | AL109669 | 5689801 | mRNA full length insert cDNA clone EUROMAGE 31839 /cds=UNKNOWN | 1 | TTCACCGAGGACATGAAACTCCACCT TGCGGGGATAAAGAGAGAAAAACA |
| 1196 | Table 3A | Hs.119155 | AL109786 | 5725475 | mRNA full length insert cDNA clone EUROMAGE 814975 /cds=UNKNOWN | 1 | TGTGCTCTTCAGTAGAGGATTTTCTG TGATCCTACAATGAAGGGAAAGCT |
| 1197 | Table 3A | Hs.75875 | AL110132 | 5817027 | ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), transcript variant 2, mRNA /cds=(69,734) | 1 | TTTGTGTAAACCACCTTTTGAAGCA GCAACTATCAAGCTGAAAAGCAA |
| 1198 | Table 3A | Hs.128797 | AL110151 | 5817052 | mRNA; cDNA DKFZp586D0824 (from clone DKFZp586D0824); partial cds /cds=(0,1080) | 1 | AGTGGGTGAATCACAGTAATTTCCCT GTAAATGTGGTACCTGAAGTCAT |
| 1199 | Table 3A | Hs.193700 | AL110164 | 5817069 | cDNA: FLJ22008 fis, clone HEP06934 /cds=UNKNOWN | 1 | TAGGCTCATAGCCTTGATTTCGTTTT AGATTGTAAGCTCAATGGCAGGG |
| 1200 | Table 3A | Hs.73851 | AL110183 | 5817095 | ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F6 (ATP5J), mRNA /cds=(1,327) | 1 | GCTCAAGCAAATGTTTGGTAATGCAG ACATGAATACATTTCCACCTTCA |
| 1201 | Table 3A | Hs.172089 | AL110202 | 5817121 | mRNA; cDNA DKFZp586I2022 (from clone DKFZp586I2022) /cds=UNKNOWN | 1 | AAGTCATCATTTGCCTTGAAAGTTTC CTCTGCATTGGGTTTGAAGTAGTT |
| 1202 | Table 3A | Hs.193784 | AL110204 | 5817123 | mRNA; cDNA DKFZp586K1922 (from clone DKFZp586K1922) /cds=UNKNOWN | 1 | GAGCAGGGGTGGGAGTGGCTGTAAC TTCACAATCCTAATACAGTAAATGT |
| 1203 | Table 3A | Hs.321022 | AL110236 | 5817178 | mRNA; cDNA DKFZp566P1124 (from clone DKFZp566P1124) /cds=UNKNOWN | 1 | TTCTTAAGGAGTCTTAACCTGGTACT TGGGTTAACGCCAGAAATTACTTT |
| 1204 | Table 3A | Hs.187991 | AL110269 | 5817043 | DKFZP564A122 protein (DKFZP564A122), mRNA /cds=(2570,2908) | 1 | TTGGTGAGTTGCCAAAGAAGCAATAC AGCATATCTGCTTTTGCCTTCTGT |
| 1205 | Table 3A | Hs.109727 | AL117407 | 5911992 | mRNA; cDNA DKFZp434D2050 (from clone DKFZp434D2050); partial cds /cds=(110,1720) | 1 | AGGCCTTGTTTTTCAGCTTCATCTGC AGTTCATGTGAAGATTGATAAAT |
| 1206 | Table 3A | Hs.26797 | AL117448 | 5911896 | mRNA; cDNA DKFZp586B1417 (from clone DKFZp586B1417); partial cds /cds=(0,3876) | 1 | TGCAACTTAGAACCAGCTACAGTAT GGCCCACTTAATAAACACCTGAA |
| 1207 | Table 3A | Hs.7200 | AL117502 | 5912009 | hypothetical protein MGC16714 (MGC16714), mRNA /cds=(394,990) | 1 | AGTTTATTGTAGCCAGGTTGCTTGA AAGGTTGAGAGTGGAGTGGTTTGG |
| 1208 | Table 3A | Hs.22583 | AL117513 | 5912025 | mRNA; cDNA DKFZp434K2235 (from clone DKFZp434K2235); partial cds /cds=(0,1086) | 1 | GCATAACTGCTCTAGCTTCTTGTTTA CCATAGTACTGTGGCTTCAGATTT |
| 1209 | Table 3A | Hs.303154 | AL117536 | 5912065 | popeye protein 3 (POP3), mRNA /cds=(147,1022) | 1 | TGTATCTTTTCTGTAAACACACAGA CCCCTCCCAATCTGGACATTGA |
| 1210 | Table 3A | Hs.6607 | AL117565 | 5912115 | URAX1 mRNA, complete cds /cds=(191,1960) | 1 | GCCTTGCCAGCCTGTGTGCTTGTGG GAACACCTTGATCTGAGCTTACAG |
| 1211 | Table 3A | Hs.154320 | AL117566 | 5912116 | ubiquitin-activating enzyme E1C (homologous to yeast UBA3) (UBE1C), mRNA /cds=(0,1328) | 1 | GCATGAATGGGCAATATTTTCTCTG TTTACTTGTAGTGCCATAGAGGCC |
| 1212 | Table 3A | Hs.4055 | AL117595 | 5912159 | mRNA; cDNA DKFZp564C2063 (from clone DKFZp564C2063) /cds=UNKNOWN | 1 | GGCCTTCTATGTGCTTAGCCATAACA ATTCCATTAGCAAGAAGGTAAGC |
| 1213 | Table 3A | Hs.180777 | AL117621 | 5912202 | mRNA; cDNA DKFZp564M0264 (from clone DKFZp564M0264) /cds=UNKNOWN | 1 | AATTGAACAATAACCATTGGTGACTG GAGCAGGTAATTATAGCCTGCAGA |
| 1214 | Table 3A | Hs.87794 | AL117637 | 5912225 | mRNA; cDNA DKFZp434I225 (from clone DKFZp434I225); partial cds /cds=(0,1281) | 1 | AGGGGTCCCAAGAGCCTGTCTCTTT TGTTCAAATACATCTTGAAACGT |
| 1215 | Table 3A | Hs.79709 | AL117644 | 5912234 | phosphatidylinositol transfer protein (PITPN), mRNA /cds=(216,1028) | 1 | CCTGCTGGGACTCCCTGACTTACTTT GGTGGTTCCTAGTGCTACTTGTT |
| 1216 | Table 3A | NA | AL120453 | 5926352 | (synonym: hamy2) cDNA clone DKFZp761I208 5' | 1 | GGAAAGCTCGTCAGTTTAGTAGGCTC CGAAATAGAATTAGCAGTTGTCACT |
| 1217 | Table 3A | Hs.6986 | AL121406 | 5927407 | glucose transporter pseudogene /cds=UNKNOWN | 1 | AGAAGGTAACCTTATAGAAGTAACAC CAATATCCTAGTCTGCTTGCCCCG |
| 1218 | Table 3A | Hs.274481 | AL121735 | 6012990 | cellular growth-regulating protein (LOC51038), mRNA /cds=(612,785) | 1 | GCTGCTCCCTGGTTCCTCTGGAGA GTAATCTGGGACATCTAGTGTTC |
| 1219 | Table 3A | Hs.272307 | AL133015 | 6453493 | mRNA; cDNA DKFZp434O2417 (from clone DKFZp434O2417); partial cds /cds=(0,724) | 1 | CTCTCCTCTCCACCTCTGTATCCC ACACAGGCATCTGGTGATGTTCTC |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|--|---|-----------------------------|
| 1220 | Table 3A | Hs.75497 | AL133074 | 6453517 | p53DINP1 mRNA for p53DINP1b, complete cds /cds=(39,533) | 1 | ACACCTGTTCTTTGTAATTGGGTTGT |
| 1221 | Table 3A | Hs.76853 | AL133096 | 6453550 | mRNA; cDNA DKFZp434N1728 (from clone DKFZp434N1728) /cds=UNKNOWN | 1 | GGTGCAATTTTGCACCTACCTGGAGT |
| 1222 | Table 3A | Hs.109150 | AL133111 | 6453598 | mRNA; cDNA DKFZp434H068 (from clone DKFZp434H068) /cds=UNKNOWN | 1 | AGCCTAGGTGAAATCTATTATAAAT |
| 1223 | Table 3A | Hs.199009 | AL133572 | 6599150 | PCCX2 mRNA for protein containing CXXC domain 2, partial cds /cds=(0,2483) | 1 | GGACCACAACTCTGGGGTGTCTGT |
| 1224 | Table 3A | Hs.25362 | AL133611 | 6599222 | mRNA; cDNA DKFZp434O1317 (from clone DKFZp434O1317) /cds=UNKNOWN | 1 | CATGAAGCTCTCAAGTCTGCATCCT |
| 1225 | Table 3A | Hs.224680 | AL133721 | 6601909 | DKFZp761H09121_r1 cDNA, 5' end /clone=DKFZp761H09121 /clone_end=5' | 1 | GAGGATCCAGATGGATGACAAGGA |
| 1226 | Table 3A | Hs.306155 | AL133879 | 6602066 | chorionic somatomammotropin hormone 1 (placental lactogen) (CSH1), transcript variant 2, mRNA /cds=(116,886) | 1 | GGTGGTGTTCCTAGACCTTCCTCGA |
| 1227 | Table 3A | Hs.322456 | AL136542 | 12044472 | hypothetical protein DKFZp761D0211 (DKFZP761D0211), mRNA /cds=(164,1822) | 1 | TGCGATTTTACCTTTGTTGAATTT |
| 1228 | Table 3A | Hs.258503 | AL136549 | 6807648 | mRNA; cDNA DKFZp761I12121 (from clone DKFZp761I12121); complete cds /cds=(138,3899) | 1 | ACGATGCTGTTTGCTCTGGAATGTTT |
| 1229 | Table 3A | Hs.177537 | AL136558 | 13276622 | hypothetical protein DKFZp761B1514 (DKFZp761B1514), mRNA /cds=(72,1028) | 1 | ATCTTTTAGACAGGTTTTGGCTCA |
| 1230 | Table 3A | Hs.245798 | AL136607 | 12052739 | hypothetical protein DKFZp564I0422 (DKFZP564I0422), mRNA /cds=(510,1196) | 1 | TCCGAGGGATGAGATTAAGGCAGAG |
| 1231 | Table 3A | Hs.4750 | AL136610 | 12052745 | hypothetical protein DKFZp564K0822 (DKFZP564K0822), mRNA /cds=(9,527) | 1 | GCAAAAGTTTCACACAAAGTTCTG |
| 1232 | Table 3A | Hs.108548 | AL136640 | 12052805 | mRNA; cDNA DKFZp564F163 (from clone DKFZp564F163); complete cds /cds=(149,532) | 1 | GCCACAACCTCCCATAGTGCCATGT |
| 1233 | Table 3A | Hs.27181 | AL136656 | 12052835 | nuclear receptor binding factor-2 (NRBF-2), mRNA /cds=(179,1042) | 1 | TTTGATAGCCTCAGTTTCTCAACG |
| 1234 | Table 3A | Hs.57209 | AL136703 | 12052925 | hypothetical protein DKFZp566J091 (DKFZP566J091), mRNA /cds=(212,529) | 1 | TGACCCACCCACCAAGGAAGAAAGC |
| 1235 | Table 3A | Hs.166254 | AL136711 | 12052941 | hypothetical protein DKFZp566I133 (DKFZP566I133), mRNA /cds=(133,1353) | 1 | AGAATAAACATTTTTGCACTGCCTG |
| 1236 | Table 3A | Hs.324275 | AL136739 | 12052996 | WW domain-containing protein 1 (WWP1), mRNA /cds=(10,2778) | 1 | CATGCTCTCCCATGACATCTCCATGC |
| 1237 | Table 3A | Hs.273294 | AL136797 | 12053106 | mRNA; cDNA DKFZp434N031 (from clone DKFZp434N031); complete cds /cds=(18,3608) | 1 | TGGTTTCTCCATAGCATAAATGAA |
| 1238 | Table 3A | Hs.76698 | AL136807 | 12053124 | mRNA; cDNA DKFZp434L1621 (from clone DKFZp434L1621); complete cds /cds=(315,515) | 1 | GGTGCCGTGCATCACCAATGAAAGT |
| 1239 | Table 3A | Hs.238996 | AL136828 | 12053164 | hypothetical protein DKFZp434K0427 (DKFZP434K0427), mRNA /cds=(341,1813) | 1 | TTGTATTTAACGAGGAGGTGCTTT |
| 1240 | Table 3A | Hs.146037 | AL136874 | 12053252 | hypothetical protein DKFZp434C135 (DKFZP434C135), mRNA /cds=(118,1206) | 1 | AAATCCTCTCTGCTGTTACATTATCC |
| 1241 | Table 3A | Hs.103378 | AL136885 | 12053268 | hypothetical protein MGC11034 (MGC11034), mRNA /cds=(245,640) | 1 | TTTGTTTAACGTATGAACCAGGT |
| 1242 | Table 3A | Hs.37892 | AL136932 | 12053358 | KIAA0922 protein (KIAA0922), mRNA /cds=(122,3841) | 1 | GTGTAGAATTCGCGAGCGTCCGTG |
| 1243 | Table 3A | Hs.37892 | AL136932 | 12053358 | KIAA0922 protein (KIAA0922), mRNA /cds=(122,3841) | 1 | GTTCAGAGTAACTTGAAGCAGATC |
| 1244 | Table 3A | Hs.108338 | AL136941 | 12053376 | hypothetical protein DKFZp586C1924 (DKFZp586C1924), mRNA /cds=(105,692) | 1 | TGGTAGGTTAAGCTGCCATACGTGT |
| 1245 | Table 3A | Hs.194718 | AL136945 | 12053384 | mRNA; cDNA DKFZp586O012 (from clone DKFZp586O012) /cds=UNKNOWN | 1 | TCAGTGTGAATAGTGTTTAAGTTG |
| 1246 | Table 3A | Hs.7392 | AL137423 | 6807979 | nucleolar protein GU2 (GU2), mRNA /cds=(107,2320) | 1 | TGATGCAAGAGTGACGTAATGCTAG |
| 1247 | Table 3A | Hs.21015 | AL137576 | 6808287 | mRNA; cDNA DKFZp564L0864 (from clone DKFZp564L0864); partial cds /cds=(0,566) | 1 | TTGGCAGTATTTTATTGTGAAGAAA |
| 1248 | Table 3A | Hs.122752 | AL137601 | 6808346 | TATA box binding protein (TBP)-associated factor, RNA polymerase II, B, 150kD (TAF2B), mRNA /cds=(57,3656) | 1 | TCAGTAAAAATGCCTGTTGTGAGATG |
| | | | | | | | AACCTCCTGTAACCTTCATCTGTT |
| | | | | | | | GGGCCATTTTATGATGCATTGCACAC |
| | | | | | | | CCTCTGGGGAATTGATCTTTAAA |
| | | | | | | | AAAATGCTGCTGGCTTTTCTGAAGAC |
| | | | | | | | AGGTGCTTGAACCTTGTCAGTTTGT |
| | | | | | | | CGCCCCAAAAGTCTGTTCTGATGGCA |
| | | | | | | | CTGAGTTTTCATTGTTCTGGATGT |
| | | | | | | | TGTTGTGCTAAATTCATAGCAGGTG |
| | | | | | | | CCTTATTCTTTGCTTTTAGTCAAA |
| | | | | | | | TTTGCCAGGGTAATCTTCAGTTGGCC |
| | | | | | | | CTGATTCAATTAATGGCCTTAAT |
| | | | | | | | ACACTCCTTAAGTCCAAATGTTTTCC |
| | | | | | | | GCTAATAGTCTGTCTAAAGCCT |
| | | | | | | | AGGACTCTTGACATCTGAGCAGTTT |
| | | | | | | | TGTGCTTTGAGCCACTTTTTGACA |
| | | | | | | | CGCCTATATGAACCTGGACATATGGA |
| | | | | | | | CTACCACAGCGAATAGGAATGCAA |
| | | | | | | | CGCCTATATGAACCTGGACATATGGA |
| | | | | | | | CTACCACAGCGAATAGGAATGCAA |
| | | | | | | | TTTCCTATTTTGCTCCAGACATGTTT |
| | | | | | | | TCAGCATACCTTGGGTCTGAACA |
| | | | | | | | TTGTGCTTTCTGTATTTAAACTTTGG |
| | | | | | | | CTGTACTAAGCAAATGCAAGGTT |
| | | | | | | | GGTCATCATAGTTGAGGTATGTGTCT |
| | | | | | | | GCTATTTGCAAGAAAGTTGGTCGT |
| | | | | | | | TTCAGGACCCTAGAGGAGAGCTTTAT |
| | | | | | | | ACAATTACCGATGTGAATTTCTCT |
| | | | | | | | TGTTTTGCTTAATGTGGACAATTTACA |
| | | | | | | | CACCCACACATACTGTTTCCAA |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|--|---|---|
| 1249 | Table 3A | Hs.145612 | AL137608 | 6808357 | RNA helicase (RIG-I), mRNA /cds=(157,2934) | 1 | GAGATCAACGGGATGAGGTGTTACA GCTGCCTCCCTCTTCATGCAATCTG |
| 1250 | Table 3A | Hs.173912 | AL137681 | 6807931 | eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA /cds=(15,1238) | 1 | AGGTAGGGTTTAATCCCCAGTAAAT TGCCATATTGCACATGCTTAATG |
| 1251 | Table 3A | Hs.306195 | AL137721 | 6808159 | over-expressed breast tumor protein (OBTP), mRNA /cds=(0,224) | 1 | AGGGGGTGATTTTTGCTCTGTCTCTG AGAAATAACAGTGTGTTTTAAAA |
| 1252 | Table 3A | Hs.12144 | AL137753 | 6808455 | mRNA; cDNA DKFZp434K1412 (from clone DKFZp434K1412) /cds=UNKNOWN | 1 | ACTTGAGTGGGGTTTTCTTTTCCCC CAATTCTAAGAGAATATAATGTGT |
| 1253 | Table 3A | Hs.77646 | AL137938 | 6851002 | mRNA; cDNA DKFZp761M0223 (from clone DKFZp761M0223) /cds=UNKNOWN | 1 | GCGTCTGTTGTTAGCAAAGAATAGAT TCACACAGTCTAAGGTTTCTTCC |
| 1254 | Table 3A | Hs.235390 | AL157426 | 7018455 | mRNA; cDNA DKFZp761B101 (from clone DKFZp761B101) /cds=UNKNOWN | 1 | CCCTCTTAGCCTATCCATCTTAAGCC CCAAGCTGAGTGTGGTTCTGGTAA |
| 1255 | Table 3A | Hs.66151 | AL157438 | 7018513 | mRNA; cDNA DKFZp434A115 (from clone DKFZp434A115) /cds=UNKNOWN | 1 | TAAGGAGAATTAGACTCCCAAGTAGA CACCAGAGTCACTGTTTGGTTGGT |
| 1256 | Table 3A | Hs.110702 | AL157477 | 7018497 | mRNA; cDNA DKFZp761E212 (from clone DKFZp761E212) /cds=UNKNOWN | 1 | ACGTGTTTTTGGGATATGTTTCCAAT CTTTAAATGACCTTGCCCTGTCCA |
| 1257 | Table 3A | Hs.250535 | AL157499 | 7018548 | mRNA; cDNA DKFZp434N2412 (from clone DKFZp434N2412) /cds=UNKNOWN | 1 | AACCATTTGTAACTGTACTGAAGGT GTGTCCTCAAGAAAGAGTGTTC |
| 1258 | Table 3A | Hs.170171 | AL161952 | 7328002 | mRNA; cDNA DKFZp434M0813 (from clone DKFZp434M0813); partial cds /cds=(430,788) | 1 | AAACAACTGTGTAAGTGCCTAAAGC AGCACTTATAAATCAGCCTAACAT |
| 1259 | Table 3A | Hs.71252 | AL161991 | 7328122 | mRNA; cDNA DKFZp761C169 (from clone DKFZp761C169); partial cds /cds=(996,2474) | 1 | AACTGATCACACTGACTGGATCTGT CCACGACATGGAAAAATAACTGGA |
| 1260 | Table 3A | Hs.99908 | AL162047 | 7328089 | nuclear receptor coactivator 4 (NCOA4), mRNA /cds=(140,1984) | 1 | TTGCATTGATGAATTTTGTATCTGCTT CCATTAAGCATACAGCCACA |
| 1261 | Table 3A | Hs.78829 | AL162049 | 7328093 | mRNA; cDNA DKFZp762E1712 (from clone DKFZp762E1712); partial cds /cds=(0,2477) | 1 | ATCTCTCCTTCAGTCTGCTCTGTTAA TTCTGCTGTCTCTCTCTCTAA |
| 1262 | Table 3A | Hs.302649 | AL162068 | 7328143 | HSP22-like protein interacting protein (LOC64165), mRNA /cds=(0,155) | 1 | TTGAAGTTTTAAGGGACGTCAGTGT TATGCCATTTTCCAGTTCCAAAA |
| 1263 | Table 3A | Hs.17377 | AL162070 | 7328146 | mRNA; cDNA DKFZp762H186 (from clone DKFZp762H186); complete cds /cds=(0,1489) | 1 | GGTCGGCTCTTATAGAGTGGCCATAG TGTTCTGTCAAAACACTTGCTTCC |
| 1264 | Table 3A | Hs.155191 | AL162086 | 7328174 | villin 2 (ezrin) (VIL2), mRNA /cds=(117,1877) | 1 | TTCTCCTTCACAGCTAAGATGCCATG TGCAGGTGGATTCCATGCCGAGA |
| 1265 | Table 3A | Hs.3576 | AL357536 | 8249879 | Homo sapiens, Similar to RIKEN cDNA 5730494N08 gene, clone MGC:13348 IMAGE:4132400, mRNA, complete cds /cds=(132,494) | 1 | CATGATTCCAAGGATCAGCCTGGATG CCTAGAGGACTAGATCACCTTAGT |
| 1266 | Table 3A | Hs.29797 | AL359585 | 8655645 | mRNA; cDNA DKFZp762B195 (from clone DKFZp762B195) /cds=UNKNOWN | 1 | AGTGAAGATCTGGCTGAACAGTTCC ACAAGTTACTGTATACATAGCCT |
| 1267 | Table 3A | Hs.252588 | AL359626 | 8655704 | mRNA; cDNA DKFZp564F172 (from clone DKFZp564F172) /cds=UNKNOWN | 1 | AGGCCATCATCTATACCTCATTTAA GCCATTGTTATCAAGGGTTTACCC |
| 1268 | Table 3A | Hs.33756 | AL359654 | 8670873 | mRNA full length insert cDNA clone EUROIMAGE 196784 /cds=UNKNOWN | 1 | AGAGTACATGAAAGTTAGGTGTTCA AATTCACATCTAATTTCCCTGGGA |
| 1269 | Table 3A | Hs.3640 | AL359940 | 8977897 | mRNA; cDNA DKFZp762P1915 (from clone DKFZp762P1915) /cds=UNKNOWN | 1 | GTTTTAGTTTTCCCTTTACAGTCTT CTCCCTCACCTCCAGGACCTC |
| 1270 | Table 3A | Hs.318501 | AL360190 | 8919391 | stimulated trans-acting factor (50 kDa) (STAF50), mRNA /cds=(122,1450) | 1 | ATCCTTCAGAAATGTGTTGGTTTACCA GTGACACCCCATATTCATCACAAA |
| 1271 | Table 3A | Hs.7104 | AL390127 | 9368821 | mRNA; cDNA DKFZp761P06121 (from clone DKFZp761P06121) /cds=UNKNOWN | 1 | GTCTGGCCTTGCTGCTCGGATAAA ACTTTGTATGATTTTGTATGGCA |
| 1272 | Table 3A | Hs.49822 | AL390132 | 9368828 | mRNA; cDNA DKFZp547E107 (from clone DKFZp547E107) /cds=UNKNOWN | 1 | TGCTGAGCATGGGAATGTGGCTGCT TGCAGAGACGTTATGAACACTTCT |
| 1273 | Table 3A | Hs.98026 | AL442083 | 10241762 | mRNA for KIAA1784 protein, partial cds /cds=(0,3505) | 1 | TCTCCATCCTTGTAATGTCTCGTC TGTTTCAAATACAGTGCAGTCAGT |
| 1274 | Table 3A | Hs.77868 | AL513780 | 12777274 | ORF (LOC51035), mRNA /cds=(135,1031) | 1 | TGGTTCTTCTGATGAGCAAGGGAACA ACACTGAGAATGAGGAGGAAGGAGT |
| 1275 | Table 3A | Hs.181309 | AL520892 | 12784385 | proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2), mRNA /cds=(0,704) | 1 | TGAAGTTAAGGATTACTTGCTGCCA TAGCATAACAATGAAGTGACTGAA |
| 1276 | Table 3A | Hs.16648 | AL523085 | 12786578 | AL523085 cDNA /clone=CS0DC001YF21-(5-prime) | 1 | GGCTTTCTGTTTTGGTGTCTGGAG TGCTGGGTAAAGTTCACTGGATAT |
| 1277 | Table 3A | Hs.37617 | AL532303 | 12795796 | 602144947F1 cDNA, 5' end /clone=IMAGE:4308683 /clone_end=5' | 1 | CTATCTACACCATCATGCGTGGTTC CGGAGACACAAGGTGCGGGCTCAC |

Table 8

| | | | | | | | |
|------|----------|-----------|-----------|----------|---|---|--|
| 1278 | Table 3A | Hs.83583 | AL532406 | 12795899 | actin related protein 2/3 complex, subunit 2 (34 kD) (ARPC2), mRNA /cds=(84,986) | 1 | GAAGCGGCTGGCAACTGAAGGCTGG AACACTTGCTACTGGATAATCGTAG |
| 1279 | Table 3A | Hs.30120 | AL533737 | 12797230 | 602272333F1 cDNA, 5' end /clone=IMAGE:4360233 /clone_end=5' | 1 | AAGCAAGAGATTGTAAACCGGGTACA GAATCCAAGAGATGAGAGAGGACC |
| 1280 | Table 3A | Hs.179999 | AL534564 | 12798057 | Homo sapiens, clone IMAGE:3457003, mRNA /cds=UNKNOWN | 1 | AGACGAATGCTTGTCAGTTGTAGCTT TCCAGGATTCTGCTCCAATGAGGA |
| 1281 | Table 3A | Hs.159065 | AL538276 | 12801769 | AL538276 cDNA /clone=CS0DF027YC09-(5-prime) | 1 | CAAAGTATTGCGGGGAGGGGACTT GAGTATGGGGAGAGGCTGCAAAAGA |
| 1282 | Table 3A | Hs.285401 | AL540399 | 12870508 | colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), mRNA /cds=(28,2721) | 1 | GAACATCAGGAGAGGAGTCCAGAGC CCACGCTACTGCGGAAAAGTCAGG |
| 1283 | Table 3A | Hs.181400 | AL542592 | 12874788 | 602650370T1 cDNA, 3' end /clone=IMAGE:4761353 /clone_end=3' | 1 | AGTTGGAGAGTTACTCGAACCTCAGG TGACAGTTGTAAGGCAGACATAGT |
| 1284 | Table 3A | Hs.271599 | AL550229 | 12886998 | cDNA FLJ12347 fis, clone MAMMA1002298 /cds=UNKNOWN | 1 | CTCCTCCAGGCCTCTCGGATGCCTCT GTTGGGACAGCTAAGTTCCTCTTC |
| 1285 | Table 3A | NA | NC_001807 | 13959823 | Mitochondrial Sequence | 1 | TCCTCCATATATCCAACAACAAAGC ATAATATTTGCCCCACTAAGCCAA |
| 1286 | Table 3A | Hs.218329 | AL556016 | 12898299 | mRNA for KIAA1245 protein, partial cds /cds=(701,3379) | 1 | TGCTGTTGCAAAAGAGAAGACATCT CTGCCTGAGTTTAAATTTTGCCA |
| 1287 | Table 3A | Hs.250465 | AL556919 | 12900027 | mRNA; cDNA DKFZp434E2023 (from clone DKFZp434E2023) /cds=UNKNOWN | 1 | TTTCTGCTGGAGTCCCTGTGTCTCTC AGCCATCCCAAGAAGGGTTTGCTG |
| 1288 | Table 3A | Hs.90035 | AL558028 | 12902157 | AL558028 cDNA /clone=CS0DJ002YF02-(5-prime) | 1 | CTGGTTGGATCTGCATCTCACGCCCA CTGCACACCGTTCTCTCCATCTG |
| 1289 | Table 3A | Hs.301756 | AL559029 | 12904124 | Homo sapiens, clone MGC:17544 IMAGE:3462146, mRNA, complete cds /cds=(256,894) | 1 | ACCTCGACTCCCTGGTCTCTTTGCA GAGTTGGGCAGTGAAATTACCTTT |
| 1290 | Table 3A | Hs.119274 | AL559422 | 12904908 | RAS p21 protein activator (GTPase activating protein) 3 (Ins(1,3,4,5)P4-binding protein) (GAP1IP4BP), mRNA /cds=(46,2550) | 1 | ATACACAGCAGACGATCCTTGTTAC CGACTTCTCCCGTTCTTGTTGA |
| 1291 | Table 3A | Hs.218329 | AL559555 | 12905153 | mRNA for KIAA1245 protein, partial cds /cds=(701,3379) | 1 | GTAATTAGGAAGACACAGCTAGATGG ACAACAGCATTGGGAGGCTTAGCC |
| 1292 | Table 3A | Hs.33026 | AL561074 | 12908145 | mRNA for FLJ00037 protein, partial cds /cds=(3484,3921) | 1 | CATCTCTGGTTGTGTCTGTGCCGACT CGGTGTTGAATCAAATCAGGTGTG |
| 1293 | Table 3A | Hs.335863 | BE262306 | 9135208 | 601462961T1 cDNA, 3' end /clone=IMAGE:3866222 /clone_end=3' | 1 | CAACAATAGGAGGTGGAATGCTGCAA GGGGCTGCAAAATGAGGGCAATGCA |
| 1294 | Table 3A | NA | NC_001807 | 13959823 | mitochondrial COX3 | 1 | ATATTTCACTTTACATCCAAACATCAC TTTGGCTTCGAAGCCGCCGCTG |
| 1295 | Table 3A | Hs.287797 | AU117298 | 10932256 | mRNA for FLJ00043 protein, partial cds /cds=(0,4248) | 1 | TGGCAAATTCGCGAGTGTGATAATT TCAACTGTGATAGATCCAATGGCT |
| 1296 | Table 3A | Hs.1600 | AU118159 | 10933184 | Homo sapiens, clone IMAGE:3543711, mRNA, partial cds /cds=(0,1620) | 1 | TCTCAGATGTCCATTGAAACCAACCCA AACCAAAACAAAGCATAAGCTGG |
| 1297 | Table 3A | Hs.181165 | AU120731 | 10935966 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(53,1441) | 1 | TCCAGGATGTCTACAAAATTGGTGGT ATTGGTACTGTTCTGTTGGCCGA |
| 1298 | Table 3A | Hs.172028 | AU135154 | 10995693 | a disintegrin and metalloproteinase domain 10 (ADAM10), mRNA /cds=(469,2715) | 1 | TGGACATAGCAGCACATACTACTTCA GAGTTCATGATGATGTCTGGT |
| 1299 | Table 3A | NA | AV686223 | 10288086 | AV686223 cDNA, 5' end /clone=GKCGXH11 /clone_ | 1 | AACAGAAGACGAGGACACAGAGCGA GAATAAGCACAACTCAGACAACACA |
| 1300 | Table 3A | Hs.343475 | AV687530 | 10289393 | 601556208T1 cDNA, 3' end /clone=IMAGE:3826392 /clone_end=3' | 1 | TGACCACTTATGCATTTCTGAATTTG CTTTCCATGCTCAGAGTTCTGCT |
| 1301 | Table 3A | NA | AV689330 | 10291193 | cDNA clone GKCDJE03 5' | 1 | CTTTGACCCACCTTGTTGGAACCCCA GCTGTCTACTGGCAGACATTGGTG |
| 1302 | Table 3A | Hs.28739 | AV691642 | 10293505 | 602593745F1 cDNA, 5' end /clone=IMAGE:4721002 /clone_end=5' | 1 | AAACACCAAGTTGCAGGAAGAAAGGA AGAGAATTGGAATTGCTTCTGGAA |
| 1303 | Table 3A | NA | AV693913 | 13959823 | mitochondrion, complete genome | 1 | CCCTACCATGAGCCCTACAAACAACCT AACCTGCCACTAATAGTTATGTCA |
| 1304 | Table 3A | Hs.324602 | AW969923 | 8159767 | EST382001 cDNA | 1 | AGTCGTATTAGAGCCTTGGCGTAATC ATGGTCATAGCTGTTTCTGTGTG |
| 1305 | Table 3A | Hs.301570 | AV702152 | 10718482 | 602585120F1 cDNA, 5' end /clone=IMAGE:4712861 /clone_end=5' | 1 | TTGCTGCCTGATCTGACATACATGAT CCATCGGGTTTTGTCAAGGAAC |
| 1306 | Table 3A | Hs.7312 | AV702692 | 10719022 | AV702692 cDNA, 5' end /clone=ADBBQC12 /clone_end=5' | 1 | CATGTTTCATAGGTAATCTTTGTACTCT GTGTGCAGCAGTATTTGGTTTGC |
| 1307 | Table 3A | NA | AV705900 | 10723195 | Partial Cloning Vector | 1 | AATTCGCCCTATAGTGAGTCGATTAC CAATCACTGCCCGCGTTTACACG |
| 1308 | Table 3A | Hs.167130 | AV706014 | 10723303 | hypothetical protein (PRED22), mRNA /cds=(245,1021) | 1 | ACAGGTAAGTGAAGATCAAAGTAAAG CAACAGAGGAATGTACATCTACCT |

Table 8

| | | | | | | | |
|------|----------|-----------|-----------|----------|---|---|---|
| 1309 | Table 3A | Hs.134829 | AV706481 | 10723761 | AV706481 cDNA, 5' end /clone=ADBBYF02 /clone_end=5' | 1 | AACAGTTGGGCACCCTGAATGGCAAA TGGCAAATTTGGAGCGCTAATAAT |
| 1310 | Table 3A | NA | NC_001807 | 13959823 | mitochondrion, complete genome | 1 | GCCAACTACTTTATTGACTCTAGCC GCAGACCTCCTCATTCTAACCTGA |
| 1311 | Table 3A | Hs.90960 | AV710415 | 10729044 | 602563938F1 cDNA, 5' end /clone=IMAGE:4688769 /clone_end=5' | 1 | ATGTGGGAGGGGCGATGGCAGCTATG AAGGACCTCTACCTCTGTTTCTG |
| 1312 | Table 3A | Hs.316785 | AV710763 | 10730069 | AV710763 cDNA, 5' end /clone=CuAAJH09 /clone_end=5' | 1 | CATGGGACGGGGAGAAAAAGCAAAAC CCTGGCACTTGGGAATACTTATACC |
| 1313 | Table 3A | Hs.135167 | AV712376 | 10731682 | AV712376 cDNA, 5' end /clone=DCAAND12 /clone_end=5' | 1 | TTGTGCCCTTGACTGGGTATTTCTTG AAGCCCTTGGATCTACCTTTGGTC |
| 1314 | Table 3A | Hs.89104 | AV716500 | 10798017 | 602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5' | 1 | ACATAATACGGTTGTGCGACGAGAGA ATCTACCTTCCACTTCTAAGCCT |
| 1315 | Table 3A | Hs.237868 | AV716565 | 10813717 | interleukin 7 receptor (IL7R), mRNA /cds=(22,1401) | 1 | CCAGCCTTTGCTCTTCTTCAATGT GGTTTCCATGGGAATTTGCTTCAG |
| 1316 | Table 3A | Hs.178703 | AV716627 | 10813779 | AV716627 cDNA, 5' end /clone=DCBBCH05 /clone_end=5' | 1 | AAAACCTCGAGTCATGGTGAATGAGT GTCTCGGAGTTGCTCGTGTGTGTA |
| 1317 | Table 3A | Hs.17481 | AV716644 | 10813796 | mRNA; cDNA DKFZp434G2415 (from clone DKFZp434G2415) /cds=UNKNOWN | 1 | GTGAGCACGGACATGCGGCATCATC GAGTGAGACTGGTGTCCAAGATTC |
| 1318 | Table 3A | Hs.256959 | AV719442 | 10816594 | AV719442 cDNA, 5' end /clone=GLCBNA01 /clone_end=5' | 1 | CACCACAGTCTCAGTGCAGGGCTGG GAAGTGAAAGACGATTACACGACC |
| 1319 | Table 3A | NA | AV719659 | 10816811 | cDNA clone GLCGR09 5' | 1 | TTTGTGGGTGGGTGATTAGTCTGTGC TGATGAGATATTTTGGGGTGGGG |
| 1320 | Table 3A | Hs.127160 | AV719938 | 10817090 | AV659177 cDNA, 3' end /clone=GLCFUC08 /clone_end=3' | 1 | ACCTTGTAGTGCCTAAGAAATGAGA CTACAAGCTCCATTTCAGCAGGAC |
| 1321 | Table 3A | Hs.21536 | AV720984 | 10818136 | yf69a03.s1 cDNA, 3' end /clone=IMAGE:27414 /clone_end=3' | 1 | GCCGAGACTCTGCTCAGCATACATGG CTTCCACTATAGGGTTCTACAGTGT |
| 1322 | Table 3A | Hs.119908 | AV721008 | 10818160 | nucleolar protein NOP5/NOP58 (NOP5/NOP58), mRNA /cds=(0,1589) | 1 | AAATCAGAATTCATTTAGCTCACCAC ATCTCTTGAATGTGATTGACCTAC |
| 1323 | Table 3A | Hs.247474 | AV723437 | 10826838 | hypothetical protein FLJ21032 (FLJ21032), mRNA /cds=(235,1005) | 1 | AGGTGTTTAAACAGTGTATTTTGCCA CTGGTAATGTGTAACCTGTGAGTG |
| 1324 | Table 3A | Hs.76728 | AV724531 | 10829010 | 602570065F1 cDNA, 5' end /clone=IMAGE:4694321 /clone_end=5' | 1 | TGGAGTTTCCAGGAGAAAAATAATCA CCTTTGAAGGTTTTAGAGCATGT |
| 1325 | Table 3A | Hs.280261 | BE382869 | 9328234 | 601297762F1 cDNA, 5' end /clone=IMAGE:3627806 /clone_end=5' | 1 | GGTAACAACATCCGTCTGAAAGGGTC GGACCTCGTCCAAAGGAGATAGGC |
| 1326 | Table 3A | Hs.21351 | AV724665 | 10829278 | qd15g09.x1 cDNA, 3' end /clone=IMAGE:1723840 /clone_end=3' | 1 | ACATTTTGATTTCTTCTCTGTGGG GTGGCAAGTTGAGGGAGCATCTT |
| 1327 | Table 3A | Hs.44656 | AV726117 | 10832185 | AV726117 cDNA, 5' end /clone=HTCAXB05 /clone_end=5' | 1 | CGTAAACCAATGTGGTACACTAGTTG GCCCGAAGTTGGTATAAACCGCCT |
| 1328 | Table 3A | Hs.245798 | AV727063 | 10836484 | hypothetical protein DKFZp564I0422 (DKFZP564I0422), mRNA /cds=(510,1196) | 1 | TCTTTAAGTCTGTCAAAGCAGAACTC TTTGAAGCACTTTGAACAATGCCC |
| 1329 | Table 3A | Hs.316771 | AV729160 | 10838581 | AV729160 cDNA, 5' end /clone=HTCCAB04 /clone_end=5' | 1 | AGCTGGCGTAATAGCGAAGAGGCCCC GCACCGATCGCCTTTCCAACAAGTG |
| 1330 | Table 3A | Hs.22003 | AV730135 | 10839556 | solute carrier family 6 (neurotransmitter transporter, GABA), member 1 (SLC6A1), mRNA /cds=(234,2033) | 1 | AGATGCATTTTAAATGTCTATAAATGG TGTCATACTAGAGCACGGGCGT |
| 1331 | Table 3A | Hs.175971 | AV734916 | 10852461 | AV734916 cDNA, 5' end /clone=cdAAHE11 /clone_end=5' | 1 | ATTTAAACGCTTGGAAGAAAATCCCC TTTTGGCAGGTGGGGGAAAAAGCA |
| 1332 | Table 3A | NA | AV735258 | 10852803 | mitochondrion, complete genome | 1 | ATTTCAACCAATAGCCCTTGCCTACC GCCTACCCGTAACATTACTGGAGG |
| 1333 | Table 3A | NA | NC_001807 | 10855754 | Mitochondrial Sequence | 1 | CGCCTATAGCACTCGAATAATTCTTC TCACCCTAACAGGTCAACCTCGCT |
| 1334 | Table 3A | Hs.246796 | AV739961 | 10857542 | AV739961 cDNA, 5' end /clone=CBFBRA10 /clone_end=5' | 1 | GTTGTGCATGATTTCCCACTGTCTC TGTTTATCCAGATAAGAAAGATA |
| 1335 | Table 3A | Hs.122431 | AV743635 | 10861216 | AV713062 cDNA, 5' end /clone=DCAADD12 /clone_end=5' | 1 | TCTTTTAGGATTTGTCTTTTAGAATCT CCAGCTCTACAGGAAAAACCCCT |
| 1336 | Table 3A | Hs.42915 | AV745692 | 10865139 | ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA /cds=(74,1258) | 1 | TGGGTGGAGTATTATGTTTAACTGGA GTTGTCAAGTATGAGTCCCTCAGG |
| 1337 | Table 3A | Hs.26670 | AV749844 | 10907692 | PAC clone RP3-515N1 from 22q11.2- q22 /cds=(0,791) | 1 | ACCTCATTCTGACACCTGCATATAGT GTGGGAAATTGCTCTGCATTGAC |
| 1338 | Table 3A | Hs.31409 | AV752358 | 10910206 | 602685862F1 cDNA, 5' end /clone=IMAGE:4818566 /clone_end=5' | 1 | GTTCTGGAGGACAGGAAGGGTGACC CACAGAGGATTATACCACCGGGGTG |
| 1339 | Table 3A | Hs.335863 | AV755117 | 10912965 | 601462961T1 cDNA, 3' end /clone=IMAGE:3866222 /clone_end=3' | 1 | GCCGCAGACCTCCTCATTCTAACCTG AATCGAAGGACAACCACTAAGCTA |
| 1340 | Table 3A | Hs.339696 | AV755367 | 10913215 | ribosomal protein S12 (RPS12), mRNA /cds=(80,478) | 1 | TGAGTCGTATTACAATCACTGGCCG TCGTTTTACAACGTCGTGACTGGG |
| 1341 | Table 3A | Hs.181165 | AV756188 | 10914036 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(53,1441) | 1 | TAAGATTATCAACCTTGGGGTCGTTT TGTTGTTCCGGGATTGAGCACGGA |
| 1342 | Table 3A | Hs.58643 | AV760147 | 10917995 | 602438603F1 cDNA, 5' end /clone=IMAGE:4564968 /clone_end=5' | 1 | CTGGGCTGAAGCCTATTCCTATGGG GCTCTGGAATGTTGTGACTGAATG |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|--|---|---|
| 1343 | Table 3A | Hs.93194 | AV762642 | 10920490 | apolipoprotein A-I (APOA1), mRNA /cds=(38,841) | 1 | TTGTCCATTTGGAACAGAGTCACTAT AAAGAACGGGCTCAACTGGGCACC |
| 1344 | Table 3A | Hs.301553 | AW021037 | 5874567 | karyopherin alpha 6 (importin alpha 7) (KPNA6), mRNA /cds=(55,1665) | 1 | GCAGACATAGGCGAAGAAACATGG CATTGAGTGTGCTGAGTCCAGACAA |
| 1345 | Table 3A | Hs.232400 | AW021551 | 5875081 | heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1), transcript variant B1, mRNA /cds=(169,1230) | 1 | CTTTTCCCACCCCTCCCCCTCCATG TGAAGATTTGGGTGCTTAACATAT |
| 1346 | Table 3A | Hs.95835 | AW248322 | 6591315 | RST8356 cDNA | 1 | GGCACTGCCTCCTTACCTGTGAGGAA TGCAAAATAAAGCATGGATTAAGT |
| 1347 | Table 3A | Hs.340753 | AW362008 | 6866658 | tw50h12.x1 cDNA, 3' end /clone=IMAGE:2263175 /clone_end=3' | 1 | AAACCACACCAGGAACCTCTTGATG GCAAAAGCTGAACAGTACAAATCC |
| 1348 | Table 3A | Hs.127574 | BG436386 | 13342892 | 602509044F1 cDNA, 5' end /clone=IMAGE:4619579 /clone_end=5' | 1 | ACACAGTCATCCCCATGCAGAAACCT CAGAAAACACCAATGTATTACACA |
| 1349 | Table 3A | Hs.8024 | AW390233 | 6894892 | IK cytokine, down-regulator of HLA II (IK), mRNA /cds=(111,1784) | 1 | GTCTGAACGAGACTCAATTCCTCTCC GAGGCTCCCCAAACAAATTGTAGC |
| 1350 | Table 3A | NA | AW402007 | 6920693 | UI-HF-BK0-aao-g-02-0-UI.r1 NIH_MGC_36 cDNA clone IMAGE:3054530 5' | 1 | GTGCAGTCCATCAGATCCAAGCCTGT CTCTTGAGGAACAACCGCGCAGAC |
| 1351 | Table 3A | Hs.181125 | AW405863 | 6924920 | Homo sapiens, clone MGC:12849 IMAGE:4308973, mRNA, complete cds /cds=(24,725) | 1 | GACCCAGGCTATGGATGAGGCTGAC TATTACTGTCAGCGCTGGGACAGCA |
| 1352 | Table 3A | NA | AW499658 | 7111531 | UI-HF-BR0p-ajj-c-07-0-UI.r1 NIH_MGC_52 cDNA clone IMAGE:3074677 5' | 1 | TGGTGGCAAATCTGATTTTTGGAAAC GAGTATTGGAGGACTATAAAACAA |
| 1353 | Table 3A | NA | AW499828 | 7111870 | UI-HF-BN0-ake-c-06-0-UI.r1 NIH_MGC_50 cDNA clone IMAGE:3076619 5' | 1 | ACATTTCTTGTGGCACTACAGCAAC CACATACAGTACAGACAACCTCCA |
| 1354 | Table 3A | Hs.181461 | AW499829 | 7111872 | ariadne (Drosophila) homolog, ubiquitin-conjugating enzyme E2-binding protein, 1 (ARIH1), mRNA /cds=(314,1987) | 1 | TGGGATAAAGGTGTGTCGGTTTTAGCA CCTCTGGAAGACCTATCTAGAGCT |
| 1355 | Table 3A | Hs.145668 | AW500534 | 7113240 | fmc5 cDNA /clone=CR6-21 | 1 | CCTGGCACATGTTGTCTGGAGTCTGG CACACTGGTTATCAATAGCACATT |
| 1356 | Table 3A | Hs.304900 | AW501528 | 7115141 | 602288147F1 cDNA, 5' end /clone=IMAGE:4373963 /clone_end=5' | 1 | GCATGTTCTCACCGTGAAGGAGAGT GATGCAGGGAGATACTACTGTGCAG |
| 1357 | Table 3A | Hs.37892 | AW504212 | 7141879 | KIAA0922 protein (KIAA0922), mRNA /cds=(122,3841) | 1 | AAAGTGGGTGGAAGACTTCTCGGTG CAGGAGGCTCACTCCGATTAAAGT |
| 1358 | Table 3A | Hs.120996 | AW504293 | 7141960 | serine/threonine kinase 17b (apoptosis-inducing) (STK17B), mRNA /cds=(261,1379) | 1 | CTGTGGTCTGTTATATGAGAGAGATC CTTTAACTAGAGCAAAGAGGGAGT |
| 1359 | Table 3A | Hs.182937 | AW630825 | 7377615 | peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA /cds=(44,541) | 1 | GCTTGCTGTTCCCTAGAAATTTGCCTT GTAAGTTCTAGCTCAAGTTGGGG |
| 1360 | Table 3A | Hs.102647 | AW651682 | 7412932 | 602271536F1 cDNA, 5' end /clone=IMAGE:4359609 /clone_end=5' | 1 | TTTCTCAGAGCTGGAGTTGCTGGG CACCTAAATGATGTTTCATGATAGC |
| 1361 | Table 3A | NA | AW792856 | 7844778 | UM0001 cDNA | 1 | CTTTTTGTAAGTTACAACATTCCACTG GATCCTTATATTGCCTGTAGTGG |
| 1362 | Table 3A | NA | AW810442 | 7903436 | ST0125 cDNA | 1 | CTCATCTATGTCTCTAAAGCTTTTCT GCATCTCTCCACCTGGGATTCAA |
| 1363 | Table 3A | NA | AW812896 | 7905890 | RC3-ST0186-250200-018-a11 cDNA /gb=AW812896 | 1 | CTGCTTTTGAAGGAGACACAAGAAC CTGATAACATTGGTTGTCTTCGGG |
| 1364 | Table 3A | Hs.44577 | AW813133 | 7906127 | 602388170F1 cDNA, 5' end /clone=IMAGE:4517129 /clone_end=5' | 1 | AAACAAGAACCACCTTAAACACAGCA TCAAACCTCTACCATGAAATGAAGA |
| 1365 | Table 3A | Hs.23128 | AW819894 | 7912888 | Homo sapiens, Similar to RIKEN cDNA 4931428D14 gene, clone MGC:15407 IMAGE:4309613, mRNA, complete cds /cds=(123,1151) | 1 | TTCTTCTGGTCATATTCCTCTTTTGA TTTTCTAAGAACTTCCCTCAGGA |
| 1366 | Table 3A | Hs.165695 | AW850041 | 7945558 | IL3-CT0216-170300-097-C07 cDNA | 1 | ACACAAGATACTGCCACTTTCTCTAC ACAAAGACCCACCCAAACACCAGC |
| 1367 | Table 3A | Hs.301756 | AW866426 | 8000476 | Homo sapiens, clone MGC:17544 IMAGE:3462146, mRNA, complete cds /cds=(256,894) | 1 | CTTTCTCAGGAAGTGGCTCTGCCAGG CAGGACTATGTGGGAAAGGGTTTT |
| 1368 | Table 3A | Hs.130729 | AW898615 | 8062820 | RC1-NN0073-090500-012-f02 cDNA | 1 | ATTACATGCTAACTCAAACCTACAAAA TCAAGCTCTCTGTGATCCTGGTT |
| 1369 | Table 3A | Hs.166975 | AW949461 | 8139088 | splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(218,541) | 1 | GATTAAGGCTTCCATCGATTGGGTA GTGTCCTTCAAGTGGGTGGCGAAG |
| 1370 | Table 3A | Hs.172028 | AW954112 | 8143795 | a disintegrin and metalloproteinase domain 10 (ADAM10), mRNA /cds=(469,2715) | 1 | TGTATTAAACAGGCTTATTGCTATGCA GGGAAATAGAAGGGGCATTACAAA |
| 1371 | Table 3A | Hs.76728 | AW954476 | 8144159 | 602570065F1 cDNA, 5' end /clone=IMAGE:4694321 /clone_end=5' | 1 | TGGTGGATGGATGGAAACACATACCT CCTAATTAACTGTTGGTGGAAAC |
| 1372 | Table 3A | Hs.292457 | AW954580 | 8144263 | Homo sapiens, clone MGC:16362 IMAGE:3927795, mRNA, complete cds /cds=(498,635) | 1 | GCCTTGGAGTGTGACATTTCTGCGAG AATGCTTAAATACCGATTTCCTCCG |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|---|---|--|
| 1373 | Table 3A | Hs.95835 | AW955265 | 8144948 | RST8356 cDNA | 1 | AGGGAGTCGTTTTACCAATTCAGTGG CCCGTGTTTTACAAACGCTGACT |
| 1374 | Table 3A | Hs.205353 | AW957139 | 8146822 | ectonucleoside triphosphate diphosphohydrolase 1 (ENTPD1), mRNA /cds=(67,1599) | 1 | TGGAGAGCTTGGGACAAGGTGAGAA TGAAACATACCAGTCAATCCTGCT |
| 1375 | Table 3A | Hs.289088 | AW958538 | 8148222 | heat shock 90kD protein 1, alpha (HSPCA), mRNA /cds=(60,2258) | 1 | ACCTGTGCTCTTTGGATACCTAATGC GACATTTAAGTTGTATTTGACAGT |
| 1376 | Table 3A | Hs.14453 | AW960484 | 8150168 | interferon consensus sequence binding protein 1 (ICSBP1), mRNA /cds=(47,1327) | 1 | AGGCTGGGCACAAAGGAGAAAGGAG GACATGGAAAATCCGACAATTCGAA |
| 1377 | Table 3A | Hs.198427 | AW960593 | 8150277 | hexokinase 2 (HK2), mRNA /cds=(1490,4243) | 1 | ATCTCAAATCCTTGAGCACTCAGTCT AGTGAAGATGTTGTCTATTATGTACA |
| 1378 | Table 3A | Hs.237868 | AW963171 | 8153007 | interleukin 7 receptor (IL7R), mRNA /cds=(22,1401) | 1 | GGGTCATAGGTTTCATGGGTTTGTGA GAATTGTGGCTCCTGGTTTCTGGT |
| 1379 | Table 3A | Hs.56205 | AW964218 | 8154054 | insulin induced gene 1 (INSIG1), mRNA /cds=(414,1247) | 1 | GCCTTCTTCTGCTGACTGGGGGCTT TCATTTAAAGGAGTCTTTTTAAT |
| 1380 | Table 3A | Hs.30212 | AW965078 | 8154914 | thyroid receptor interacting protein 15 (TRIP15), mRNA /cds=(15,1346) | 1 | TGTAAACAGTGGCAGGAGCGTGGAC TTAAACAAGGCTTGCTTATTTGGT |
| 1381 | Table 3A | Hs.124764 | AW965490 | 8155326 | 602386504F1 cDNA, 5' end /clone=IMAGE:4515481 /clone_end=5' | 1 | GCCCTTTGGGTTAAGCCTTTACATT ATGAAGACCCCTCCAGGGTAGAAT |
| 1382 | Table 3A | Hs.132739 | AW965987 | 8155823 | EST378060 cDNA / | 1 | AAAAGGAAAACGAAAAGGAAAAGGT GGCCAATGTGAAAAAGTTTCAAT |
| 1383 | Table 3A | Hs.293418 | AW966098 | 8155934 | EST385296 cDNA | 1 | ACTCTCAGGAGCCATGAAAGCTGCAC AGTTACTTTATATACCACGAGGCA |
| 1384 | Table 3A | Hs.25130 | AW967388 | 8157225 | cDNA FLJ14923 fis, clone PLACE1008244, weakly similar to VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 /cds=UNKNOWN | 1 | TTATGTCACCAGAATGTTTGCCAACA CCCCGAAAAGGAACAGAGGACTT |
| 1385 | Table 3A | Hs.343615 | AW968561 | 8158402 | 602621493F1 cDNA, 5' end /clone=IMAGE:4755166 /clone_end=5' | 1 | AGGTTATTTGAGCACAGTGAAGCAG AGTACTATGTTGTCCAACACAGG |
| 1386 | Table 3A | Hs.82712 | AW969359 | 8159203 | fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA /cds=(12,1877) | 1 | GGCCTGCCATCCGAGGGACTGTGTT GTAGATTGTGATCAAGGTTGATTGG |
| 1387 | Table 3A | Hs.199160 | AW969546 | 8159390 | translocation T(4:11) of ALL-1 gene to chromosome 4 /cds=UNKNOWN | 1 | ACAGGTAGTTGAATAATTGTTTCAAG AGCTCAACAGATGACAGCTTCTT |
| 1388 | Table 3A | Hs.293744 | AW973953 | 8165036 | 602279577F1 cDNA, 5' end /clone=IMAGE:4367322 /clone_end=5' | 1 | AATACACTTGTGCTCAAGGGAAGAAC ACTGCATGCCCTGGGTCTTCAGTC |
| 1389 | Table 3A | Hs.43148 | AW993524 | 8253690 | 602554063F1 cDNA, 5' end /clone=IMAGE:4663887 /clone_end=5' | 1 | GGGAAGTGGAGGTGAGAAGCATTAT AATAGCCTCTCTGCCTTTATCTACA |
| 1390 | Table 3A | Hs.238990 | AY004255 | 9652559 | Homo sapiens, Similar to cyclin- dependent kinase inhibitor 1B (p27, Kip1), clone MGC:5304 IMAGE:3458141, mRNA, complete cds /cds=(377,973) | 1 | ACAAGCCAAAGTGGCATGTTTTGTGC ATTTGTAAATGCTGTGTTGGGTAG |
| 1391 | Table 3A | Hs.16773 | AY007106 | 9955998 | clone TCCCI00427 mRNA sequence /cds=UNKNOWN | 1 | AACAGACTGTCTAGAAAAGTGTCTT TGCTTCCAAATCAGCAGAGGACCA |
| 1392 | Table 3A | Hs.285013 | AY007110 | 9956004 | putative HLA class II associated protein I (PHAP1), mRNA /cds=(148,897) | 1 | GCCCTCAGAAGAGCCAACTTTGAG TTTTATGTCTGTTGTCTATTGATA |
| 1393 | Table 3A | Hs.24435 | AY007126 | 9956024 | clone CDABP0028 mRNA sequence /cds=UNKNOWN | 1 | CCTTGTTGTCCACGGGAATAGGAAGA ATTAGTTACTGACTTCACCTGAGA |
| 1394 | Table 3A | Hs.330838 | BE910568 | 10407295 | 601501121F1 cDNA, 5' end /clone=IMAGE:3903053 /clone_end=5' | 1 | CCCACAATTGGACTGATAGGGGGAG AAAATCCAAAGAGACGGAGCAACTG |
| 1395 | Table 3A | Hs.250820 | AY007158 | 9956071 | hypothetical protein FLJ14827 (FLJ14827), mRNA /cds=(468,1277) | 1 | AACGGCAACTGGGAGATTGTGAGT GAACACTGTTTCATCTTAATATGCT |
| 1396 | Table 3A | Hs.173274 | AY007165 | 9956080 | integrin cytoplasmic domain-associated protein 1 (ICAP-1A), transcript variant 1, mRNA /cds=(168,770) | 1 | ACATCTGAGAAACCCTGAATCCTGCA ATCAAGTAGAAGTCACTTCATCT |
| 1397 | Table 3A | Hs.105484 | AY007243 | 12621025 | regenerating gene type IV (REG-IV), mRNA /cds=(181,657) | 1 | GCCATAGGAAGGTTTACCAGTAGAAT CCTTGCTAGGTTGATGTGGGCCAT |
| 1398 | Table 3A | Hs.5298 | AY029066 | 14017398 | CGI-45 protein (LOC51094), mRNA /cds=(182,1294) | 1 | TCATCTCAACTAGTATTATACCCACA CCCACCCAAGAAGAGGGTTTGT |
| 1399 | Table 3A | Hs.79070 | BC000141 | 12652778 | v-myc avian myelocytomatosis viral oncogene homolog (MYC), mRNA /cds=(558,1877) | 1 | GACTGAAAGATTTAGCCATAATGTAA ACTGCCTCAAATTGGACTTTGGGC |
| 1400 | Table 3A | Hs.334602 | BC000167 | 13096801 | cDNA FLJ14539 fis, clone NT2RM2001345, weakly similar to VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 /cds=(7,1434) | 1 | GGCACTGTCTGTGTCCTTCTTGAAC TGTCTACCCTGTTGCTTTTCACAA |
| 1401 | Table 3A | Hs.75458 | BC000374 | 12653212 | ribosomal protein L18 (RPL18), mRNA /cds=(15,581) | 1 | GGCCAGCCGAGGCTACAAAACTAA CCCTGGATCCTACTCTCTTATTA |
| 1402 | Table 3A | Hs.278544 | BC000408 | 12653278 | acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase) (ACAT2), mRNA /cds=(37,1230) | 1 | ACTAGGTTGCAATATGTGAAATCAGA GGACCAAAGTACAGATGAAACCA |

Table 8

| | | | | | | | |
|------|------------|-----------|----------|----------|--|---|---|
| 1403 | Table 3A | Hs.183704 | BC000449 | 12653358 | ubiquitin mRNA, complete cds /cds=(135,2192) | 1 | CCCTGTCTGACTACAACATCCAGAAA GAGTCCACTCTGCACCTTGGTCTCG |
| 1404 | Table 3A | Hs.151242 | BC000514 | 12653484 | serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1 (SERPING1), mRNA /cds=(60,1562) | 1 | GGCATCGCCCATGCTCTCACCTGTGA TTTTGTAATCAGAAATAAATTGCT |
| 1405 | Table 3A | Hs.180450 | BC000523 | 12653502 | ribosomal protein S24 (RPS24), transcript variant 1, mRNA /cds=(37,429) | 1 | AAAGCAACGAAAGGAACGCAAGAAC AGAATGAAGAAAGTCAGGGGGACTG |
| 1406 | Table 3A | Hs.272822 | BC000530 | 12653516 | RuvB (E coli homolog)-like 1 (RUVBL1), mRNA /cds=(76,1446) | 1 | TCCCACTTTGTCTGTACATACTGGCC TCTGTGATTACATAGATCAGCCAT |
| 1407 | Table 3A | Hs.83583 | BC000590 | 12653624 | actin related protein 2/3 complex, subunit 2 (34 kD) (ARPC2), mRNA /cds=(84,986) | 1 | GAAGCGGCTGGCAACTGAAGGCTGG AACACTTGCTACTGGATAATCGTAG |
| 1408 | literature | Hs.153026 | BC000616 | 12653666 | mRNA for KIAA0640 protein, partial cds /cds=(0,1812) | 1 | CAGTCACGTCAGTTATGTAGATACTG CATGGCAGGAGAGCTTTACGCTAA |
| 1409 | Table 3A | Hs.321677 | BC000627 | 12653684 | signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3), mRNA /cds=(220,2532) | 1 | GCCACCCCTCACACAGCCAAACCC AGATCATCTGAAACTACTAATTG |
| 1410 | Table 3A | Hs.5662 | BC000672 | 12653772 | guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 (GNB2L1), mRNA /cds=(95,1048) | 1 | GCAGGTGACCATTGGCACACGCTAG AAGTTTATGGCAGAGCTTTACAAAT |
| 1411 | Table 3A | Hs.4147 | BC000687 | 12653796 | Homo sapiens, translocating chain-associating membrane protein, clone MGC:784 IMAGE:3347823, mRNA, complete cds /cds=(91,1215) | 1 | TGCCATGCTGCTAGGAAATTGTCCTT TTTCTTTCTAGCTGTTAACCTACT |
| 1412 | Table 3A | Hs.44468 | BC000758 | 12653928 | Homo sapiens, clone MGC:2698 IMAGE:2820737, mRNA, complete cds /cds=(168,266) | 1 | AACCTATTCCAGTGTTGATCGCAAGC TGTTGATGCACAGGCGTCTTGTTGG |
| 1413 | Table 3A | Hs.101514 | BC000764 | 12653940 | hypothetical protein FLJ10342 (FLJ10342), mRNA /cds=(533,1144) | 1 | TGAAAAGGATTAAAGCTGGTATTCTA GAACATGCCCTTCACTGGTGTGT |
| 1414 | Table 3A | Hs.85844 | BC000771 | 12653954 | neurotrophic tyrosine kinase, receptor, type 1 (NTRK1), mRNA /cds=(0,2390) | 1 | GGTAAGGTTTCTAGGAGGTCTGTTAG GTGTACATCTGCAGCTTATTGGC |
| 1415 | Table 3A | Hs.195870 | BC000967 | 13111833 | chronic myelogenous leukemia tumor antigen 66 mRNA, complete cds, alternatively spliced /cds=(232,1983) | 1 | TGATTCTGTAAGCTGTGGAATGAAG CTGCAGATTAGAGAACATTGGCT |
| 1416 | Table 3A | Hs.299214 | BC001077 | 12654494 | Homo sapiens, clone IMAGE:2822295, mRNA, partial cds /cds=(0,661) | 1 | CGATTTTACACGGCTGGGTAGAATTT GTAGAAAAGATCCACAGGGCAAGC |
| 1417 | Table 3A | Hs.82193 | BC001169 | 12654662 | cDNA FLJ11763 fis, clone HEMBA1005679 /cds=UNKNOWN | 1 | GCTACTACTTCATTGCAACCTTTATTA CTGACCACATCAGACATCATGCT |
| 1418 | Table 3A | Hs.240770 | BC001255 | 12654824 | Homo sapiens, nuclear cap binding protein subunit 2, 20kD, clone MGC:4991 IMAGE:3458927, mRNA, complete cds /cds=(26,496) | 1 | GGGCTGAAGTACCTAAGTGTGAATGT CTCTCCCGTTAAACTGAGTGTA |
| 1419 | Table 3A | Hs.73957 | BC001267 | 12654846 | Homo sapiens, RAB5A, member RAS oncogene family, clone MGC:5048 IMAGE:3463669, mRNA, complete cds /cds=(165,812) | 1 | AGGAAAACGGTTCACCAGTGTTTAGT TTTATATTGAGGTGCTCAGGTTGG |
| 1420 | Table 3A | Hs.73965 | BC001303 | 12654914 | splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(155,820) | 1 | CCGGGCCTTGTCATATAAATAACGGAG CATACAGTGAGCACATCTAGCTGA |
| 1421 | Table 3A | Hs.62954 | BC001399 | 12655094 | ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(91,663) | 1 | ATAATGAAAGCTAAGCCTCGGGCTAA TTTCCCCATAGCCGTGGGGTGA |
| 1422 | Table 3A | Hs.288036 | BC001412 | 12655120 | tRNA isopentenylpyrophosphate transferase (IPT), mRNA /cds=(60,1040) | 1 | TGCATCGTAAACCTTCAGAAAGGAAA GGAGAATGTTTTGTGGACCACTTT |
| 1423 | Table 3A | Hs.3459 | BC001413 | 13937593 | cDNA: FLJ22003 fis, clone HEP06764 /cds=UNKNOWN | 1 | TGCTCTGTTCTGGTTTCTGTTTTCAAA TCAATGCGCTGTTTGGGAGGAGA |
| 1424 | Table 3A | Hs.51299 | BC001632 | 12804450 | NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD) (NDUFV2), mRNA /cds=(18,767) | 1 | CAAAATCCCAAAACAGGGCCAAGG AGTGAGCGCTTCTCTGTGAGCCAG |
| 1425 | Table 3A | Hs.155101 | BC001637 | 12804460 | mRNA for KIAA1578 protein, partial cds /cds=(0,3608) | 1 | ACAAATTTCTTGGCTGGATTGAAGC TTAAACTCCTGTGGATTACATCA |
| 1426 | Table 3A | Hs.318069 | BC001646 | 12804476 | cDNA FLJ20350 fis, clone HEP13972, highly similar to Z184_ZINC FINGER PROTEIN 184 /cds=UNKNOWN | 1 | TCCACGGTTGTGCCTTATTGTTCCAT TAAATTTGATCTTCCGATCCATCA |
| 1427 | Table 3A | Hs.8297 | BC001660 | 12804498 | cDNA FLJ10907 fis, clone OVARC1000060 /cds=(319,696) | 1 | GGTCTGAGAGTCTGTGAAGATGGCC CAGTCTTCTATCCCCACCTAAAAA |
| 1428 | Table 3A | Hs.17279 | BC001697 | 12804560 | tyrosylprotein sulfotransferase 1 (TPST1), mRNA /cds=(81,1193) | 1 | ACACACAGGAGGAAAAATCCTGGGA TTCTTTTCTAGGGATGTAATACAT |
| 1429 | Table 3A | Hs.284291 | BC001798 | 12804732 | sorting nexin 6 (SNX6), mRNA /cds=(497,1369) | 1 | CTGTTTGAACCTGTTGAGTTTCCGTTG CTGGCTGAGTGCCTTTTGTCTTC |
| 1430 | Table 3A | Hs.8297 | BC001819 | 12804758 | cDNA FLJ10907 fis, clone OVARC1000060 /cds=(319,696) | 1 | GGTCTGAGAGTCTGTGAAGATGGCC CAGTCTTCTATCCCCACCTAAAAA |
| 1431 | Table 3A | Hs.77502 | BC001854 | 12804818 | Homo sapiens, methionine adenosyltransferase II, alpha, clone MGC:4537 IMAGE:3010820, mRNA, complete cds /cds=(116,1303) | 1 | GGTACAGAGAAGCCAGCTTGTTTACA TGCTTATTCCATGACTGCTTGCCC |

Table 8

| | | | | | | | |
|------|----------|-----------|-----------|----------|---|---|---|
| 1432 | Table 3A | Hs.77502 | BC001854 | 12804818 | Homo sapiens, methionine adenosyltransferase II, alpha, clone MGC:4537 IMAGE:3010820, mRNA, complete cds /cds=(116,1303) | 1 | GGTACAGAGAAGCCAGCTTGTTTACA TGCTTATTCATGACTGCTTGCCC |
| 1433 | Table 3A | Hs.13580 | BC001909 | 12804912 | Homo sapiens, clone IMAGE:3537447, mRNA, partial cds /cds=(0,790) | 1 | GGGAGAATGAATGTGCAACGTGGCT GAAATCTATTTTGTGTAATAAAGG |
| 1434 | Table 3A | Hs.157236 | BC001913 | 12804920 | Homo sapiens, clone MGC:3015 IMAGE:3162543, mRNA, complete cds /cds=(332,1234) | 1 | CCCCACCACCCATTACCACAGCTGC CTTTGTGTGTTGTGTCAATAAAA |
| 1435 | Table 3A | Hs.318885 | BC001980 | 12805046 | superoxide dismutase 2, mitochondrial (SOD2), mRNA /cds=(4,672) | 1 | CCAGCAAGATAATGTCTGTCTTCTA AGATGTGCATCAAGCCTGGTACAT |
| 1436 | Table 3A | Hs.288061 | BC002409 | 12803202 | actin, beta (ACTB), mRNA /cds=(73,1200) | 1 | CCAACCTTGAGATGTATGAAGGCTTTT GGTCTCCCTGGGAGTGGGTGGAGG |
| 1437 | Table 3A | Hs.284214 | BC002435 | 12803242 | putative zinc finger protein (LOC55818), mRNA /cds=(299,3937) | 1 | GCTACTAGAGAGCAAGGGCTTTCTT ACCACCACTGCTGAGGAGAAAAAGT |
| 1438 | Table 3A | Hs.334822 | 12803270 | 12803270 | Homo sapiens, Similar to ribosomal protein L4, clone MGC:2966 IMAGE:3139805, mRNA, complete cds /cds=(1616,2617) | 1 | ACCAAGAAACCAAGCCCTGAAAAGAA GCCTGCAGAGAAGAAACCTACTAC |
| 1439 | Table 3A | Hs.104879 | BC002538 | 12803428 | Homo sapiens, serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9, clone MGC:2131 IMAGE:3140427, mRNA, complete cds /cds=(92,1222) | 1 | TTTCCTCATCTATGAATTGTCATTAC ACACCTACTTTTCTGCTTCGTTT |
| 1440 | Table 3A | Hs.104879 | BC002538 | 12803428 | Homo sapiens, serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9, clone MGC:2131 IMAGE:3140427, mRNA, complete cds /cds=(92,1222) | 1 | TTTCCTCATCTATGAATTGTCATTAC ACACCTACTTTTCTGCTTCGTTT |
| 1441 | Table 3A | Hs.146409 | BC002711 | 12803746 | cell division cycle 42 (GTP-binding protein, 25kD) (CDC42), mRNA /cds=(69,644) | 1 | AATAATGACAAATGCCCTGCACCTAC CCACATGCACCTCGTGTGAGACAAG |
| 1442 | Table 3A | Hs.322824 | BC002746 | 12803812 | Homo sapiens, Similar to dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase), clone MGC:3903 IMAGE:3630566, mRNA, complete cds /cds=(15,872) | 1 | GTGCCCTGTGGGTCCCAGGGAGGT CTTAAACAAGGTATTTTCAACTTA |
| 1443 | Table 3A | Hs.46446 | BC002796 | 12803898 | lymphoblastic leukemia derived sequence 1 (LYL1), mRNA /cds=(0,803) | 1 | CAGTGAAGACGTGAGGGGCAAGGTC TCGGGGGTCCGGAAGGGTGATCATC |
| 1444 | Table 3A | Hs.322404 | BC002837 | 12803976 | hypothetical protein MGC4175 (MGC4175), mRNA /cds=(221,577) | 1 | TGCAAGGGAGACATATCCTAGATCAC TTTGCTTTTTCTTTAAGGAGCTGA |
| 1445 | Table 3A | Hs.288036 | BC002845 | 12803990 | tRNA isopentenylpyrophosphate transferase (IPT), mRNA /cds=(60,1040) | 1 | TGCATCGTAAACCTTCAGAAGGAAA GGAGAATGTTTTGTGGACCACTTT |
| 1446 | Table 3A | Hs.318693 | BC002867 | 12804028 | Homo sapiens, clone IMAGE:3940519, mRNA, partial cds /cds=(0,902) | 1 | TTGGGGGAGGTTAGGGACTTATCCT GTGCTTGTAATAAATAAGGTCATG |
| 1447 | Table 3A | Hs.181309 | BC002900 | 12804094 | proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2), mRNA /cds=(0,704) | 1 | ACTTGGCTGCCATAGCATAACAATGA AGTGACTGAAAAATCCAGAAATTC |
| 1448 | Table 3A | Hs.96757 | 12804148 | 12804148 | suppressor of Ty (S.cerevisiae) 3 homolog (SUPT3H), mRNA /cds=(71,1024) | 1 | AAAATATTAACACAAACTACCACCTA CCTCCCTCACCAGGCCATAAA |
| 1449 | Table 3A | Hs.1600 | BC002971 | 12804224 | Homo sapiens, clone IMAGE:3543711, mRNA, partial cds /cds=(0,1620) | 1 | AGCTGTTTGGTAACCATAGTTTCACT TGTTCAAAGCTGTGTAATCGTGGG |
| 1450 | Table 3A | Hs.1600 | BC002971 | 12804224 | Homo sapiens, clone IMAGE:3543711, mRNA, partial cds /cds=(0,1620) | 1 | AGCTGTTTGGTAACCATAGTTTCACT TGTTCAAAGCTGTGTAATCGTGGG |
| 1451 | Table 3A | Hs.75193 | BC003090 | 13111846 | COP9 homolog (COP9), mRNA /cds=(49,678) | 1 | TGTCGCCTTTTGAAGGAGAAACTTA AGTGTGGAATGCATTATATGGGCA |
| 1452 | Table 3A | Hs.334861 | BC003137 | 13111932 | hypothetical protein FLJ23059 (FLJ23059), mRNA /cds=(41,1681) | 1 | TCCTTGGCAGCTGTATICTGGAGTCT GGATGTTGCTCTCTAAAGACCTTT |
| 1453 | Table 3A | Hs.326456 | BC003352 | 13097158 | hypothetical protein FLJ20030 (FLJ20030), mRNA /cds=(1,1239) | 1 | TTTGGAGTGGAGGCATTGTTTTAAG AAAAACATGTCATGTAGGTTGTCT |
| 1454 | Table 3A | Hs.77091 | NM_006730 | 5803006 | deoxyribonuclease I-like 1 (DNASE1L1), mRNA /cds=(794,1702) | 1 | TGGCTGGGACGCTAGAAGGGTCATG TGTTAACTATAATCACATTATGGT |
| 1455 | Table 3A | Hs.24697 | BC003406 | 13097305 | cDNA FLJ20709 fis, clone KAIA1124, highly similar to D86324 mRNA for CMP-N-acetylneuraminic acid /cds=UNKNOWN | 1 | ATTCTGGTTAACCGCTCACATGCATA ACAATAATGCTAGAAATTCAGGAA |
| 1456 | Table 3A | Hs.42712 | BC003525 | 13097617 | Homo sapiens, Similar to Max, clone MGC:10775 IMAGE:3607261, mRNA, complete cds /cds=(115,570) | 1 | TGCTGATTTCTAGTGATACTCTGTA GTCTCAGTTCGTGTTGATTCAT |
| 1457 | Table 3A | Hs.5322 | BC003563 | 13097716 | guanine nucleotide binding protein (G protein), gamma 5 (GNG5), mRNA /cds=(333,539) | 1 | AAATGAATCTTTCAAAGGTTTCCAAA CCACTCCTTATGATCCAGTGATA |
| 1458 | Table 3A | Hs.334861 | BC003577 | 13097758 | hypothetical protein FLJ23059 (FLJ23059), mRNA /cds=(41,1681) | 1 | TCCTTGGCAGCTGTATTCTGGAGTCT GGATGTTGCTCTCTAAAGACCTTT |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|---|---|-----------------------------|
| 1459 | Table 3A | Hs.56851 | BC003581 | 13097767 | hypothetical protein MGC2668 (MGC2668), mRNA /cds=(20,325) | 1 | TGCGTGTGCCCTCAGTTTCCTCCTCCA |
| 1460 | Table 3A | Hs.188757 | BC003697 | 13277575 | Homo sapiens, clone MGC:5564, mRNA, complete cds /cds=(227,304) | 1 | GGGATGTGGAGGATTTTGTGAAGTG |
| 1461 | Table 3A | Hs.215595 | BC004186 | 13278842 | guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA /cds=(280,1302) | 1 | TCAATCGAAGTTAAAAAGCAAGGG |
| 1462 | Table 3A | Hs.111334 | BC004245 | 13279004 | PR02760 mRNA, complete cds /cds=UNKNOWN | 1 | AGCTCTCTGCACCCCTTACCCCTTTCC |
| 1463 | Table 3A | Hs.70333 | BC004258 | 13279043 | mRNA for KIAA1844 protein, partial cds /cds=(0,1105) | 1 | ACCTTTTGATTTAATTTTAAAGT |
| 1464 | Table 3A | Hs.9788 | BC004317 | 13279217 | hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5 (MGC10924), mRNA /cds=(104,769) | 1 | CCCTCCAGCCAAATAGGCAGCTTTCTT |
| 1465 | Table 3A | Hs.254105 | BC004458 | 13325286 | enolase 1, (alpha) (ENO1), mRNA /cds=(94,1398) | 1 | AACATCTCTAACAAGCCTTGGACC |
| 1466 | Table 3A | Hs.155101 | BC004521 | 13325447 | mRNA for KIAA1578 protein, partial cds /cds=(0,3608) | 1 | CGTGGTTGTGGGAGGGGAAAGAGGA |
| 1467 | Table 3A | Hs.17132 | BC004805 | 13937690 | 602326676F1 cDNA, 5' end /clone=IMAGE:4427970 /clone_end=5' | 1 | AACAGAGCTAGTCAGATGTGAATTG |
| 1468 | Table 3A | Hs.103378 | BC004872 | 13436100 | hypothetical protein MGC11034 (MGC11034), mRNA /cds=(245,640) | 1 | ACAATGTGTTAGCAGAAACCAGTGGG |
| 1469 | Table 3A | Hs.151242 | BC004900 | 13436172 | serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1 (SERPING1), mRNA /cds=(60,1562) | 1 | TTATAATGTAGAATGATGTGCTTT |
| 1470 | Table 3A | Hs.74335 | BC004928 | 13436256 | heat shock 90kD protein 1, beta (HSPCB), mRNA /cds=(0,2174) | 1 | GCTAGATCCCCGGTGGTTTTGTGCTC |
| 1471 | Table 3A | Hs.336916 | BC004994 | 13436445 | death-associated protein 6 (DAXX), mRNA /cds=(147,2369) | 1 | AAAATAAAAGCCTCAGTGACCCA |
| 1472 | Table 3A | Hs.60377 | BC005101 | 13937700 | mRNA for KIAA1298 protein, partial cds /cds=(55,2271) | 1 | ACAAATTTCTTGGCTGGATTGGAAGC |
| 1473 | Table 3A | Hs.99858 | BC005128 | 13477308 | ribosomal protein L7a (RPL7A), mRNA /cds=(31,831) | 1 | TAAACTCCTGTGGATTACATCA |
| 1474 | Table 3A | Hs.177507 | BC005187 | 13528770 | hypothetical protein (HSPC155), mRNA /cds=(240,743) | 1 | GCTGTGGTTGGTTGCCATTACATGACA |
| 1475 | Table 3A | Hs.251531 | BC005361 | 13529190 | proteasome (prosome, macropain) subunit, alpha type, 4 (PSMA4), mRNA /cds=(59,844) | 1 | CAGAAAAGTCTCCTCTACCTCACG |
| 1476 | Table 3A | Hs.100000 | BC005928 | 13543538 | S100 calcium-binding protein A8 (calgranulin A) (S100A8), mRNA /cds=(55,339) | 1 | GCCCTGGTAGGCTCCTTTAGAAGGA |
| 1477 | Table 3A | Hs.334573 | BC006008 | 13937718 | clone IMAGE:4285740, mRNA /cds=UNKNOWN | 1 | CCATTTCTGTTCCTAGAGCTTAACT |
| 1478 | Table 3A | Hs.101150 | BC006176 | 13544094 | clone IMAGE:4054156, | 1 | GGCATCGCCCATGCTCCTCACCTGTA |
| 1479 | Table 3A | Hs.108824 | BC006282 | 13623362 | hypothetical protein MGC10540 (MGC10540), mRNA /cds=(49,579) | 1 | TTTTCCCTCTCCTGTCTTGTGTTGAA |
| 1480 | Table 3A | Hs.239884 | BC006464 | 13623674 | H2B histone family, member L (H2BFL), mRNA /cds=(0,380) | 1 | GGCAGTAACTAAGGGGTGCAAGC |
| 1481 | Table 3A | Hs.19574 | BC006849 | 13905123 | hypothetical protein MGC5469 (MGC5469), mRNA /cds=(69,1124) | 1 | AGACTGGAAATGGGGATGAGGGTGT |
| 1482 | Table 3A | Hs.252716 | BC007004 | 13937807 | oxysterol-binding protein-related protein 1 (FLJ10217), mRNA /cds=(174,3026) | 1 | AAATTGTATTGAAAAAGATCGCGAA |
| 1483 | Table 3A | Hs.180909 | BC007063 | 13937906 | peroxiredoxin 1 (PRDX1), mRNA /cds=(60,659) | 1 | CCATGAGTTGTTGGTTTCCAGAAG |
| 1484 | Table 3A | Hs.238730 | BC007203 | 13938171 | hypothetical protein MGC10823 (MGC10823), mRNA /cds=(63,1235) | 1 | CTGCCAGTGGGTTCCCGTGAATTG |
| 1485 | Table 3A | Hs.334637 | BC007277 | 13938298 | hypothetical protein MGC15619 (MGC15619), mRNA /cds=(744,1454) | 1 | GATACGATGAGATCCGCCGTCCTG |
| 1486 | Table 3A | Hs.298262 | BE250027 | 9120132 | ribosomal protein S19 (RPS19), mRNA /cds=(69,506) | 1 | GGGTGGCAATGTCCTGGGTCTTAAG |
| 1487 | Table 3A | Hs.297095 | BE253125 | 9123276 | 601116648F1 cDNA, 5' end /clone=IMAGE:3357178 /clone_end=5' | 1 | CATCAATAAAGCTCTGCGATCAACC |
| 1488 | Table 3A | NA | BE253336 | 9123402 | cDNA clone IMAGE:3357826 5' | 1 | CGATGATGTTACCTTTCATGGACGT |
| 1489 | Table 3A | Hs.75313 | BE254064 | 9124489 | aldo-keto reductase family 1, member B1 (aldose reductase) (AKR1B1), mRNA /cds=(45,995) | 1 | CTTAATCTCCACACACATCCCCCT |
| 1490 | Table 3A | Hs.314898 | BE255377 | 9125816 | 601115405F1 cDNA, 5' end /clone=IMAGE:3355872 /clone_end=5' | 1 | GGCCCCCTGGACATGTACCTGCAGAA |
| 1491 | Table 3A | Hs.296183 | BE259480 | 9129916 | 601106571F1 cDNA, 5' end /clone=IMAGE:3342929 /clone_end=5' | 1 | TAATAAAGTCATCAATACCTAAAAA |
| | | | | | | 1 | GCAAACCTGCAGATTCCTCAAGATGTT |
| | | | | | | 1 | CACGAGCTTGTGCTTTCTAAAGAA |
| | | | | | | 1 | TCCCCATTGTCCGCGCTTTATCAATT |
| | | | | | | 1 | GCCTGTTTTGTTTTGTTTTTTTT |
| | | | | | | 1 | CTTTAGCTGCTGTTGCCCTCCCTCTC |
| | | | | | | 1 | AGGCTGGTGCTGGATCCTCTCCTAG |
| | | | | | | 1 | CTGCTTATGGCACAATTGGCTCAAAA |
| | | | | | | 1 | ATCCATTCCAAGTTGTATATTGTT |
| | | | | | | 1 | CTGCTTCTGGGTGCATGGTAGACTTT |
| | | | | | | 1 | GTGGCATTGATACAACCTTGGACA |
| | | | | | | 1 | CTTATAGTATTTCACCCCAACCC |
| | | | | | | 1 | CAGACTGAGATACTGCTCCAGGG |
| | | | | | | 1 | GAGAGACCAGCCTTTCTTCTTTGGT |
| | | | | | | 1 | AGGAATGGCCTGAGTTGGCGTTGT |
| | | | | | | 1 | CAGAGGTGGGAGTAAGTCTGGTAG |
| | | | | | | 1 | TGCCCTCTTTGGTTGTGTTGCTCAG |
| | | | | | | 1 | CTGTGTGCCCGAGCTGCATCAGCCA |
| | | | | | | 1 | GCTTCTAGGTGGCTCCATTGTTTT |
| | | | | | | 1 | AGAGCAGAATAGCAATATAAGAGCAC |
| | | | | | | 1 | AGACGAACATAGACACGACGCGA |
| | | | | | | 1 | CTATTAGGACCCAGTGATTATGCTAC |
| | | | | | | 1 | CTTGCCACGGTTAGGGTACTGCGG |
| | | | | | | 1 | AAAGAAGCATGCACACTTATCACAAA |
| | | | | | | 1 | CAACTCTCTCAGGTGGCCAGTCTG |
| | | | | | | 1 | TGCTGCCTATATGAAGTCTTTGAGAA |
| | | | | | | 1 | AGCCCCCTCTTGAGAGTCTGTGCCCT |
| | | | | | | 1 | GATATACGAGGACAAAACCCATCTAC |
| | | | | | | 1 | CAGGCAGCTAACAAACGCCGCCCA |
| | | | | | | 1 | GCCACTTTATTAGTAATGGTCGATAG |
| | | | | | | 1 | TCCGAATCGATGGCTAGGGTGACT |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|--|---|---|
| 1492 | Table 3A | Hs.301809 | BE260041 | 9131017 | 601150579F1 cDNA, 5' end /clone=IMAGE:3503419 /clone_end=5' | 1 | TAATCTGGCGGGTTATACCCCCGTGT TCTCCGGATTATATTTCCGGGACAC |
| 1493 | Table 3A | Hs.308154 | BE264564 | 9138121 | 601192330F1 cDNA, 5' end /clone=IMAGE:3536383 /clone_end=5' | 1 | GCTGGATTTGTGGGTATGGGGGCGG TTTTTGGGCGAAGGTTGGTTGTAC |
| 1494 | Table 3A | Hs.279429 | BE279328 | 9154319 | 601157666F1 cDNA, 5' end /clone=IMAGE:3504328 /clone_end=5' | 1 | CCACATCATCGGGGGCGAAATAGAA GCCCAGAGAGAGGCTAGGTGTAGGA |
| 1495 | Table 3A | Hs.95835 | BE292793 | 9175433 | RST8356 cDNA | 1 | AGGGAGACTCTCAGCCTTCAGCTTCC TAAATTCTGTGTCTGTGACTTTCCG |
| 1496 | Table 3A | Hs.142737 | BE293343 | 9176462 | 601143756F1 cDNA, 5' end /clone=IMAGE:3051493 /clone_end=5' | 1 | TTGTCAAGCTGCTGCTGTCTTCAAGA TCTACCTGGTCAGAATCTCCTGCT |
| 1497 | Table 3A | Hs.337986 | BE297329 | 9180903 | Homo sapiens, clone MGC:17431 IMAGE:2984883, mRNA, complete cds /cds=(1336,1494) | 1 | GGCCAGTCTCTATGTGTCTTAAATCCC TTGCCTTCATTAAGCAAGCAAACT |
| 1498 | Table 3A | Hs.192755 | BE298181 | 9181768 | 601118566F1 cDNA, 5' end /clone=IMAGE:3028193 /clone_end=5' | 1 | TCTCTCACATTCTGTCTTTCCCTCCT CCTTCACCTTCCCTCCGTCCCTC |
| 1499 | Table 3A | Hs.336628 | BE311727 | 9148186 | ribosomal protein L36a (RPL36A), mRNA /cds=(30,350) | 1 | ACACGAGACTATAGAGAATGCAGCAC ACAGATGAGAGCAGAGCAAATAGA |
| 1500 | Table 3A | Hs.129872 | BE379820 | 9325198 | sperm associated antigen 9 (SPAG9), mRNA /cds=(110,2410) | 1 | GCATCCAGATGGTGGTTTACTCTGCA ACAGTCTAATGTTCTTCACTTCCA |
| 1501 | Table 3A | Hs.231510 | BE407125 | 9343575 | 601301818F1 cDNA, 5' end /clone=IMAGE:3636412 /clone_end=5' | 1 | GGGGTTTCCACCTACCTAAGATGC TTTAATTGCTGTTTCCAAATTGT |
| 1502 | Table 3A | Hs.315263 | BE410105 | 9346555 | 601302278F1 cDNA, 5' end /clone=IMAGE:3637002 /clone_end=5' | 1 | ATGCCTAACCAAGCAACATGATCCTAT AAATCCACCCCAAGCCAATCTGGT |
| 1503 | Table 3A | Hs.258494 | BE531180 | 9759916 | Homo sapiens, Similar to hypothetical protein FLJ22376, clone MGC:16044 IMAGE:3610443, mRNA, complete cds /cds=(478,1776) | 1 | CCACCATCTGGTACGTTTTTACTTCC TCACCCGCGTGACTCCGATTACC |
| 1504 | Table 3A | Hs.13328 | BE537908 | 9766464 | 602268829F1 cDNA, 5' end /clone=IMAGE:4356966 /clone_end=5' | 1 | GAGTATATTCCCCCAGTTATTTGCTC TTCCCCACACAGGGTGGTAGTACC |
| 1505 | Table 3A | Hs.125819 | BE538333 | 9766978 | putative dimethyladenosine transferase (HSA9761), mRNA /cds=(78,1019) | 1 | CAAAGGAAGGGGCGTGAAGGGGTGA GAAAATATGGGACCCAAATGTGG |
| 1506 | Table 3A | Hs.5122 | BE539096 | 9767741 | 602293015F1 cDNA, 5' end /clone=IMAGE:4387778 /clone_end=5' | 1 | TTTCCTTACAGGCGGTAAACCCGGTC CACACAGTTCTTGCCAAAACAAAG |
| 1507 | Table 3A | Hs.180549 | BE540238 | 9768883 | 601059809F1 cDNA, 5' end /clone=IMAGE:3446283 /clone_end=5' | 1 | AATTTTCTCTCACCTCATCACTCGGG ACCTCCCCAGTGATAATAACCCGG |
| 1508 | Table 3A | Hs.155101 | BE547584 | 9776229 | mRNA for KIAA1578 protein, partial cds /cds=(0,3608) | 1 | GCGGGTGTAAAGGGGATATCTTGATAA ACTGGAGCCCAGGAAGATTACAAA |
| 1509 | Table 3A | Hs.74861 | BE549137 | 9777782 | activated RNA polymerase II transcription cofactor 4 (PC4), mRNA /cds=(0,383) | 1 | ACGCCGACAATCAAGAAATGTGAGT TATAACGGACAAGGTTGTATTATG |
| 1510 | Table 3A | NA | BE569141 | 9812861 | cDNA clone IMAGE:3681180 5' | 1 | GATATTGGTAGTAAAGGGGTTACCTG TGAACCTTCCAAAATTCCTTGGGGC |
| 1511 | Table 3A | NA | BE612847 | 9894444 | 601452239F1 5' end /clone=IMAGE:3856304 | 1 | TAAAGATGTCGGGTACACTTCGCCA AGGGTTAGCGCTTTTGGGCATTTC |
| 1512 | Table 3A | Hs.194362 | BE618004 | 9888942 | DNA sequence from clone RP11- 248N6 on chromosome 13 Contains ESTs, STSs and GSSs. Contains two olfactory receptor pseudogenes, an NPM1 (nucleophosmin, nucleolar phosphoprotein B23, numatrin) pseudogene and a BCR (breakpoint cluster region) pseudogene /cds=(0,887) | 1 | TCCTAATTTCTCTGTGTGAACCTCTCA AATCCCCAGCATGCGTGTAGTG |
| 1513 | Table 3A | Hs.294309 | BE621121 | 9892059 | 601493943F1 cDNA, 5' end /clone=IMAGE:3896051 /clone_end=5' | 1 | CTGCATGATGTCATCAACCTGCTGTA GTGCGGAAACGACCACAACACACA |
| 1514 | Table 3A | Hs.184582 | BE730026 | 10144018 | ribosomal protein L24 (RPL24), mRNA /cds=(39,512) | 1 | AAAGACGAACGAGACACGAAAGCAA CGAACGAACACAGAGACGCCGCAC |
| 1515 | Table 3A | Hs.76572 | BE730376 | 10144368 | ATP synthase, H ⁺ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O), mRNA /cds=(36,677) | 1 | TTTCAACACGCATCCCTTATGGGCGA ACTGTCCTCAAACAACAACAGTG |
| 1516 | Table 3A | Hs.77496 | BE737246 | 10151226 | small nuclear ribonucleoprotein polypeptide G (SNRPG), mRNA /cds=(83,313) | 1 | TAGGACGAGAAACGAAGAAGGACAG AGCGAGAACAAAGTAAGCAGGGACAC |
| 1517 | Table 3A | Hs.271272 | BE737348 | 10151340 | DKFZp434K1715_r1 cDNA, 5' end /clone=DKFZp434K1715 /clone_end=5' | 1 | GGTGGAGAATCAAAACGACCCCGCA AATAACATGGCGATTTGGCTTGGG |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|---|---|---|
| 1518 | Table 3A | Hs.58066 | BE739287 | 10153279 | 602389077F1 cDNA, 5' end /clone=IMAGE:4517875 /clone_end=5' | 1 | TGGCCTTTTAAATAACTGGGCTTCTC ACAACCATAGTGAACAGAAACAGC |
| 1519 | Table 3A | Hs.127951 | BE745645 | 10159637 | hypothetical protein FLJ14503 (FLJ14503), mRNA /cds=(19,2217) | 1 | ATTGTGACATGGTGTATGCCTCATTGC TGATATGGTCTGTGTTATGTGC |
| 1520 | Table 3A | Hs.276718 | BE747210 | 10161202 | 601473284T1 cDNA, 3' end /clone=IMAGE:3876165 /clone_end=3' | 1 | GGAAGAGATAACACCACAACGAAAGA GCAGGCAAGAGAGACCAAGCACA |
| 1521 | Table 3A | Hs.285647 | BE747224 | 10161216 | cDNA FLJ14704 fis, clone NT2RP3000526 /cds=UNKNOWN | 1 | GGTAAAGGCGTTACTCTCCGCCCTC TTCAAGGAACGGCCAAGAGATATAA |
| 1522 | Table 3A | Hs.293842 | BE748123 | 10162115 | 601571679F1 cDNA, 5' end /clone=IMAGE:3838675 /clone_end=5' | 1 | ACCCAAGGGTCTCGCCAGTGGGGTT AAGTCAATATTACTACACAAGGG |
| 1523 | Table 3A | Hs.283674 | BE778549 | 10199747 | hypothetical protein MGC2495 (MGC2495), mRNA /cds=(0,416) | 1 | ACAGTACACAATCACCTGCAAGGGAC ATAGCACACAACCGCTAAAGAGG |
| 1524 | Table 3A | Hs.61472 | BE779284 | 10200482 | 601464557F1 cDNA, 5' end /clone=IMAGE:3867566 /clone_end=5' | 1 | TCTCACAGCGAGAGGAGGAGACGGG ATGACCGAGAGGTAGACGATTATAC |
| 1525 | Table 3A | Hs.43273 | BE781009 | 10202207 | 602642428F1 cDNA, 5' end /clone=IMAGE:4773534 /clone_end=5' | 1 | CGCTGGTGTGTCCCAAGTGATTTA TTCTACTGGAGTGCTGGTGTCTT |
| 1526 | Table 3A | Hs.102558 | BE781611 | 10202895 | 601467463F1 cDNA, 5' end /clone=IMAGE:3870902 /clone_end=5' | 1 | TTCCGGCTTTTAAACAACACACACCA CACTAACACAACAACACAAACAAA |
| 1527 | Table 3A | Hs.40334 | BE782824 | 10204022 | 602557448F1 cDNA, 5' end /clone=IMAGE:4686562 /clone_end=5' | 1 | AAGACTTGCCTCTTTAAATGTCTTTG TTTTCTGCAGTACTATCTGTGGT |
| 1528 | Table 3A | Hs.79914 | BE783628 | 10204826 | lumican (LUM), mRNA /cds=(84,1100) | 1 | GAACTCGTCCACTCTTCTCGGGCCAC TATTCTGGTTTCAGGGAATCTTGGG |
| 1529 | Table 3A | Hs.135056 | BE786820 | 10208018 | DNA sequence from clone RP5-850E9 on chromosome 20. Contains part of the gene for a novel C2H2 type zinc finger protein similar to Drosophila Scratch (Scr), Slug and Xenopus Snail, a novel gene similar to Drosophila CG6762, STSs, GSSs and five CpG islands /cds=(0,397) | 1 | AGCAATAAACCGAAGCAGCTAGACAG CGAAGAAGTACAGCAAGAGACGA |
| 1530 | Table 3A | Hs.11355 | BE788546 | 10209744 | thymopoietin (TMPO), mRNA /cds=(204,2288) | 1 | CGCCCATACTAGAGAAGTTTGCCCTC TATTGTCTCTCACACCACAATGAG |
| 1531 | Table 3A | Hs.75458 | BE790474 | 10211672 | ribosomal protein L18 (RPL18), mRNA /cds=(15,581) | 1 | CACAGACATCCACGGACACAAAGG CGGGGACCACCACCAATGAACAC |
| 1532 | Table 3A | Hs.20225 | BE792125 | 10213323 | tufelin-interacting protein (TIP39), mRNA /cds=(263,2776) | 1 | CGCTCGATTGATATCAGACAGCATCG TCTCTCGAGCACAAGATCTGTT |
| 1533 | Table 3A | Hs.11607 | BE794595 | 10215793 | 602429913F1 cDNA, 5' end /clone=IMAGE:4547787 /clone_end=5' | 1 | GGAACAGGGTTAATGGCCAGGCCCT TTGCCGCCCTTTTAAAGGGAATCC |
| 1534 | Table 3A | Hs.58297 | BE867841 | 10316617 | CLL8 protein (CLL8), mRNA /cds=(825,2984) | 1 | ACAGAGTAACATGGGATATGGGTATG AGTGGGATGTGCTGAGAAGGAAGT |
| 1535 | Table 3A | Hs.179703 | BE868389 | 10317165 | tripartite motif protein 14 (TRIM14), mRNA /cds=(10,1230) | 1 | GGGGGCAAGAAAGTACATTGGGTG AAAATTTAAAAAGGTATGGAGCATT |
| 1536 | Table 3A | NA | BE871962 | 10320738 | 601448005F1 cDNA, 5' end /clone=IMAGE:3852001 | 1 | CAAACGAACGCGAAGACAACAACTC ACGATGCTGCACAACGCGACCAAC |
| 1537 | Table 3A | Hs.31314 | BE872245 | 10321021 | retinoblastoma-binding protein 7 (RBBP7), mRNA /cds=(287,1564) | 1 | ACATTTTATAAGGCATTGTGTGATGCC ACTCAGTCATCTTTGGGTGCTGC |
| 1538 | Table 3A | Hs.47334 | BE872760 | 10321536 | hypothetical protein FLJ14495 (FLJ14495), mRNA /cds=(83,1141) | 1 | GTCACAGCAACGTGTCGCTCCCCAG ATCATTTATTAGCGTCGATTGTTGT |
| 1539 | Table 3A | Hs.6820 | BE875609 | 10324385 | 602418418F1 cDNA, 5' end /clone=IMAGE:4525397 /clone_end=5' | 1 | ATTCCAAACGGGATCTGCTGAGACCT CACAGAGGTGGGCCGCGATTATAA |
| 1540 | Table 3A | Hs.158164 | BE876375 | 10325061 | transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) (TAP1), mRNA /cds=(30,2456) | 1 | CCTAGGGTGAAACACGTGACAGAAG AATAAAGACTATTGAATAGTCTCT |
| 1541 | Table 3A | Hs.237868 | BE877115 | 10325891 | interleukin 7 receptor (IL7R), mRNA /cds=(22,1401) | 1 | CCAGCCTTTGCCTCTTCTTCAATGT GGTTTCCATGGGAATTTGCTTCAG |
| 1542 | Table 3A | Hs.24181 | BE877357 | 10326133 | 601485590F1 cDNA, 5' end /clone=IMAGE:3887951 /clone_end=5' | 1 | CCCCTGTTTACTCTGTCTGTATGTAT GTCAAAAGCGTGGCAAAACCTCT |
| 1543 | Table 3A | Hs.237868 | BE878973 | 10327749 | interleukin 7 receptor (IL7R), mRNA /cds=(22,1401) | 1 | CATGATCTCAGAGGAACTGTGCTG ACCCTGGACATGGGTACGTTTGAC |
| 1544 | Table 3A | NA | BE879482 | 13959823 | mitochondrion, complete genome | 1 | CCTCTACCTGCACGACAATACATAAT GACCCACCAATCACATGCCTATCA |
| 1545 | Table 3A | NA | BE881113 | 10329889 | cDNA clone IMAGE:3894306 5' | 1 | ATTTGGAAGCGCCACCTAGCAAAATA TACAAACCATTAACCTTCCCTCT |
| 1546 | Table 3A | Hs.323950 | BE881351 | 10330127 | zinc finger protein 6 (CMPX1) (ZNF6), mRNA /cds=(1265,3361) | 1 | TTTACCAATGATTTTCAGGTGACCTG GGCTAAGTCATTTAACTGGGTCT |
| 1547 | Table 3A | Hs.111554 | BE882335 | 10331111 | ADP-ribosylation factor-like 7 (ARL7), mRNA /cds=(14,592) | 1 | AGTTTACATATCGACAGCATATCCAC TGATTTCTAAATGGGCTGGTCCCA |
| 1548 | Table 3A | NA | BE884898 | 10333674 | cDNA clone IMAGE:3908551 5' | 1 | ATCTGGAGTGGGACCCTTCAACCAT GTCTGTGCTTATGCGGGAAACAAAT |
| 1549 | Table 3A | Hs.142838 | BE886127 | 10340315 | nucleolar protein interacting with the FHA domain of pKi-67 (NIFK), mRNA /cds=(54,935) | 1 | GCGGAGAGAAGAAGAGGTAGATATG AGAACAGTGTGTGGTATATGATAGT |

Table 8

| | | | | | | | |
|------|----------|-----------|-----------|----------|---|---|--|
| 1550 | Table 3A | Hs.301486 | BE886472 | 10340792 | 601509688F1 cDNA, 5' end /clone=IMAGE:3911301 /clone_end=5' | 1 | GAAATCCCACCGGCAAGTTAAGGTCA CGGAGCAAGTGAATAAACCGCGGAG |
| 1551 | Table 3A | Hs.250824 | BE887646 | 10343176 | cDNA: FLJ23435 fis, clone HRC12631 /cds=UNKNOWN | 1 | GTGATCAAAACAAATTCACAGCACAGA CACCGCGCAACAAACGCAACTTCTC |
| 1552 | Table 3A | Hs.320836 | BE888304 | 10344472 | 601514033F1 cDNA, 5' end /clone=IMAGE:3915177 /clone_end=5' | 1 | GGTATTTGTGTTGTTGAGTATTGTGT CTGGGTGTGGGTATTGTGTTCTTT |
| 1553 | Table 3A | Hs.169274 | BE888744 | 10345354 | AL528777 cDNA /clone=CS0DD001YG24-(3-prime) | 1 | GGGTTTCGTCCAGGGCTCGCTAAAT TATTCTCAATGATTTGTCTCTTTGC |
| 1554 | Table 3A | Hs.71941 | BE889075 | 10346019 | hypothetical protein MGC15677 (MGC15677), mRNA /cds=(298,807) | 1 | CAATGACGCAGTCGGACCCCTCGGAT CCAAGTCCTGCTTTGGGTGTGGACC |
| 1555 | Table 3A | Hs.188757 | BE891242 | 10350376 | Homo sapiens, clone MGC:5564, mRNA, complete cds /cds=(227,304) | 1 | GGGTTATAATAGATGGACGGGTCTTT CACGGTGGTGACAGCACCCCTTTCC |
| 1556 | Table 3A | Hs.171802 | BE891269 | 10350433 | RST31551 cDNA | 1 | TCCGCTGCAATTTGAGTTTAGCTTTA CAGATTGTGCCGGGTGTTTAACCT |
| 1557 | Table 3A | Hs.4055 | BE891928 | 10351744 | mRNA; cDNA DKFZp564C2063 (from clone DKFZp564C2063) /cds=UNKNOWN | 1 | CTCCTTCCCAAAGACTTGAGTGGAAAC TTCCCTTTTCATGTGCGTATCGGTC |
| 1558 | Table 3A | Hs.3297 | BE895166 | 10358288 | ribosomal protein S27a (RPS27A), mRNA /cds=(38,508) | 1 | AAATTAGTCGCCTTCGTGAGAGTGC CCTTCTGATGAATGTGGCTGGG |
| 1559 | Table 3A | NA | BE896691 | 10361375 | cDNA clone IMAGE:3925062 5' | 1 | GACAGTACTCCTAAGACCCCTGTGTG TGTCCCGATGAGATCATGACTGGG |
| 1560 | Table 3A | NA | NC_001807 | 13959823 | COX2 gene of mitochondria | 1 | CATGCCCATCGTCTAGAATTAATTC CCCTAAAAATCTTTGAAATAGGGC |
| 1561 | Table 3A | NA | BE899595 | 10367264 | cDNA clone IMAGE:3952215 5' | 1 | GGCGTATCATCAACTGGTGAGCCCG AAGGGATATTATTTCTAAGGCCTCT |
| 1562 | Table 3A | Hs.285122 | BE901218 | 10390179 | Homo sapiens, hypothetical protein FLJ21839, clone MGC:2851 IMAGE:2967512, mRNA, complete cds /cds=(444,2618) | 1 | CCAGAATCGTAAGGGGGCTGACGGGA GGATGAGAGGGGGGCACCCAGAGATC |
| 1563 | Table 3A | Hs.293515 | BE905040 | 10397924 | 602286727T1 cDNA, 3' end /clone=IMAGE:4375662 /clone_end=3' | 1 | CGGTGTTTTCTGATCGGTTTTTGT CTGCTTACATATGATGTACTTGT |
| 1564 | Table 3A | Hs.278704 | BE973840 | 10587176 | RST30930 cDNA | 1 | ACAGAATGCAGCGGTGCAACACCGG CAAGGTTCCACACGCCACAAAGAAA |
| 1565 | Table 3A | Hs.217493 | D00017 | 219909 | annexin A2 (ANXA2), mRNA /cds=(49,1068) | 1 | TGGAAGTGAAGTCTATGATGTGAAAC ACTTTGCCTCCTGTGTACTGTGTC |
| 1566 | Table 3A | Hs.25 | D00022 | 219653 | Homo sapiens, Similar to ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide, clone MGC:19754 IMAGE:3629237, mRNA, complete cds /cds=(12,1601) | 1 | CCAAAAAGCTTCATTTTTCTATATAGG CTGCACAAGAGCCTTGATTGAAG |
| 1567 | Table 3A | Hs.76549 | D00099 | 219941 | mRNA for Na,K-ATPase alpha-subunit, complete cds /cds=(318,3389) | 1 | TCACAAGACAGTCATCAGAACCAGTA AATATCCGTCTGCCAGTTCGATCA |
| 1568 | Table 3A | Hs.76549 | D00099 | 219941 | mRNA for Na,K-ATPase alpha-subunit, complete cds /cds=(318,3389) | 1 | TCACAAGACAGTCATCAGAACCAGTA AATATCCGTCTGCCAGTTCGATCA |
| 1569 | Table 3A | Hs.154890 | D10040 | 219899 | fatty-acid-Coenzyme A ligase, long- chain 2 (FACL2), mRNA /cds=(13,2109) | 1 | GCTGTCAATTTGTACATTTAAAGCAGC TGTTTTGGGGTCTGTGAGAGTACA |
| 1570 | Table 3A | Hs.46 | D10202 | 219975 | platelet-activating factor receptor (PTAFR), mRNA /cds=(25,1053) | 1 | TATCCTGAGTCCCTTAATCTTATGGG GCCGGAAGGAATGTCAGGGCCAGG |
| 1571 | Table 3A | Hs.155342 | D10495 | 520586 | protein kinase C, delta (PRKCD), mRNA /cds=(58,2088) | 1 | CTCTGCCTTCGGAGGGAAATTGTAAA TCCTGTGTTTCATTACTTGAATGT |
| 1572 | Table 3A | Hs.330716 | D10522 | 219893 | cDNA FLJ14368 fis, clone HEMBA1001122 /cds=UNKNOWN | 1 | AAACTCCTGCTTAAGGTGTTCTAATTT TCTGTGAGACACTAAAGCTTCTGTTGA |
| 1573 | Table 3A | Hs.137555 | D10923 | 219866 | putative chemokine receptor; GTP- binding protein (HM74), mRNA /cds=(60,1223) | 1 | GGGTGCACGTTCCTCCTGGTTCCTTC GCTTGTGTTTCTGTACTTACCAAA |
| 1574 | Table 3A | Hs.301921 | D10925 | 219862 | chemokine (C-C motif) receptor 1 (CCR1), mRNA /cds=(62,1129) | 1 | GGGGTTGGGAGGAAGTGTCTACTAG GAGGGTGGGTGAGATCTGTGTTGAT |
| 1575 | Table 3A | Hs.238893 | D11086 | 303611 | od15g01.s1 cDNA /clone=IMAGE:1368048 | 1 | ATCTACCCTCCGATTGTTCTGTAACC GATGAGAAATAAAGTTTCTGTGTA |
| 1576 | Table 3A | Hs.61153 | D11094 | 219930 | proteasome (prosome, macropain) 26S subunit, ATPase, 2 (PSMC2), mRNA /cds=(66,1367) | 1 | AAGTCTTATGCCAAATTCAGTGCTAC TCCTCGTTACATGACATACAACTG |
| 1577 | Table 3A | Hs.36 | D12614 | 219911 | lymphotoxin alpha (TNF superfamily, member 1) (LTA), mRNA /cds=(140,757) | 1 | CACACGGAGGCATCTGCACCCTCGA TGAAGCCCAATAAACCTCTTTTCTC |
| 1578 | Table 3A | Hs.333114 | D13316 | 286022 | AV713318 cDNA, 5' end /clone=DCAAAC09 /clone_end=5' | 1 | ACAACGTCGTGACTGGGAAAACCTT GGCGTTACCCAACCTTAATCGCCTTG |
| 1579 | Table 3A | Hs.15071 | D13627 | 286010 | chaperonin containing TCP1, subunit 8 (theta) (CCT8), mRNA /cds=(28,1674) | 1 | CCAAGCCTCCAAGTGGGAAGAAAGA CTGGGATGATGACCAAAATGATTGA |
| 1580 | Table 3A | Hs.195614 | D13642 | 285998 | splicing factor 3b, subunit 3, 130kD (SF3B3), mRNA /cds=(156,3809) | 1 | CAACTACTTGTGGCATGCTTGGCAC TCGGAATAAAGCGCACTATTGTCA |
| 1581 | Table 3A | Hs.2471 | D13645 | 286008 | KIAA0020 gene product (KIAA0020), mRNA /cds=(418,1944) | 1 | GAAGGGGTAGGGTCCAGCTACTGCG TAATTGGGGTACTCTGTATATGTGT |

Table 8

| | | | | | | | |
|------|----------|-----------|--------|---------|---|---|-------------------------------|
| 1582 | Table 3A | Hs.278573 | D14041 | 2326266 | H-2K binding factor-2 (LOC51580), mRNA /cds=(238,1500) | 1 | GCTCAGTTCCATATTTTCATCCGTGAA |
| 1583 | Table 3A | Hs.43910 | D14043 | 219924 | CD164 antigen, sialomucin (CD164), mRNA /cds=(79,648) | 1 | AACTTGAACATACGAGCAGTTTCA |
| 1584 | Table 3A | Hs.111894 | D14696 | 285962 | lysosomal-associated protein transmembrane 4 alpha (LAPTM4A), mRNA /cds=(148,849) | 1 | AATTGTCTATTTTACCTGGGTATGAATTC |
| 1585 | Table 3A | Hs.232068 | D15050 | 457560 | transcription factor 8 (represses interleukin 2 expression) (TCF8), mRNA /cds=(3,3377) | 1 | CCTGACACACATTCATGTCAACA |
| 1586 | Table 3A | Hs.279607 | D16217 | 303598 | calpastatin (CAST), mRNA /cds=(66,1358) | 1 | GTGACTTGACTGTGGAAGATGATGGT |
| 1587 | Table 3A | Hs.146812 | D16481 | 473711 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB), mRNA /cds=(46,1470) | 1 | TGCATGTTTCTAGTTTGTATATGT |
| 1588 | Table 3A | Hs.50651 | D17042 | 598768 | Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA /cds=(75,3503) | 1 | CAGTGCTGTAATACAGACGGCAATGC |
| 1589 | Table 3A | Hs.180828 | D17391 | 440365 | collagen, type IV, alpha 4 (COL4A4), mRNA /cds=(208,5280) | 1 | AATAGCCTATTTAAAGAACTACGT |
| 1590 | Table 3A | Hs.178658 | D21090 | 498147 | RAD23 (S. cerevisiae) homolog B (RAD23B), mRNA /cds=(313,1542) | 1 | AGCTGGTGGATGGTGACTTTTGAAGA |
| 1591 | Table 3A | Hs.75337 | D21262 | 434764 | mRNA for KIAA0035 gene, partial cds /cds=(0,2125) | 1 | ACAAAAGGCTTTGGCAACAGAAAA |
| 1592 | Table 3A | Hs.79768 | D21853 | 434770 | KIAA0111 gene product (KIAA0111), mRNA /cds=(214,1449) | 1 | TCTGTTGCTACTAAAGACTAAATGAG |
| 1593 | Table 3A | Hs.334822 | D23660 | 432358 | Homo sapiens, Similar to ribosomal protein L4, clone MGC:2966 IMAGE:3139805, mRNA, complete cds /cds=(1616,2617) | 1 | GGTTTGCAGTTGGGAAAGAGGTCA |
| 1594 | Table 3A | Hs.75512 | D23662 | 432362 | neural precursor cell expressed, developmentally down-regulated 8 (NEDD8), mRNA /cds=(99,344) | 1 | GCGGAGTTGACCAAAATAATATCTGA |
| 1595 | Table 3A | Hs.35804 | D25215 | 517114 | hect domain and RLD 3 (HERC3), mRNA /cds=(166,3318) | 1 | GGATGATTGCTTTTCCCTGCTGCC |
| 1596 | Table 3A | Hs.173737 | D25274 | 464185 | ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) (RAC1), transcript variant Rac1b, mRNA /cds=(0,635) | 1 | CATCTTGAACCTTGGCCTGAGAACATT |
| 1597 | Table 3A | Hs.172199 | D25538 | 436217 | adenylate cyclase 7 (ADCY7), mRNA /cds=(265,3507) | 1 | TTCTGGGAAGAGGTAAGGGTGACA |
| 1598 | Table 3A | Hs.82502 | D26018 | 436221 | mRNA for KIAA0039 gene, partial cds /cds=(0,1475) | 1 | TCTGTGGAATCTCCTTCATTGGCATT |
| 1599 | Table 3A | Hs.169303 | D26121 | 785998 | mRNA for ZFM1 protein alternatively spliced product, complete cds /cds=(382,624) | 1 | GTTATTTAATCATAACGGGGCAG |
| 1600 | Table 3A | Hs.90315 | D26488 | 452522 | mRNA for KIAA0007 gene, partial cds /cds=(0,2062) | 1 | TGTACTGTTTCATGCTGACACAGATAT |
| 1601 | Table 3A | Hs.17719 | D28589 | 460714 | EBP50-PDZ interactor of 64 kD (EPI64), mRNA /cds=(24,1550) | 1 | TTCAGTCTGCATGGTAAAGTTCT |
| 1602 | Table 3A | Hs.198248 | D29805 | 474986 | UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1 (B4GALT1), mRNA /cds=(72,1268) | 1 | TAATGGGGTTTATATGGAATTTCTCT |
| 1603 | Table 3A | Hs.79709 | D30036 | 1060902 | phosphatidylinositol transfer protein (PITPN), mRNA /cds=(216,1028) | 1 | CATAAATGGCCTGCCGTCTCCCT |
| 1604 | Table 3A | Hs.115263 | D30783 | 2381480 | epiregulin (EREG), mRNA /cds=(166,675) | 1 | ACCAAGAAACAGCCCTGAAAAGAA |
| 1605 | Table 3A | Hs.75416 | D31767 | 505091 | DAZ associated protein 2 (DAZAP2), mRNA /cds=(69,575) | 1 | GCCTGCAGAGAAGAACTACTAC |
| 1606 | Table 3A | Hs.3094 | D31884 | 505095 | KIAA0063 gene product (KIAA0063), mRNA /cds=(279,887) | 1 | AGTCCTGTGTGCTTCCCTCTCTTATG |
| 1607 | Table 3A | Hs.75249 | D31885 | 505097 | mRNA for KIAA0069 gene, partial cds /cds=(0,680) | 1 | ACTGTGTCCTTGTTGTCAATAAA |
| 1608 | Table 3A | Hs.3100 | D32053 | 2366751 | lysyl-tRNA synthetase (KARS), mRNA /cds=(40,1833) | 1 | ACCCACCACCTCTTGCACTCTCGCTT |
| 1609 | Table 3A | Hs.181244 | D32129 | 699597 | major histocompatibility complex, class I, A (HLA-A), mRNA /cds=(0,1097) | 1 | TTGGAGCAAGTTGCATTAACATT |
| 1610 | Table 3A | Hs.89887 | D38081 | 533325 | thromboxane A2 receptor (TBXA2R), mRNA /cds=(991,2022) | 1 | TGACAGTGTGCTGATCTTTGCTATGC |
| 1611 | Table 3A | Hs.138593 | D38524 | 633070 | 5'-nucleotidase (purine), cytosolic type B (NT5B), mRNA /cds=(83,1768) | 1 | TTTACATTGATCTTTTGCTAATGC |
| 1612 | Table 3A | Hs.77257 | D38549 | 559702 | Homo sapiens, Similar to selective hybridizing clone, clone MGC:13167 IMAGE:3163591, mRNA, complete cds /cds=(52,3813) | 1 | ATGACAGACACACGTATCTAACAAAC |
| 1613 | Table 3A | Hs.81848 | D38551 | 1531549 | RAD21 (S. pombe) homolog (RAD21), mRNA /cds=(184,2079) | 1 | AAACAAACAGTGACCTTCTCCATG |

Table 8

| | | | | | | | |
|------|------------|-----------|--------|---------|---|---|---|
| 1614 | Table 3A | Hs.81964 | D38555 | 559716 | SEC24 (S. cerevisiae) related gene family, member C (SEC24C), mRNA /cds=(114,3491) | 1 | ACCTGGGATGCCCTGCTCTGGACC TCTCATTTCTCTTCATTGGTTTATT |
| 1615 | Table 3A | Hs.78871 | D42039 | 577290 | mRNA for KIAA0081 gene, partial cds /cds=(0,702) | 1 | ATCTATCCTTGCCAGCCTTGGGCATC ACATTTACCAGTTTAATAGATTGT |
| 1616 | Table 3A | Hs.75243 | D42040 | 577292 | bromodomain-containing 2 (BRD2), mRNA /cds=(1701,4106) | 1 | GCCCTGATCTGGAGTTACCTGAGGC CATAGCTGCCCTATTTCACTTCTAAG |
| 1617 | Table 3A | Hs.79123 | D42043 | 577298 | mRNA for KIAA0084 gene, partial cds /cds=(0,1946) | 1 | CTTGACCAAAACCCACAGCCTGTCTCT TCTCTTGTTTAGTTACTTACGGCA |
| 1618 | literature | Hs.1560 | D42045 | 577302 | mRNA for KIAA0086 gene, complete cds /cds=(918,4040) | 1 | CCTTAGAAGAGGAAGCAAAGGCAGA TTCAGGGACCAAAAGGATTAATGAT |
| 1619 | Table 3A | Hs.151791 | D42054 | 577310 | KIAA0092 gene product (KIAA0092), mRNA /cds=(53,1477) | 1 | ATGTGTCAACCAACATTTTCAGCTATT AAAACTCCTGTTATCTCCTTGT |
| 1620 | Table 3A | Hs.129914 | D43968 | 966996 | AML1 mRNA for AML1b protein (alternatively spliced product), complete cds /cds=(1578,2939) | 1 | AGCCACCAAGAGCCTTCTCTCTTTGT ACCACAGTTTCTTCTGTAATCCA |
| 1621 | Table 3A | Hs.183706 | D44640 | 1572115 | HUMSUPY040 cDNA /clone=035-00-1 | 1 | ACATGAAATATAGTTGCATATATGGA CACCGACTTGGGAGGACAGGTCCT |
| 1622 | Table 3A | Hs.1119 | D49728 | 1813881 | nuclear receptor subfamily 4, group A, member 1 (NR4A1), mRNA /cds=(110,1906) | 1 | CTTTCCAGCCTCCTGCTGGGCTCTCT CTTCCTACCTCCTTCCACATGTA |
| 1623 | Table 3A | Hs.83077 | D49950 | 1405318 | interleukin 18 (interferon-gamma-inducing factor) (IL18), mRNA /cds=(177,758) | 1 | AGATAGCCAGCCTAGAGGTATGGCT GTAATCTCTCTGTGAAGTGTGAGA |
| 1624 | Table 3A | Hs.155543 | D50063 | 971269 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) (PSMD7), mRNA /cds=(83,1057) | 1 | TGGCATCCTCAGGGGTTGTGATCCA GCTCCATATATTGTTACCTTCAAA |
| 1625 | Table 3A | Hs.182255 | D50420 | 2618577 | non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA /cds=(94,480) | 1 | CATGAGGAGAGTGCTAGTTCATGTGT TCTCCATTCTGTGAGCATCCTAA |
| 1626 | Table 3A | Hs.699 | D50525 | 1167502 | peptidylprolyl isomerase B (cyclophilin B) (PPIB), mRNA /cds=(21,671) | 1 | CAGCAAATCCATCTGAAGTGTGGAGG AGAAGCTCTCTTTACTGAGGGTGC |
| 1627 | Table 3A | Hs.82028 | D50683 | 1827474 | mRNA for TGF-beta1R alpha, complete cds /cds=(1572,3275) | 1 | TCAGCATAAACTGGAATGTAGTGTCA GAGGATACTGTGGCTGTTTGT |
| 1628 | Table 3A | Hs.90998 | D50918 | 1469178 | mRNA for KIAA0128 gene, partial cds /cds=(0,1276) | 1 | TGGTGAACAAAACAGTCATTAGAA ATGGTCTGTGCTTTTATTTCCCA |
| 1629 | Table 3A | Hs.70359 | D50926 | 1469194 | genomic DNA, chromosome 21q22.2, PCR fragment from BAC clone:KB739C11, CBR1-HLCS region /cds=(0,2854) | 1 | ACTATGCTTTATTGGTCCCATGTTTTG TGCAATTTTAAAGAGATGGCTTT |
| 1630 | Table 3A | Hs.198899 | D50929 | 1469200 | eukaryotic translation initiation factor 3, subunit 10 (theta, 150/170kD) (EIF3S10), mRNA /cds=(113,4261) | 1 | AAAGATGAACTATTTGGTCTCATTGA AGCCAACACAGAACTTGCTGCTGT |
| 1631 | Table 3A | Hs.77152 | D55716 | 1255616 | minichromosome maintenance deficient (S. cerevisiae) 7 (MCM7), mRNA /cds=(544,2175) | 1 | GGAGCCCTCTTTCTCCCATGCTGCA CTTACTCCTTTTGCTAATAAAAGT |
| 1632 | Table 3A | Hs.181418 | D63486 | 1469885 | KIAA0152 gene product (KIAA0152), mRNA /cds=(128,1006) | 1 | CCTTCCATGTCCACCCCACTCCAC CAAAAAGTACAAAATCAGGATGTT |
| 1633 | Table 3A | Hs.3195 | D63789 | 1754608 | small inducible cytokine subfamily C, member 1 (lymphotactin) (SCYC1), mRNA /cds=(20,364) | 1 | TGATGGTAACCATATGGAAGAGATT CTGGCTAGTGCTATCAGAGGTGA |
| 1634 | Table 3A | Hs.274472 | D63874 | 968887 | high-mobility group (nonhistone chromosomal) protein 1 (HMG1), mRNA /cds=(52,699) | 1 | GTCCTGGTGGTATCTTCAATAGCCAC TAACCCTGCCTGGTACAGTATGGG |
| 1635 | Table 3A | Hs.87726 | D63876 | 961443 | ADP-ribosylation factor-binding protein GGA3 (GGA3), mRNA /cds=(8,2080) | 1 | CCCAGCTCTGCTGCCCTGTTTTGCT GCATGTTAAATAAAACCATTTTCA |
| 1636 | Table 3A | Hs.155595 | D63878 | 961447 | neural precursor cell expressed, developmentally down-regulated 5 (NEDD5), mRNA /cds=(258,1343) | 1 | CCCACACTGTACACTTCTGATCCCC TTTGGTTTTACTACCCAAATCTAA |
| 1637 | Table 3A | Hs.182741 | D64015 | 2281005 | TIA1 cytotoxic granule-associated RNA-binding protein-like 1 (TIAL1), transcript variant 2, mRNA /cds=(157,954) | 1 | CTGTAATACCTCCTCCTAACCAAGCC GGATATGGTATGGCAAGTTACCAA |
| 1638 | Table 3A | Hs.75232 | D67029 | 1669536 | SEC14 (S. cerevisiae)-like 1 (SEC14L1), mRNA /cds=(303,2450) | 1 | CCCTTGTAAGGGAATTTCTGGGGCAG CTATGGTTTGAGTATGCAGTTTGCA |
| 1639 | Table 3A | Hs.155968 | D76444 | 1945614 | zinc finger protein homologous to Zfp103 in mouse (ZFP103), mRNA /cds=(922,2979) | 1 | ACAATCTCTGTCCAGCACCTTGGT TAAATAATGTATGCTGTGAGACAT |
| 1640 | Table 3A | Hs.80905 | D79990 | 1136395 | Ras association (RalGDS/AF-6) domain family 2 (RASSF2), mRNA /cds=(196,1176) | 1 | ACAGGGCCTCAGCAAGGGAGCCATA CATTTTTGTAACATTTTGATATGTT |
| 1641 | Table 3A | Hs.76666 | D80005 | 1136425 | mRNA for KIAA0183 gene, partial cds /cds=(0,3190) | 1 | TTGACTGTGCGATGGATTGTGGTGTGG TGTATCTGAAGGCTATTGAATGCA |
| 1642 | Table 3A | Hs.322903 | D80006 | 1136427 | mRNA for KIAA0184 gene, partial cds /cds=(0,2591) | 1 | TTCTGTCCAAACAAGTATTTCTGTAGA TCCAAATGGATTACCAAGTGTGCT |
| 1643 | Table 3A | Hs.79389 | D83018 | 1827484 | nel (chicken)-like 2 (NELL2), mRNA /cds=(96,2546) | 1 | ATCTTCAGAAATCAGTTAGGTTCTCA CTGCAAGAAATAAATGTCAGGCA |
| 1644 | Table 3A | Hs.89385 | D83243 | 1304113 | nuclear protein, ataxia-telangiectasia locus (NPAT), mRNA /cds=(34,4317) | 1 | TGAAGCTTACTGCAAAAACCTTGAT GTAAGAAATTTGTATGGTGTGGCA |

Table 8

| | | | | | | | |
|------|----------|-----------|--------|---------|--|---|------------------------------|
| 1645 | Table 3A | Hs.12413 | D83776 | 1228034 | mRNA for KIAA0191 gene, partial cds /cds=(0,4552) | 1 | GCTGTCTCAAGGGTATCCGTACCTCA |
| 1646 | Table 3A | Hs.22559 | D83781 | 1228044 | mRNA for KIAA0197 gene, partial cds /cds=(0,3945) | 1 | ATGTCAGTTACATTCAGCAGAAAA |
| 1647 | Table 3A | Hs.343517 | D84224 | 7804467 | methionine-tRNA synthetase (MARS), mRNA /cds=(23,2725) | 1 | TTGGTCAGATTAGAGCATTCATGC |
| 1648 | Table 3A | Hs.21899 | D84454 | 1526437 | protein translocase, JM26 protein, UDP-galactose translocator, pim-2 protooncogene homolog pim-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM enhancer 3 genes, partial cds; and unknown gene /cds=(323,1504) | 1 | TCACAAGTTTTGGGAAAGTGAAAA |
| 1649 | Table 3A | Hs.300391 | D85429 | 1816451 | UI-H-B14-aq-d-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:3085848 /clone_end=3' | 1 | CCCTAAAGGCAAGAAGAAAAAGTAAA |
| 1650 | Table 3A | Hs.75842 | D86550 | 1772437 | mRNA for serine/threonine protein kinase, complete cds /cds=(1473,3737) | 1 | AGACCTTGGCTCATAGAAAGTCAC |
| 1651 | Table 3A | Hs.36927 | D86956 | 1503985 | heat shock 105kD (HSP105B), mRNA /cds=(313,2757) | 1 | GTGTGTGCATGGAAGATGCCTGGGC |
| 1652 | Table 3A | Hs.17211 | D86964 | 1504001 | mRNA for KIAA0209 gene, partial cds /cds=(0,5530) | 1 | TGTCTTTGCTATATGTAAATAGAGC |
| 1653 | Table 3A | Hs.154332 | D86967 | 1504007 | KIAA0212 gene product (KIAA0212), mRNA /cds=(58,2031) | 1 | GCCTTGGCTTTATTTGCAGGCTACTA |
| 1654 | Table 3A | Hs.110613 | D86974 | 1504021 | PI-3-kinase-related kinase SMG-1 (SMG1), mRNA /cds=(132,9227) | 1 | AAGCTGCTTTTACTTTGTAACCTT |
| 1655 | Table 3A | Hs.199243 | D86984 | 1504041 | mRNA for KIAA0231 gene, partial cds /cds=(0,1430) | 1 | ACAGTTTGGTTACAGGACTTCTGTGC |
| 1656 | Table 3A | Hs.79276 | D86985 | 6634002 | mRNA for KIAA0232 protein, partial cds /cds=(0,3836) | 1 | ATTGTAACATAAACAGCATGGAA |
| 1657 | Table 3A | Hs.10315 | D87432 | 1665758 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 (SLC7A6), mRNA /cds=(261,1808) | 1 | TGTGAAAGTGTGGAATGGAAGAAATG |
| 1658 | Table 3A | Hs.75912 | D87446 | 1665780 | mRNA for KIAA0257 gene, partial cds /cds=(0,5418) | 1 | TCGATCCTGTTGTAAGTATTGTG |
| 1659 | Table 3A | Hs.154978 | D87450 | 1665788 | mRNA for KIAA0261 gene, partial cds /cds=(0,3865) | 1 | ACAACCAACCAAGTTTCTTTCTAGCC |
| 1660 | Table 3A | Hs.192966 | D87454 | 1665796 | mRNA for KIAA0265 gene, partial cds /cds=(0,1205) | 1 | AATCATCTCTGAAGAGTTGCTGTT |
| 1661 | Table 3A | Hs.40888 | D87468 | 1944419 | mRNA for KIAA0278 gene, partial cds /cds=(0,1383) | 1 | GAACCTCCTGATTCTATACCCTCTTC |
| 1662 | Table 3A | Hs.77495 | D87684 | 1663703 | mRNA for KIAA0242 protein, partial cds /cds=(0,1590) | 1 | CTTCTTTCTGCAAGGCAGAGGAAT |
| 1663 | Table 3A | Hs.75789 | D87953 | 1596166 | N-myc downstream regulated (NDRG1), mRNA /cds=(110,1294) | 1 | CACCCCTCAGCTCCACCCCTCAGCAGAT |
| 1664 | Table 3A | Hs.75367 | D89077 | 1694681 | Src-like-adaptor (SLA), mRNA /cds=(41,871) | 1 | GATAATATCAAGACACTGCCGAG |
| 1665 | Table 3A | Hs.170311 | D89678 | 3218539 | heterogeneous nuclear ribonucleoprotein D-like (HNRPDL), transcript variant 1, mRNA /cds=(580,1842) | 1 | TTGGCCCTCAGGTTTACTGTGTAAT |
| 1666 | Table 3A | Hs.121102 | D89974 | 5541649 | vanin 2 (VNN2), mRNA /cds=(11,1573) | 1 | CTGCATTTTTTGGTGGTAAATCCCT |
| 1667 | Table 3A | Hs.73817 | D90144 | 219905 | gene for LD78 alpha precursor, complete cds | 1 | GCATTTCCATAGCACTGAAGTACCAG |
| 1668 | Table 3A | Hs.218387 | H03298 | 866231 | tc88c11.x1 cDNA, 3' end /clone=IMAGE:2073236 /clone_end=3' | 1 | TTCCATTCTCGGGCTGAGATTGT |
| 1669 | Table 3A | Hs.70258 | H06786 | 870318 | yl83g05.r1 cDNA, 5' end /clone=IMAGE:44737 /clone_end=5' | 1 | CTCCTTTTAAACGTGTTATTGACAAACC |
| 1670 | Table 3A | Hs.32149 | H14103 | 878951 | ym62a02.r1 cDNA, 5' end /clone=IMAGE:163466 /clone_end=5' | 1 | TCCCCAAAGAATATGCAATTGT |
| 1671 | Table 3A | Hs.94881 | H51796 | 991637 | 602387586F1 cDNA, 5' end /clone=IMAGE:4516388 /clone_end=5' | 1 | AACATTCAGTTGAGACCATATGCATT |
| 1672 | Table 3A | Hs.178703 | H56344 | 1004988 | AV716627 cDNA, 5' end /clone=DCBBCH05 /clone_end=5' | 1 | TTCTGTGCTGTTTGACTTGAGGT |
| 1673 | Table 3A | Hs.270192 | H57221 | 1010053 | ESTs | 1 | TTAACCCCTCAGAGAAGCTTGCAATTT |
| 1674 | Table 3A | Hs.237146 | H86841 | 1068420 | mRNA for zinc finger protein RINZF (RINZF gene) /cds=(598,3141) | 1 | AGGGTACTTGAGGCTGACTTAACT |
| 1675 | Table 3A | Hs.76807 | J00194 | 188231 | major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA /cds=(26,790) | 1 | AGCGACCTCTTCTCTAGTCCGGTGTT |
| 1676 | Table 3A | Hs.251064 | J02621 | 184229 | high-mobility group (nonhistone chromosomal) protein 14 (HMG14), mRNA /cds=(150,452) | 1 | ACGAACAGAAGTTCTGAGTTGTGC |
| | | | | | | 1 | TAAATGTGCGTCCAGGCCCTGTGCAC |
| | | | | | | 1 | CTTACCCAGAGACAGACTCTTTT |
| | | | | | | 1 | ATAAGGCTGTAAATGAGAATTCTGC |
| | | | | | | 1 | CCCTCACCTCTTACCCCACTACT |
| | | | | | | 1 | AAAAGTCGGGATTCGGGGCAAGAGA |
| | | | | | | 1 | GGCTGAGTACGGATGGGAACTATT |
| | | | | | | 1 | GAGCACCCAGAGGGATTTTTCAGTG |
| | | | | | | 1 | GGAAGCATTACACTTTGCTAAATCA |
| | | | | | | 1 | TGATTAGGTGACGAGTTGACATTGAG |
| | | | | | | 1 | ATTGTCCTTTTCCCCGTATCAAAA |
| | | | | | | 1 | TGTATGTATGGGAGTGAGGAGTTTCA |
| | | | | | | 1 | GGGCCATTGCAAAACATAGCTGTGC |
| | | | | | | 1 | ACAGAGTTATCCACTTTACAACGGAG |
| | | | | | | 1 | ACACAGTTCTGGAACATTGAAACT |
| | | | | | | 1 | ATACGGGACAATAAAATCTGCCCTTTT |
| | | | | | | 1 | GTCTGGGAGGAGATACTACCTCT |
| | | | | | | 1 | GGGCAAAACACTTTAGGAATACTAGT |
| | | | | | | 1 | TACTCACTTAACATGGAGGGCGGG |
| | | | | | | 1 | AAAGGCCGCGCAGATTGTTTAATTCT |
| | | | | | | 1 | GGAAAGTCAATCCCCGGATTAGC |
| | | | | | | 1 | GGGACTCCATGGGAATATTTGCCAG |
| | | | | | | 1 | TAATGGTAAGGAAATCTTTCGGGT |
| | | | | | | 1 | CCAGAAAGGTGATGAATGAATAGGAC |
| | | | | | | 1 | TGAGAGTCAAGTGAATGTGGCAT |
| | | | | | | 1 | TCCCAAGGTTGTTAGTGACTGATAAG |
| | | | | | | 1 | CTTCCAACTACAGTACAGTTTTT |
| | | | | | | 1 | GTTTTCTGTAGTTGCGGGTCCCTCG |
| | | | | | | 1 | CGAAAGTTCAATTCATGGCCCACT |
| | | | | | | 1 | CATGGGGCTCTCTGTGTACTTATTG |
| | | | | | | 1 | TTTAAGGTTTCTCAAACCTGTGAT |
| | | | | | | 1 | ACAAATTGAAATGTCTGTACTGATCC |
| | | | | | | 1 | TCAACCAATAAAATCTCAGCCGAA |

Table 8

| | | | | | | | |
|------|----------|-----------|--------|--------|---|---|---|
| 1677 | Table 3A | Hs.62192 | J02931 | 339501 | coagulation factor III (thromboplastin, tissue factor) (F3), mRNA /cds=(123,1010) | 1 | TGCAGGAGACATTGGTATTCTGGGCA GCTTCCTAATATGCTTTACAATCT |
| 1678 | Table 3A | Hs.1513 | J03171 | 184645 | interferon (alpha, beta and omega) receptor 1 (IFNAR1), mRNA /cds=(78,1751) | 1 | TCATCCCCGAGAACATTGGCTTCCACA TCACAGTATCTACCCTTACATGGT |
| 1679 | Table 3A | Hs.317 | J03250 | 339805 | topoisomerase (DNA) I (TOP1), mRNA /cds=(247,2544) | 1 | GGCATTGTAGTTAGTGTGTGTGCA GAGTCCATTTCCACATCTTTCCT |
| 1680 | Table 3A | Hs.81118 | J03459 | 187172 | leukotriene A4 hydrolase (LTA4H), mRNA /cds=(68,1903) | 1 | GACTGCAATGCTGGTGGGGAAAGAC TTAAAGTGGATTAAAGACCTGCGT |
| 1681 | Table 3A | Hs.177766 | J03473 | 337423 | ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase) (ADPRT), mRNA /cds=(159,3203) | 1 | GCTTTCCCTTCCAGGAATACTGAAC ATGGGAGCTCTTGAAATATGTAGT |
| 1682 | Table 3A | Hs.73792 | J03565 | 181919 | complement component (3d/Epstein Barr virus) receptor 2 (CR2), mRNA /cds=(69,3170) | 1 | TGGGAATCAAGATTTAATCCTAGAGA TTTGGTGTAACAATCAGGCTTTGG |
| 1683 | Table 3A | Hs.727 | J03634 | 181946 | inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA /cds=(85,1365) | 1 | GCAGTAGTGTGGACTAGAACAAACCCA AATAGCATCTAGAAAGCCATGAGT |
| 1684 | Table 3A | Hs.86948 | J03798 | 338264 | small nuclear ribonucleoprotein D1 polypeptide (16kD) (SNRPD1), mRNA /cds=(150,509) | 1 | TGTGTAATGTACCTGTCAGTGCCTCC TTTATTAAGGGGTTCTTTGAGAAT |
| 1685 | Table 3A | Hs.75703 | J04130 | 178017 | small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA /cds=(108,386) | 1 | CCACTGTCACTGTTTCTCTGCTGTTG CAAATACATGGATAACACATTGTA |
| 1686 | Table 3A | Hs.1799 | J04142 | 619799 | CD1D antigen, d polypeptide (CD1D), mRNA /cds=(164,1171) | 1 | AGTTTGCCCTGGATGTCATATTGGCA GTTGGAGGACACAGTTTCTATTGT |
| 1687 | Table 3A | Hs.298469 | J04144 | 178285 | dipeptidyl carboxypeptidase 1 (angiotensin I converting enzyme) (ACE), mRNA /cds=(22,3942) | 1 | CCAAGTTCCACATTCCTTCTAGCGTG CCTTACATCAGGTACTTTGTCAGC |
| 1688 | Table 3A | Hs.176663 | J04162 | 183036 | leukocyte IgG receptor (Fc-gamma-R) mRNA, complete cds /cds=(17,718) | 1 | AGCTGTCTCCTGTTTGTGAAGCTTTC AGTGCAACATTTCTTGTTCCAAT |
| 1689 | Table 3A | Hs.62954 | J04755 | 182512 | ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(91,663) | 1 | TGCATGTTGGGGTTTCTTACCTTTT CTATAAGTTGTACCAAAACATCC |
| 1690 | Table 3A | Hs.288156 | J05016 | 181507 | cDNA: FLJ21819 fis, clone HEP01185 /cds=UNKNOWN | 1 | GGGTTTGTGCTATACACTGGGATGTC TAATTGCAGCAATAAAGCCTTTCT |
| 1691 | Table 3A | Hs.80758 | J05032 | 179101 | aspartyl-tRNA synthetase (DARS), mRNA /cds=(93,1595) | 1 | GGCACAATTTCTTTTTCAGTAACCT GCTAGTGACAGGCTGTACTTTAG |
| 1692 | Table 3A | Hs.850 | J05272 | 186393 | IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA /cds=(600,2144) | 1 | CAGTCGAAGGCTTTAATCTTGCACAC TTGGGATCACAGTTGCGTCATTGT |
| 1693 | Table 3A | Hs.84298 | K01144 | 188469 | CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) (CD74), mRNA /cds=(7,705) | 1 | TTCCCTTTCCCGAGCATCACTCCCCA AGGAAGAGCCAATGTTTTCACCC |
| 1694 | Table 3A | Hs.79070 | K02276 | 188927 | v-myc avian myelocytomatosis viral oncogene homolog (MYC), mRNA /cds=(558,1877) | 1 | AGCCATAATGTAACATGCCTCAAAT GGACTTTGGGCATAAAGAAGCTTT |
| 1695 | Table 3A | Hs.1290 | K02766 | 179725 | complement component 9 (C9), mRNA /cds=(4,1683) | 1 | TTGCTTTTACTAGTCTTAGCTCTACGA TTTAAATCCATGTGTCCAAGGGG |
| 1696 | Table 3A | Hs.303157 | K02885 | 338928 | mRNA for T-cell specific protein /cds=(37,975) | 1 | CACACCTGCACACTCACGGCTGAAAT CTCCCTAACCCAGGGGGACCTTAG |
| 1697 | Table 3A | Hs.21595 | L03426 | 340386 | DNA segment on chromosome X and Y (unique) 155 expressed sequence (DXYS155E), mRNA /cds=(166,1323) | 1 | AGCTGTAACTGTCGCGTTAGGAAAGA TGGTGTTTATCCAGTTTGCAATT |
| 1698 | Table 3A | Hs.199160 | L04731 | 339921 | translocation T(4:11) of ALL-1 gene to chromosome 4 /cds=UNKNOWN | 1 | AGGGGTTCCACTAGTGTCTGCTTTCC TTTATTATTGCATGTGTGAGGTT |
| 1699 | Table 3A | Hs.234569 | L05148 | 340038 | protein tyrosine kinase related mRNA sequence /cds=UNKNOWN | 1 | CATCCTCAGGTGGTCAGGCGTAGAT CACCAGAAATAAACCCAGCTTCCCTC |
| 1700 | Table 3A | Hs.75528 | L05425 | 179284 | nucleolar GTPase (HUMAUANTIG), mRNA /cds=(79,2274) | 1 | ACACACAACGTGAAAAATAGGAACAG GAACAAAAGAGACCAATGACTC |
| 1701 | Table 3A | Hs.284192 | L06132 | 340198 | clone HQ0072 /cds=UNKNOWN | 1 | TTTAGAGTCTTCCATTTTGTGGAATT AGATCCTCCCCTTCAAATGCTGT |
| 1702 | Table 3A | Hs.1845 | L06175 | 189448 | MHC class I region ORF (P5-1), mRNA /cds=(304,735) | 1 | CTAATTTCAAGTCTTGTGCTTGGTTG TTCAGGGCCATTTCAAGTTTGGGT |
| 1703 | Table 3A | Hs.75348 | L07633 | 186512 | proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) (PSME1), mRNA /cds=(92,841) | 1 | CCAGATTTTCCCAAACTTGCTTCTG TTGAGATTTTCCCTCACCTTGCC |
| 1704 | Table 3A | Hs.324278 | L08048 | 184250 | mRNA; cDNA DKFZp566M063 (from clone DKFZp566M063) /cds=UNKNOWN | 1 | TGGGGGTTGTAATTTGGCATGGAAT TTAAAGCAGGTTCTTGTGGTGCA |
| 1705 | Table 3A | Hs.94 | L08069 | 306713 | heat shock protein, DNAJ-like 2 (HSJ2), mRNA /cds=(82,1275) | 1 | AGGTGGTGTTCAGTGTCAGACCTCTT AATGGCCAGTGAATAACACTCACT |
| 1706 | Table 3A | Hs.99899 | L08096 | 307127 | tumor necrosis factor (ligand) superfamily, member 7 (TNFSF7), mRNA /cds=(137,718) | 1 | GGGGGTAGTTTGTGGCAGGACAAGA GAAGGCATTGAGCTTTTCTTTCAT |
| 1707 | Table 3A | Hs.1652 | L08176 | 183484 | chemokine (C-C motif) receptor 7 (CCR7), mRNA /cds=(66,1202) | 1 | TCGTTAAGAGAGCAACATTTTACCCA CACACAGATAAAGTTTCCCTTGA |
| 1708 | Table 3A | Hs.211576 | L10717 | 307507 | IL2-inducible T-cell kinase (ITK), mRNA /cds=(2021,3883) | 1 | CCCTATCCCGCAAAATGGGCTTCTCG CCTGGGTTTTTCTCTCTCACATT |

Table 8

| | | | | | | | |
|------|-----------|-----------|-----------|----------|--|---|---|
| 1709 | Table 3A | Hs.3069 | L11066 | 307322 | heat shock 70kD protein 9B (mortalin-2) (HSPA9B), mRNA /cds=(29,2068) | 1 | AAACAAGGTAGGAATGAGGCTAGAC CTTTAACTTCCCTAAGGCATACTTT |
| 1710 | Table 3A | Hs.3446 | L11284 | 307183 | mitogen-activated protein kinase kinase 1 (MAP2K1), mRNA /cds=(72,1253) | 1 | TTCCCCATATCCAAGTACCAATGCTG TTGTAACAACAGTGTATAGTGCT |
| 1711 | Table 3A | Hs.1183 | L11329 | 559539 | dual specificity phosphatase 2 (DUSP2), mRNA /cds=(85,1029) | 1 | TGAGCCTTTACACCTGTGCTGGCGC TGGAAAATTATTTGTGCTCAGCTG |
| 1712 | Table 3A | Hs.220 | L11695 | 431034 | transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kD) (TGFBRI), mRNA /cds=(76,1587) | 1 | TGGGATTGTACTATACCAGTAAGTGC CACTTCTGTGCTTTCTAATGGAA |
| 1713 | Table 3A | Hs.150395 | L12052 | 179892 | cAMP phosphodiesterase PDE7 (PDE7A1) mRNA, complete cds /cds=(50,1498) | 1 | TTTTTCTCACAGGAGCGGAAGAACT AGGGGGAGCAGGAGCTGCAATGCG |
| 1714 | Table 3A | Hs.104125 | L12168 | 178083 | adenylyl cyclase-associated protein (CAP), mRNA /cds=(62,1489) | 1 | TCTACCCATTTCTGAGGCCTGTGGA AATAAACCTTTATGTACTTAAAGT |
| 1715 | Table 3A | Hs.78944 | L13463 | 292054 | regulator of G-protein signalling 2, 24kD (RGS2), mRNA /cds=(32,667) | 1 | GTGTCGGTTATGAGTGCCAAAAATCT GTCTTGAAGGCAGCTACACTTTGA |
| 1716 | Table 3A | Hs.258850 | L14542 | 292360 | killer cell lectin-like receptor subfamily C, member 3 (KLRC3), transcript variant NKG2-E, mRNA /cds=(45,767) | 1 | CTGTGCAATGCTACATGTACGTGGAC TTATATCAGACCAGTGTGGATCTT |
| 1717 | Table 3A | Hs.181125 | L21961 | 405227 | Homo sapiens, clone MGC:12849 IMAGE:4308973, mRNA, complete cds /cds=(24,725) | 1 | AGTCCCCTGTCCTGGTCATCTATCAA GATAACAAGCGGCCCTCAGGGATC |
| 1718 | Table 3A | Hs.247824 | NM_005214 | 291928 | cytotoxic T-lymphocyte-associated protein 4 (CTLA4), mRNA /cds=(0,671) | 1 | GGGTCTATGTGAAAATGCCCCCAACA GAGCCAGAATGTGAAAAGCAATTT |
| 1719 | Table 3A | Hs.179881 | L20298 | 388306 | core-binding factor, beta subunit (CBFB), transcript variant 2, mRNA /cds=(11,559) | 1 | CTTGCCCTTAAGCTACCAGATTGCTTT TGCCACCATTGGCCATACTGTGTG |
| 1720 | Table 3A | Hs.83656 | L20688 | 404044 | Rho GDP dissociation inhibitor (GDI) beta (ARHGDIB), mRNA /cds=(152,757) | 1 | CCCCTGCCAGAGGGAGTTCTTCTTTT GTGAGAGACACTGTAAACGACACA |
| 1721 | Table 3A | Hs.89582 | L20814 | 493133 | glutamate receptor, ionotropic, AMPA 2 (GRIA2), mRNA /cds=(160,2811) | 1 | TGCAGCCACTATTGTTAGTCTCTTGA TTCATAATGACTTAAGCACACTTG |
| 1722 | Table 3A | Hs.181125 | L22009 | 347313 | Homo sapiens, clone MGC:12849 IMAGE:4308973, mRNA, complete cds /cds=(24,725) | 1 | TGACTATTACTGTCCAGCGTGCGGACA CCAACACTGCGGTATTGCGCGGAG |
| 1723 | Table 3A | Hs.245710 | L23332 | 408689 | heterogeneous nuclear ribonucleoprotein H1 (H) (HNRPH1), mRNA /cds=(72,1421) | 1 | TTTGAGACGCAATACCAATACTTAGG ATTTTGGTCTTGGTGTTTGTATGA |
| 1724 | Table 3A | Hs.79117 | L23320 | 410217 | mRNA for corticotrophin releasing factor receptor /cds=(226,1473) | 1 | TCCTTCCAGGGCTTCTTTGTGTCTGT GTTCTACTGTTTCCCTCAATAGTGA |
| 1725 | Table 3A | Hs.79117 | L24498 | 403127 | mRNA for corticotrophin releasing factor receptor /cds=(226,1473) | 1 | CCATGTCCATCCCCACCTCCCCAAACC CGTGTCAGCTTTACAGCATCAAG |
| 1726 | db mining | Hs.80409 | NM_021998 | 11527399 | gadd45 gene, complete cds /cds=(2327,2824) | 1 | TGCCCTCAAGTAAAAGAAAAGCCGAA AGGGTTAATCATATTTGAAAACCA |
| 1727 | Table 3A | Hs.326801 | L25124 | 435049 | DNA sequence from PAC 75N13 on chromosome Xq21.1. Contains ZNF6 like gene, ESTs, STSs and CpG islands /cds=(567,2882) | 1 | ATGCTACTTGGGAGAAAACCTCTCACT AACTGTCTCACCGGGTTTCAAAGC |
| 1728 | Table 3A | Hs.199248 | L25080 | 407696 | prostaglandin E receptor 4 (subtype EP4) (PTGER4), mRNA /cds=(388,1854) | 1 | GGACTTTGCGAATATCAGAGACCTCA GACTCTTACAGGGTCAGGACTCA |
| 1729 | Table 3A | Hs.199248 | L25851 | 4406707 | prostaglandin E receptor 4 (subtype EP4) (PTGER4), mRNA /cds=(388,1854) | 1 | AGCTCCCTGCAAGTCACATTTCCAG TGAAACACTGAACTTATCAGAAAA |
| 1730 | Table 3A | Hs.241545 | L25931 | 438638 | Homo sapiens, Similar to hypothetical protein, clone MGC:1824 IMAGE:3509518, mRNA, complete cds /cds=(533,1504) | 1 | TTCTTTCAGGATGATCTAGAGCAGCA TGGAGCTGTTGGTAGAATATTAGT |
| 1731 | Table 3A | Hs.152931 | L29218 | 632967 | lamin B receptor (LBR), mRNA /cds=(75,1922) | 1 | GGGGAGGAAGGAAGGACATTAAATT CTTTCCTGGTAATGAAAAGAGCCC |
| 1732 | Table 3A | Hs.73986 | L26953 | 537529 | CDC-like kinase 2 (CLK2), transcript variant phck2, mRNA /cds=(129,1628) | 1 | GCCTTGACATAATACTATTCCATCCA CACAGTTTCCACCCTCACCTGCC |
| 1733 | Table 3A | Hs.29877 | L27071 | 951045 | TXK tyrosine kinase (TXK), mRNA /cds=(86,1669) | 1 | AGCAAGATAGCCAAATGTGACATCAA GCTCCATTGTTCCGGAATCCAGG |
| 1734 | Table 3A | Hs.73986 | L42572 | 1160962 | CDC-like kinase 2 (CLK2), transcript variant phck2, mRNA /cds=(129,1628) | 1 | GCCGAGTGAGGTAAACAGGTGGCAT CTACCCCATGTTTATAAGGAATTT |
| 1735 | Table 3A | Hs.78504 | L29348 | 460282 | inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA /cds=(92,2368) | 1 | TTCTTTCCATTTGCTATCATGTCAGTG AACGCCAGGAGTGCTTTCTTTGC |
| 1736 | Table 3A | Hs.1742 | L33075 | 536843 | IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA /cds=(467,5440) | 1 | TGAATTTACTTCTCCCAAGAGTTTG GACTGCCCGTCAGATTGTTCTGTC |
| 1737 | Table 3A | Hs.137232 | L33842 | 602457 | yq19a04.r1 cDNA, 5' end /clone=IMAGE:274063 /clone_end=5' | 1 | ACCCTCATTTCCAGGGGGAGCCTCA GGCCCCGAGATAAATGTGCTCCATG |

Table 8

| | | | | | | | |
|------|----------|-----------|--------|---------|--|---|---|
| 1738 | Table 3A | Hs.1697 | L35249 | 522192 | ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2 (ATP6B2), mRNA /cds=(25,1560) | 1 | TTCTCTGAGGGCTGGGGGTTGGGGG AGTCAGCATGATTATATTTTAATGT |
| 1739 | Table 3A | Hs.79107 | L35263 | 603916 | mitogen-activated protein kinase 14 (MAPK14), mRNA /cds=(362,1444) | 1 | ACTTGGCTGTAATCAGTTATGCCGTA TAGGATGTCAGACAAATCCACTGG |
| 1740 | Table 3A | Hs.75217 | L36870 | 685175 | mitogen-activated protein kinase kinase 4 (MAP2K4), mRNA /cds=(9,1208) | 1 | TGGAGCTCAGTAACATAACTGCTTCT TGGAGCTTGGAAATATTTTATCCT |
| 1741 | Table 3A | Hs.83086 | L38935 | 1008845 | GT212 mRNA /cds=UNKNOWN | 1 | AAATTTACAAAGCAATACTTTGGACC ACTGGGGTTCAGGCCCAAGAAAT |
| 1742 | Table 3A | Hs.180446 | L38951 | 893287 | importin beta subunit mRNA, complete cds /cds=(337,2967) | 1 | ACACACAAAACAGCAAACTTCAGGTA ACTATTTTGGATTGCAACAGGAT |
| 1743 | Table 3A | Hs.41726 | L40377 | 1160926 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8 (SERPINB8), mRNA /cds=(83,1207) | 1 | TCTTGCCCTTAATTAACTTCCCTGTGA CCTAGTTGGTGCAGTGGCTTGAA |
| 1744 | Table 3A | Hs.155079 | L42373 | 1000887 | protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A), mRNA /cds=(571,2031) | 1 | ACTTGCAGTTGTGTGGAAAAGTGT TGTAATGAAAGATCTTCATTGGGG |
| 1745 | Table 3A | Hs.78504 | L78440 | 1479978 | inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA /cds=(92,2368) | 1 | TGTGATCTCTACTACTGTTGATTTTGC CCTCGGAGCAAACCTGAATAAAGC |
| 1746 | Table 3A | Hs.80642 | L47345 | 992562 | signal transducer and activator of transcription 4 (STAT4), mRNA /cds=(81,2327) | 1 | TAGGAAATGTTTGACATCTGAAGCTC TCTTCACACTCCCGTGGCACTCCT |
| 1747 | Table 3A | Hs.75678 | L49169 | 1082037 | FBJ murine osteosarcoma viral oncogene homolog B | 1 | CGTCCCCTCTCCCCCTGGTTCTGCAC TGTTGCCAATAAAAAGCTCTTAAA |
| 1748 | Table 3A | Hs.80642 | M11353 | 184092 | signal transducer and activator of transcription 4 (STAT4), mRNA /cds=(81,2327) | 1 | GGGAGTGTGTGACTGAAATGCTTGA AACCAAAGCTTCAGATAAACTTGC |
| 1749 | Table 3A | Hs.181307 | M10901 | 183032 | H3 histone, family 3A (H3F3A), mRNA /cds=(374,784) | 1 | AGGGGACAGAAATCAGGTATTGGCA GTTTTCCATTTTCATTGTGTGTG |
| 1750 | Table 3A | Hs.198253 | M11124 | 188109 | major histocompatibility complex, class II, DQ alpha 1 (HLA-DQA1), mRNA /cds=(43,810) | 1 | AGCCGCCAGCTACCTAATTCCTCAG TAACATCGATCTAAAATCTCCATG |
| 1751 | Table 3A | Hs.181307 | M12679 | 187911 | H3 histone, family 3A (H3F3A), mRNA /cds=(374,784) | 1 | ACATGCAAGTACATGTTTTAATGTTG TCTGTCTTCTGTGCTGTCTCTGT |
| 1752 | Table 3A | Hs.277477 | M11717 | 184416 | major histocompatibility complex, class I, C (HLA-C), mRNA /cds=(0,1100) | 1 | CCTGTGTGGGACTGAGATGCAGGAT TTCTTCACACCTCTCCTTTGTGACT |
| 1753 | Table 3A | Hs.277477 | M12824 | 339426 | major histocompatibility complex, class I, C (HLA-C), mRNA /cds=(0,1100) | 1 | GGCATCTGAATGTGTCTGCGTTCCTG TTAGCATAATGTGAGGAGGTGGAG |
| 1754 | Table 3A | Hs.85258 | M14328 | 182113 | CD8 antigen, alpha polypeptide (p32) (CD8A), mRNA /cds=(65,772) | 1 | CTGAGAGCCCAAACCTGCTGTCCCAAA CATGCACCTCCTTGCTTAAGGTAT |
| 1755 | Table 3A | Hs.254105 | M12824 | 339426 | enolase 1, (alpha) (ENO1), mRNA /cds=(94,1398) | 1 | AAGCTCCCTGGAGCCCTGTTGGCAG CTCTAGCTTTTGCAGTCGTGAATG |
| 1756 | Table 3A | Hs.122007 | M12888 | 338836 | qn52b08.x1 cDNA, 3' end /clone=IMAGE:1901847 /clone_end=3' | 1 | AGCCCTCTTTCTCTCCACCCTGCT GCTTTCTCCTGTTTCATCCTGATGG |
| 1757 | Table 3A | Hs.82085 | M14083 | 189566 | serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 (SERPINE1), mRNA /cds=(75,1283) | 1 | TCCACAGGGGTGGTGTCAAATGCTAT TGAAATGTGTTGAATGTATGCT |
| 1758 | Table 3A | Hs.254105 | M15182 | 183232 | enolase 1, (alpha) (ENO1), mRNA /cds=(94,1398) | 1 | GCTAGATCCCCGGTGGTTTTGTGCTC AAAATAAAAGCCTCAGTGACCCA |
| 1759 | Table 3A | Hs.183868 | M14648 | 340306 | glucuronidase, beta (GUSB), mRNA /cds=(26,1981) | 1 | GACTTCCACAGCAGCAGAACAAAGTG CCTCCTGGACTGTTACGGCAGACC |
| 1760 | Table 3A | Hs.1416 | M15059 | 182447 | Fc fragment of IgE, low affinity II, receptor for (CD23A) (FCER2), mRNA /cds=(213,1178) | 1 | TATCCCCAGCTCAGGTGGTGATCCT CCTGTCCAGCCTGCATCAATAAAA |
| 1761 | Table 3A | Hs.183868 | M15330 | 186283 | glucuronidase, beta (GUSB), mRNA /cds=(26,1981) | 1 | CTGGGTTTTGTGGTCATCTATTCTAG CAGGGAACACTAAAGGTGGAAATA |
| 1762 | Table 3A | Hs.126256 | M15353 | 306486 | interleukin 1, beta (IL1B), mRNA /cds=(86,895) | 1 | AGCTATGGAATCAATTCAATTTGGAC TGGTGTGCTCTCTTTAAATCAAGT |
| 1763 | Table 3A | Hs.79306 | M16342 | 184266 | eukaryotic translation initiation factor 4E (EIF4E), mRNA /cds=(18,671) | 1 | TGGCTCAAGTAGAAGGAGTCCCAT TCATATTAAGACAGGTACAAAAC |
| 1764 | Table 3A | Hs.182447 | M15796 | 181271 | heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC), transcript variant 1, mRNA /cds=(191,1102) | 1 | AGCTCTTTGAAGCAGCTTTGAGTTAG AAGTATGTGTGTACACCCTCACA |
| 1765 | Table 3A | Hs.80887 | M16038 | 187268 | v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), mRNA /cds=(297,1835) | 1 | AACCGGATATATACATAGCATGACAT TTCTTTGTGCTTTGGCTTACTTGT |
| 1766 | Table 3A | Hs.89476 | M16336 | 180093 | CD2 antigen (p50), sheep red blood cell receptor (CD2), mRNA /cds=(6,1061) | 1 | AGCCTATCTGCTTAAGAGACTCTGGA GTTTCTTATGTGCCCTGGTGGACA |
| 1767 | Table 3A | Hs.182447 | M16342 | 188352 | heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC), transcript variant 1, mRNA /cds=(191,1102) | 1 | AAAGTTGATACTGTGGGATTTTGTG AACAGCCTGATGTTTGGGACCTTT |

Table 8

| | | | | | | | |
|------|------------|-----------|--------|--------|---|---|--|
| 1768 | Table 3A | Hs.318720 | M16660 | 184420 | Homo sapiens, clone MGC:12387 IMAGE:3933019, mRNA, complete cds /cds=(63,863) | 1 | CTTCCTTAGCTCCTGTTCTTGGCCTG AAGCCTCACAGCTTTGATGGCAGT |
| 1769 | Table 3A | Hs.318720 | M16942 | 188352 | Homo sapiens, clone MGC:12387 IMAGE:3933019, mRNA, complete cds /cds=(63,863) | 1 | TTTGTGCTTCCCTTTACCTAAACTGTC CTGCCTCCCATGCATCTGTACCC |
| 1770 | Table 3A | Hs.318720 | M16942 | 188437 | Homo sapiens, clone MGC:12387 IMAGE:3933019, mRNA, complete cds /cds=(63,863) | 1 | TTTGTGCTTCCCTTTACCTAAACTGTC CTGCCTCCCATGCATCTGTACCC |
| 1771 | Table 3A | Hs.308026 | M16967 | 182411 | major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), mRNA /cds=(29,829) | 1 | CTTGTGGCTTCTCAGCTCCTGCCCT TGGCCTGAAGTCCCAGCATTGATG |
| 1772 | Table 3A | Hs.75709 | M16985 | 187282 | mannose-6-phosphate receptor (cation dependent) (M6PR), mRNA /cds=(170,1003) | 1 | ATTTGTTTGCATCCCTCCCCACACC CTGGTGTTTTAAATGAAGAAAAA |
| 1773 | Table 3A | Hs.21858 | M17783 | 183063 | trinucleotide repeat containing 3 (TNRC3), mRNA /cds=(517,1356) | 1 | CATCCGACATAATCCTACAGGTGCTG TGTTATTCATGGGGCAGATAAACA |
| 1774 | Table 3A | Hs.694 | M20137 | 186328 | interleukin 3 (colony-stimulating factor, multiple) (IL3), mRNA /cds=(9,467) | 1 | AGTGGGGTGGGGAGCATGTTCAATTT GTACCTCGAGTTTTAACTGGTTCC |
| 1775 | Table 3A | Hs.308026 | M20430 | 187182 | major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), mRNA /cds=(29,829) | 1 | CCTAAACCGTATGGCCTCCCGTGCAT CTGTATTACCCTGTATGACAAAC |
| 1776 | Table 3A | Hs.82848 | M20681 | 183684 | selectin L (lymphocyte adhesion molecule 1) (SELL), mRNA /cds=(88,1206) | 1 | TTTCATCTCAGGCCTCCCTCAACCCC ACCACTTCTTTATAACTAGTCCT |
| 1777 | Table 3A | Hs.237519 | M20867 | 183059 | yz35c09.s1 cDNA, 3' end /clone=IMAGE:285040 /clone_end=3' | 1 | GCATGGCTTAACCTGGTGATAAAAGC AGTTATTAAGTCTACGTTTTCC |
| 1778 | Table 3A | Hs.241392 | M21121 | 339420 | small inducible cytokine A5 (RANTES) (SCYA5), mRNA /cds=(26,301) | 1 | AGCTTCCGCCGTCTCAACCCCTCACA GGAGCTTACTGGCAAACATGAAAA |
| 1779 | literature | Hs.76422 | M22430 | 190888 | phospholipase A2, group IIA (platelets, synovial fluid) (PLA2G2A), nuclear gene encoding mitochondrial protein, mRNA /cds=(135,569) | 1 | TCTCCTCCACCTCAACTCCGTGCTTA ACCAAAGAAGCTGTACTCCGGGGG |
| 1780 | db mining | Hs.51299 | M22538 | 986883 | NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD) (NDUFV2), mRNA /cds=(18,767) | 1 | ACCCAAGGGACCTGGATTTGGTGTAC AAGCAGGCCTTTAATTATATTGA |
| 1781 | Table 3A | Hs.82848 | M25280 | 188555 | selectin L (lymphocyte adhesion molecule 1) (SELL), mRNA /cds=(88,1206) | 1 | AGCTCCTCTTCTGGCTTCTTACTGA AAGGTTACCCTGTAACATGCAATT |
| 1782 | Table 3A | Hs.73798 | M25393 | 190740 | macrophage migration inhibitory factor (glycosylation-inhibiting factor) (MIF), mRNA /cds=(97,444) | 1 | GTCTACATCAACTATTACGACATGAA CGCGGCCAATGTGGGCTGGAACAA |
| 1783 | Table 3A | Hs.73798 | M25639 | 188627 | macrophage migration inhibitory factor (glycosylation-inhibiting factor) (MIF), mRNA /cds=(97,444) | 1 | CCACCCCAACCTTCTGGTGGGGAGA AATAAACGGTTTAGAGACAGCTCTG |
| 1784 | db mining | Hs.624 | M26383 | 184641 | interleukin 8 (IL8), mRNA /cds=(74,373) | 1 | GCCAAGGGCCAAGAGAATATCCGAA CTTTAATTTGAGGAATTGAATGGGT |
| 1785 | Table 3A | Hs.303649 | M26683 | 186289 | small inducible cytokine A2 (monocyte chemotactic protein 1, homologous to mouse Sig-je) (SCYA2), mRNA /cds=(53,352) | 1 | GAAATTGCTTTTCTCTTGAACCACA GTTCTACCCCTGGGATGTTTTGAG |
| 1786 | Table 3A | Hs.82112 | M26880 | 340067 | interleukin 1 receptor, type I (IL1R1), mRNA /cds=(82,1791) | 1 | CCGGTTGTTAAACTGGTTTAGCACA ATTTATATTTCCCTCTCTTGCCT |
| 1787 | Table 3A | Hs.82112 | M27492 | 180035 | interleukin 1 receptor, type I (IL1R1), mRNA /cds=(82,1791) | 1 | ATTAAAGCACCAAAATTCATGTACAGC ATGCATCAGGATCAATAGACTGT |
| 1788 | Table 3A | Hs.1309 | M28170 | 862622 | thymocyte antigen CD1a mRNA, complete cds /cds=(533,1516) | 1 | TAGCCGTACTTTGCTAACTGTGCTCC TCACCTTCTCTTCTTCAATGCAGT |
| 1789 | Table 3A | Hs.78146 | M28526 | 189775 | platelet/endothelial cell adhesion molecule (CD31 antigen) (PECAM1), mRNA /cds=(141,2357) | 1 | AGGCTAAGCTGCCGGTTCTTAAATCC ATCCTGCTAAGTTAATGTTGGGTA |
| 1790 | Table 3A | Hs.1309 | M28825 | 186279 | thymocyte antigen CD1a mRNA, complete cds /cds=(533,1516) | 1 | AATATATGCATCCCTGGTGAAGGATC TTGCCTGCATGAAACATGTTCTCA |
| 1791 | Table 3A | Hs.1722 | M28983 | 186365 | interleukin 1, alpha (IL1A), mRNA /cds=(36,851) | 1 | ACCTGGGCATTCTTGTTTCATTCAATT CCACCTGCAATCAAGTCTACAA |
| 1792 | Table 3A | Hs.237868 | M29064 | 337452 | interleukin 7 receptor (IL7R), mRNA /cds=(22,1401) | 1 | CTCCCTCACAGCACAGAGAAGACAAA ATTAGCAAAACCCACTACACAGT |
| 1793 | Table 3A | Hs.237868 | M29696 | 180259 | interleukin 7 receptor (IL7R), mRNA /cds=(22,1401) | 1 | GTTTCAGTGGCAGTCAACATGAGTCAA GAGCATCTGCTTCTACCATGTGG |
| 1794 | Table 3A | Hs.89538 | M30142 | 181464 | cholesterol ester transfer protein, plasma (CETP), mRNA /cds=(130,1611) | 1 | CTTGAGCTAGAAGTCTCCAAGGAGGT CGGGATGGGGCTTGATGACAGAAGG |
| 1795 | Table 3A | Hs.89538 | M30185 | 179039 | cholesterol ester transfer protein, plasma (CETP), mRNA /cds=(130,1611) | 1 | CTCCCAACTCCTCCCTATCCTAAAGG CCCACTGGCATTAAAGTGCTGTAT |
| 1796 | db mining | Hs.270833 | M30704 | 339994 | amphiregulin (schwannoma-derived growth factor) (AREG), mRNA /cds=(209,967) | 1 | TCGGTCCTCTTCCAGTGGATCATAA GACAATGGACCCTTTTGTATGA |
| 1797 | Table 3A | Hs.29352 | M31165 | 184485 | tumor necrosis factor, alpha-induced protein 6 (TNFAIP6), mRNA /cds=(68,901) | 1 | AACACACAGTGTATGTTGGAATCT TTTGGAACCTCTTGAATCTCACTG |

Table 8

| | | | | | | | |
|------|-----------|-----------|-----------|---------|--|---|---|
| 1798 | Table 3A | Hs.149923 | M31210 | 181948 | X-box binding protein 1 (XBP1), mRNA /cds=(48,833) | 1 | GGGGCTCTTTCCCTCATGTACTTC AAGTAAGATCAAGAATCTTTTGTG |
| 1799 | Table 3A | Hs.1012 | M31452 | 190501 | complement component 4-binding protein, alpha (C4BPA), mRNA /cds=(138,1931) | 1 | TCATCCTCTGTGTGGCTCATGTTTTT GCTTTTCAACACACAAAGCACAAA |
| 1800 | Table 3A | Hs.101047 | M31523 | 339477 | transcription factor (E2A) mRNA, complete cds /cds=(30,1994) | 1 | TGGATGATTGGGACTTTAAACGACC CTCTTTCAGGTGGATTACAGAGACC |
| 1801 | db mining | Hs.149923 | M31627 | 182473 | X-box binding protein 1 (XBP1), mRNA /cds=(48,833) | 1 | TGTAGCTTCTGAAAGGTGCTTCTCC ATTTATTTAAAACTACCCATGCA |
| 1802 | Table 3A | Hs.78864 | M31932 | 188194 | Fc fragment of IgG, low affinity IIa, receptor for (CD32) (FCGR2A), mRNA /cds=(11,958) | 1 | TGTAGCAACATGAGAAACGCTTATGT TACAGGTTACATGAGAGCAATCAT |
| 1803 | Table 3A | Hs.73931 | M32011 | 189267 | major histocompatibility complex, class II, DQ beta 1 (HLA-DQB1), mRNA /cds=(57,842) | 1 | CTGATGGCTGTGACCCTGCTTCTCTGC ACTGACCCAGAGCCTCTGCCTGTG |
| 1804 | Table 3A | Hs.256278 | M32315 | 189185 | tumor necrosis factor receptor superfamily, member 1B (TNFRSF1B), mRNA /cds=(89,1474) | 1 | TGTGTGTTGATCCCAAGACAATGAAA GTTTGCACGTATGCTGGACGGCA |
| 1805 | Table 3A | Hs.73931 | M32577 | 183628 | major histocompatibility complex, class II, DQ beta 1 (HLA-DQB1), mRNA /cds=(57,842) | 1 | CTCTCCTCAGACTGCTCAAGAGAAGC ACATGAAAACCATACCTGACTTT |
| 1806 | Table 3A | Hs.75765 | M33336 | 1526989 | GRO2 oncogene (GRO2), mRNA /cds=(74,397) | 1 | GCCAGTAAGATCAATGTGACGGCAG GGAAATGTATGTGTGCTATTTTGT |
| 1807 | Table 3A | Hs.198253 | M33906 | 184194 | major histocompatibility complex, class II, DQ alpha 1 (HLA-DQA1), mRNA /cds=(43,810) | 1 | GCAACAATGAAGTTAATGGATACCCT CTGCCTTTGGCTCAGAAATGTTAT |
| 1808 | Table 3A | Hs.87773 | M34181 | 189982 | protein kinase, cAMP-dependent, catalytic, beta (PRKACB), mRNA /cds=(47,1102) | 1 | TGTCTTTCGGTTATCAAGTGTCTCTG CATGGTAATGTATGTAATGCTG |
| 1809 | Table 3A | Hs.26045 | M34668 | 190738 | protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA /cds=(695,3103) | 1 | TATCATGGGGAGTAATAGGACCAGAG CGGTATCTCTGGCACCACACTAGC |
| 1810 | Table 3A | Hs.119663 | M34671 | 180152 | CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) (CD59), mRNA /cds=(29,415) | 1 | TGATCTTGGCTGTATTTAATGGCATA GGCTGACTTTTGAGATGGAGGAA |
| 1811 | Table 3A | Hs.250811 | M35416 | 190851 | v-rat simian leukemia viral oncogene homolog B (ras related; GTP binding protein) (RALB), mRNA /cds=(170,790) | 1 | AGTACTGAGAAAAATCCCTTCAGCTC TAAGAACACTGAAAAATCCACCGA |
| 1812 | Table 3A | Hs.87149 | M35999 | 183532 | integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) (ITGB3), mRNA /cds=(16,2382) | 1 | ACTTTGCACACATTTGCATCCACATAT TAGGGAAGGAATAAGTAGCTGCA |
| 1813 | Table 3A | Hs.75765 | M36820 | 183628 | GRO2 oncogene (GRO2), mRNA /cds=(74,397) | 1 | ATGCAGTGTTCCTCTGTGTTAGAG CAGAGAGGTTTCGATATTTATTGA |
| 1814 | Table 3A | Hs.89690 | M36821 | 183632 | GRO3 oncogene (GRO3), mRNA /cds=(77,397) | 1 | TGCTGAAGTTTCCCTTAGACATTTTAT GTCTTGCTTGTAGGGCATAATGC |
| 1815 | Table 3A | Hs.82212 | M37033 | 184059 | CD53 antigen (CD53), mRNA /cds=(93,752) | 1 | CACTGGACCATTGTCAACCCCTCTG TTTCTCTTTGACTAAGTGCCCTGG |
| 1816 | Table 3A | Hs.119192 | M37583 | 179968 | H2A histone family, member Z (H2AFZ), mRNA /cds=(106,492) | 1 | AAGTGTTACTGTGGCTTCAAAGAAGC TATTGATTCTGAAGTAGTGGGTTT |
| 1817 | Table 3A | Hs.173894 | NM_000757 | 4503074 | macrophage-specific colony-stimulating factor (CSF-1) mRNA, complete cds /cds=(105,1769) | 1 | GCTGCTTATATTTAATAATAAAAGA AGTGCAACAAGCTGCCGTTGACGT |
| 1818 | Table 3A | Hs.119192 | M37583 | 189988 | H2A histone family, member Z (H2AFZ), mRNA /cds=(106,492) | 1 | AACAAACATTTGGTTTTTGTACAGCT TATTTCCACTCTGGTGATAAGT |
| 1819 | Table 3A | Hs.315366 | M55284 | 189988 | protein kinase C, eta (PRKCH), mRNA /cds=(166,2214) | 1 | GAGAGAGGGCAGAGAACCCAAAGG AATAGAGATTCTCCAGGAATTTCTCT |
| 1820 | Table 3A | Hs.315366 | M55284 | 189988 | protein kinase C, eta (PRKCH), mRNA /cds=(166,2214) | 1 | TTCCAGCATCAGCCTTAGAACAGA ACCTTACCTTCAAGGAGCAAGTGA |
| 1821 | Table 3A | Hs.171862 | M55543 | 829176 | guanylate binding protein 2, interferon-inducible (GBP2), mRNA /cds=(156,1931) | 1 | CTGTCCAGCTCCCTCTCCCCAAGAAA CAACATGAATGAGCAACTTCAGAG |
| 1822 | Table 3A | Hs.2055 | M58028 | 340071 | ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing) (UBE1), mRNA /cds=(32,3208) | 1 | CTGTAACGACGAGAGCGGCGAGGAT GTCGAGGTTCCCTATGTCCGATACA |
| 1823 | Table 3A | NA | M55674 | 189870 | one single clone, artifact ? | 1 | ACCTAGTCATCAGGACACTGAGCCAG GGCTGCAACCACTCCATGAGTTTG |
| 1824 | Table 3A | Hs.72918 | M57506 | 184505 | small inducible cytokine A1 (I-309, homologous to mouse Tca-3) (SCYA1), mRNA /cds=(72,362) | 1 | CCCCAACCTCTGGGCTCTGGATT CAGAGTGAAACTTGATGGCATTG |
| 1825 | Table 3A | Hs.193717 | M57627 | 186270 | interleukin 10 (IL10), mRNA /cds=(30,566) | 1 | TCAATTCTCTGGGAATGTTACATTG TTTGTCTGTCTTCATAGCAGATT |
| 1826 | Table 3A | Hs.1051 | M57888 | 183154 | granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), mRNA /cds=(33,776) | 1 | ACCAGTTTCTTCCCTTCTAGATCAC CCTGTTCTGAAGCCAGCCTCTCTC |
| 1827 | Table 3A | Hs.2055 | M58028 | 189177 | ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing) (UBE1), mRNA /cds=(32,3208) | 1 | CTACCTGAACCCCTCTTGCCACTGCC TTCTACCTGTTTGAAACCTGAAT |

Table 8

| | | | | | | | |
|------|----------|-----------|--------|---------|--|---|--|
| 1828 | Table 3A | Hs.83428 | M58597 | 182070 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) (NFKB1), mRNA /cds=(397,3303) | 1 | AACTCGAGACCTTTTCAACTTGGCTT CCTTCTTGGTTCATAAATGAATT |
| 1829 | Table 3A | Hs.83428 | M58603 | 186496 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) (NFKB1), mRNA /cds=(397,3303) | 1 | AGCTGCTGCTGGATCACAGCTGCTTT CTGTTGTCAATTGCTGTTGCCCTC |
| 1830 | Table 3A | Hs.265829 | M59465 | 177865 | integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), transcript variant a, mRNA /cds=(73,3228) | 1 | GGCTGTGTCCTAAGGCCCAATTGAGA AGCTGAGGCTAGTTCAAAAACCT |
| 1831 | Table 3A | Hs.2175 | M59820 | 183048 | colony stimulating factor 3 receptor (granulocyte) (CSF3R), mRNA /cds=(169,2679) | 1 | ATCCAGCCCCACCCAATGGCCTTTTG TGCTTGTTCCTATAACTTCAGTA |
| 1832 | Table 3A | Hs.265829 | M60278 | 183866 | integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), transcript variant a, mRNA /cds=(73,3228) | 1 | CCTTCTTTGTATATAGGCTTCTCACC GCGACCAATAAACAGCTCCAGTT |
| 1833 | Table 3A | Hs.799 | M60724 | 189507 | diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) (DTR), mRNA /cds=(261,887) | 1 | AAAACGATGAAGGTATGCTGTCATGG TCCTTCTGGAAGTTTCTGGTGCC |
| 1834 | Table 3A | Hs.86858 | M60626 | 182662 | ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1), mRNA /cds=(27,1604) | 1 | AATGCGAAATTATTGGTTGGTGTGAA GAAAGCCAGACAACCTCTGTTTCT |
| 1835 | Table 3A | Hs.86858 | M61906 | 189424 | ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1), mRNA /cds=(27,1604) | 1 | CTGTGGCTCGTTTGAGGGATTGGGG TGGACCTGGGGTTATTTTCAGTAA |
| 1836 | Table 3A | Hs.6241 | M61199 | 181122 | P13-kinase associated p85 mRNA sequence /cds=UNKNOWN | 1 | GCTTCCCCACCCCAGTTTTTGTGCT TGAATAATTTGTTGTCCTCGGATTT |
| 1837 | Table 3A | Hs.6241 | M61906 | 190734 | P13-kinase associated p85 mRNA sequence /cds=UNKNOWN | 1 | TGGACTGTTTTGTTGGGCAGTGCCCTG ATAAGCTTCAAGGCTGCTTTATTC |
| 1838 | Table 3A | Hs.50651 | M63180 | 339679 | Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA /cds=(75,3503) | 1 | CCTGCCGTGCCACCTAACTGCCA GATGAGGTTTATCAGCTTATGAGAA |
| 1839 | Table 3A | Hs.84318 | M63488 | 337488 | replication protein A1 (70kD) (RPA1), mRNA /cds=(69,1919) | 1 | CGAGCTGAGAAGCGGTCATGAGCAC CTGGGGATTTTAGTAAGTGTCTT |
| 1840 | Table 3A | Hs.50651 | M64174 | 190446 | Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA /cds=(75,3503) | 1 | ACCATCCAATCGGACAAGCTTTCAGA ACCTTATTGAAGGATTTGAAGCAC |
| 1841 | Table 3A | Hs.82159 | M64992 | 178996 | proteasome (prosome, macropain) subunit, alpha type, 1 (PSMA1), mRNA /cds=(105,896) | 1 | TGCTGATGAACCTGCAGAAAAGGCTG ATGAACCAATGGAACATTAAGTGA |
| 1842 | Table 3A | Hs.11482 | M69043 | 187290 | splicing factor, arginine/serine-rich 11 (SFRS11), mRNA /cds=(83,1537) | 1 | TCTTATGCACACGGTGATTTTCATGTT ATATATGCAAAGTAGGCAACTGTT |
| 1843 | Table 3A | Hs.155160 | M72709 | 179073 | Homo sapiens, Similar to splicing factor, arginine/serine-rich 2 (SC-35), clone MGC:2622 IMAGE:3501687, mRNA, complete cds /cds=(30,878) | 1 | AACATAGGAGTGGATTCTGCCCCAA CCAAACCGCATTCTGTGGATTTT |
| 1844 | Table 3A | Hs.1117 | M73047 | 339879 | tripeptidyl peptidase II (TPP2), mRNA /cds=(23,3772) | 1 | AATAAATTTGCAAAACCAAGATCACA GTACACCATATGCACCTCTGGTACC |
| 1845 | Table 3A | Hs.178112 | M73547 | 190161 | polyposis locus (DP1 gene) mRNA, complete cds /cds=(82,639) | 1 | AAATGACCTCATGTTGTGGTTTAAAC AGCAACTGCACCCACTAGCACAGC |
| 1846 | Table 3A | Hs.11482 | M74002 | 184045 | splicing factor, arginine/serine-rich 11 (SFRS11), mRNA /cds=(83,1537) | 1 | TGTGCAGTAGAAACAAAAGTAGGCTA CAGCTGTGGCATGTTGATGTACA |
| 1847 | Table 3A | Hs.811 | M74525 | 189511 | ubiquitin-conjugating enzyme E2B (RAD6 homolog) (UBE2B), mRNA /cds=(421,879) | 1 | CTGTTTATTCTGGGAAATGTTTAAATG CCAGGGCCTGCTGAGTTGCTTCT |
| 1848 | Table 3A | Hs.172766 | M80359 | 182353 | MAP/microtubule affinity-regulating kinase 3 (MARK3), mRNA /cds=(171,2312) | 1 | CCTTAAGACCAGTTCATAGTTAATAC AGGTTTACAGTTCATGCCTGTGGT |
| 1849 | Table 3A | Hs.153179 | M81601 | 339442 | fatty acid binding protein 5 (psoriasis-associated) (FABP5), mRNA /cds=(48,455) | 1 | TCATCACTTTGGACAGGAGTTAATTA AGAGAATGACCAAGCTCAGTTCAA |
| 1850 | Table 3A | Hs.119537 | M88108 | 189499 | GAP-associated tyrosine phosphoprotein p62 (Sam68) (SAM68), mRNA /cds=(106,1437) | 1 | AGTCTGCCTAAATAGGTAGCTTAAAC TTATGTCAAATGTCTGCAGCAGT |
| 1851 | Table 3A | Hs.89575 | M89957 | 179311 | CD79B antigen (immunoglobulin-associated beta) (CD79B), transcript variant 1, mRNA /cds=(94,783) | 1 | CTGGCCTCCAGTGCCTTCCCCCGTG GAATAACGGTGTGCTCGAGAAAC |
| 1852 | Table 3A | Hs.181967 | M90356 | 179575 | BTF3 protein homologue gene, complete cds | 1 | AGCTAATTAAGCTGCAGAACGTGGGA AATAAAGTTGCAAAACAAAGTTAA |
| 1853 | Table 3A | Hs.82127 | M90391 | 4153827 | putative IL-16 protein precursor, mRNA, complete cds /cds=(303,2198) | 1 | GGACAGGTGTGCCGACAGAAAGGAAC CAGCGTGTATATGAGGGTATCAAA |
| 1854 | Table 3A | Hs.73722 | M92444 | 183779 | apurinic/apyrimidinic endonuclease (HAP1) gene, complete cds | 1 | CCCTTCGTGGGGCTACACATTCTCTT CCTCATATTTTCATGCACACAAGT |
| 1855 | Table 3A | Hs.145279 | M93651 | 338038 | SET translocation (myeloid leukemia-associated) (SET), mRNA /cds=(3,836) | 1 | TTCTGCACAGGTCTCTGTTTAGTAAA TACATCACTGTATACCGATCAGGA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|--|
| 1856 | Table 3A | Hs.7647 | M94046 | 187393 | MYC-associated zinc finger protein (purine-binding transcription factor) (MAZ), mRNA /cds=(91,1584) | 1 | CACCCCTCCACCCCTTCCTTTTGC GCGGACCCCATTAACAATAATTTTAA |
| 1857 | Table 3A | Hs.153179 | M95585 | 184223 | fatty acid binding protein 5 (psoriasis-associated) (FABP5), mRNA /cds=(48,455) | 1 | CATGCAGCTATTTCAAAGTGTGTTGGATTAATTAGGATCATCCCTTTGGT |
| 1858 | Table 3A | Hs.250692 | M95585 | 337810 | hepatic leukemia factor (HLF) mRNA, complete cds /cds=(322,1209) | 1 | TGGAGAATTGTGGAAGGATTGTAACA TGGACCATCCAAATTTATGGCCGT |
| 1859 | Table 3A | Hs.74592 | M96982 | 338262 | special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's) (SATB1), mRNA /cds=(214,2505) | 1 | TTCACGGGATGCACCAAAGTGTGTAC CCCGTAAGCATGAAACCAGTGTTT |
| 1860 | Table 3A | Hs.296381 | M96995 | 181975 | growth factor receptor-bound protein 2 (GRB2), mRNA /cds=(78,731) | 1 | TCTGTCCATCAGTGCATGACGTTTAA GGCCACGTATAGTCCTAGCTGACG |
| 1861 | Table 3A | Hs.74592 | M97856 | 184432 | special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's) (SATB1), mRNA /cds=(214,2505) | 1 | TCCTATAATTATTTCTGTAGCACTCCA CACTGATCTTTGGAACCTTGCCC |
| 1862 | Table 3A | Hs.243886 | M97935 | 2281070 | nuclear autoantigenic sperm protein (histone-binding) (NASP), mRNA /cds=(85,2448) | 1 | GGGACACTGGAGGCTGGAGCTACAG TTGAAAGCACTGCATGTTAAGAGGG |
| 1863 | Table 3A | Hs.21486 | M98399 | 180112 | signal transducer and activator of transcription 1, 91kD (STAT1), mRNA /cds=(196,2448) | 1 | TGCTACCACAACATATATTATCATGCAA ATGCTGTATTCTTCTTTGGTGGA |
| 1864 | Table 3A | Hs.75613 | N27575 | 1142056 | CD36 antigen (collagen type I receptor, thrombospondin receptor) (CD36), mRNA /cds=(132,1550) | 1 | GCAACTTACGCTTGGCATCTTCAGAA TGCTTTCTAGCATTAAAGAGATGT |
| 1865 | Table 3A | Hs.198427 | N25486 | 1139799 | hexokinase 2 (HK2), mRNA /cds=(1490,4243) | 1 | TTTACAAGAAATGTCCATGTGCTTCC CTAGGCTGAGCTGGCATTGGTCTG |
| 1866 | Table 3A | Hs.198427 | N99577 | 1271009 | hexokinase 2 (HK2), mRNA /cds=(1490,4243) | 1 | AAACTTCCCACCCCTACTTTTCCAAG AGTGGCCTGTGATTCTGAAATCTG |
| 1867 | Table 3A | Hs.73965 | N28843 | 1147079 | splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(155,820) | 1 | TAGACCAATTCTCTGATCTCGAGTTG TTTTGTGTTGGATACAGCCCTTTT |
| 1868 | Table 3A | Hs.5122 | N31700 | 1152099 | 602293015F1 cDNA, 5' end /clone=IMAGE:4387778 /clone_end=5' | 1 | AACATTCTACATAGCACAGGAGCTTA AGAGTGGCATTATCTTCTCGCCTT |
| 1869 | Table 3A | Hs.66151 | N3426 | 1155403 | mRNA; cDNA DKFZp434A115 (from clone DKFZp434A115) /cds=UNKNOWN | 1 | AGATACGCAGACATTGTGGCATCTGG GTAGAAGAATACTGTATTGTGTGT |
| 1870 | Table 3A | Hs.73965 | Z22642 | 296907 | splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(155,820) | 1 | TTTGACCAGAAGCCCTTAGTAAGTAC GTGCCGTGAACTGAAACCATGTGC |
| 1871 | Table 3A | Hs.166563 | L14922 | 307337 | DNA-binding protein (PO-GA) mRNA, complete cds /cds=(393,3836) | 1 | ACACCTGGCTTGGAGTCAGATTTAGT TAACAATAATGAGCCTGGAGCAGT |
| 1872 | literature | Hs.75772 | M10901 | 183032 | nuclear receptor subfamily 3, group C, member 1 (NR3C1), mRNA /cds=(132,2465) | 1 | TCTAATAGCGGGTTACTTTCACATAC AGCCCTCCCCAGCAGTTGAATGA |
| 1873 | literature | Hs.74561 | NM_000014 | 6226959 | alpha-2-macroglobulin (A2M), mRNA /cds=(43,4467) | 1 | CTGAAAAGTGCTTTGCTGGAGTCCTG TTCTCTGAGCTCCACAGAAGACAC |
| 1874 | db mining | Hs.172670 | NM_000020 | 4557242 | activin A receptor type II-like 1 (ACVRL1), mRNA /cds=(282,1793) | 1 | AAGCCTAAAGTGATTCAATAGCCAG GAGCACCTGATTCCTTTCTGCCTG |
| 1875 | Table 3A | Hs.1217 | NM_000022 | 4557248 | adenosine deaminase (ADA), mRNA /cds=(95,1186) | 1 | TGGGCATGGTTGAATCTGAAACCCCTC CTCTGTGGCACTTGTACTGAAA |
| 1876 | Table 3A | Hs.99931 | NM_000023 | 4506910 | sarcoglycan, alpha (50kD dystrophin-associated glycoprotein) (SGCA), mRNA /cds=(11,1174) | 1 | GGGGTGGGTGGGGTGAGAGTGTGT GGAGTAAGGACATTCAGAATAAATA |
| 1877 | literature | Hs.207776 | NM_000027 | 4557272 | aspartylglucosaminidase (AGA), mRNA /cds=(170,1210) | 1 | AGAAGTTGTGCGCGTGCTTTCTCAGC AGCATTTTTCTTCAAATCATCT |
| 1878 | Table 3A | Hs.159546 | NM_000033 | 7262392 | ATP-binding cassette, sub-family D (ALD), member 1 (ABCD1), mRNA /cds=(386,2623) | 1 | CTTGCCAGCCAGGAGTGCGGACACC ATGTTCCCAGCTCAGTGCCAAAGAG |
| 1879 | Table 3A | Hs.75081 | NM_000038 | 4557318 | adenomatosis polyposis coli (APC), mRNA /cds=(38,8569) | 1 | ATTTGGGGAGAGAAAACCTTTTAAAG CATGGTGGGGCACTCAGATAGGAG |
| 1880 | literature | Hs.36820 | NM_000057 | 4557364 | Bloom syndrome (BLM), mRNA /cds=(74,4327) | 1 | ACCCTCTTTCTGTTTGTGTCAGCATCT GACCATCTGTGACTATAAAGCTGT |
| 1881 | literature | Hs.34012 | NM_000059 | 4502450 | breast cancer 2, early onset (BRCA2), mRNA /cds=(228,10484) | 1 | TGGTCATCCAAACTCAAACCTTGAGAA AATATCTTGCTTTCAAATTGACAC |
| 1882 | Table 3A | Hs.159494 | NM_000061 | 4557376 | Bruton agammaglobulinemia tyrosine kinase (BTK), mRNA /cds=(163,2142) | 1 | ACCGAATTTGGCAAGATGAAATGGT GTCATAAAGATGGGAGGGGAGGGT |
| 1883 | Table 3A | Hs.1282 | NM_000065 | 4559405 | complement component 6 (C6), mRNA /cds=(155,2959) | 1 | AGCCTGTGACATTAAAGCATTCTCACA ATTAGAAATAAGAAATAAACCCAT |
| 1884 | Table 3A | Hs.2259 | NM_000073 | 4557428 | CD3G antigen, gamma polypeptide (TIT3 complex) (CD3G), mRNA /cds=(37,585) | 1 | AAAAAATAAAAAATAACTGTGTTTCA GAAGCGCCACCTATTGGGAAAAA |
| 1885 | Table 3A | Hs.36508 | NM_000081 | 4502838 | Chediak-Higashi syndrome 1 (CHS1), mRNA /cds=(189,11594) | 1 | TTATCACAAGCTCTGTTACCTTTATAT ACGCTGCCTCTTCAATTTGGAAA |
| 1886 | literature | Hs.32967 | NM_000082 | 4557466 | Cockayne syndrome 1 (classical) (CKN1), mRNA /cds=(36,1226) | 1 | GCAGAAAAATCCTGGCAGGGAATCT GGCTTAAACATGAAATGCTGTAAT |
| 1887 | Table 3A | Hs.154654 | NM_000104 | 13325059 | cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1), mRNA /cds=(372,2003) | 1 | TGTGTGCATAATAGCTACAGTGCATA GTTGTAGACAAAGTACATTCTGGG |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|---|
| 1888 | literature | Hs.77602 | NM_000107 | 4557514 | damage-specific DNA binding protein 2 (49kD) (DDB2), mRNA /cds=(175,1458) | 1 | TCTCAGTGGGTGGTAGCAGAGGGAT CAAGCAGTTATTGTGTTGTGCTCT |
| 1889 | Table 3A | Hs.74635 | NM_000108 | 5016092 | dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD), mRNA /cds=(82,1611) | 1 | GTCTATTTACGGAACCTCAAATACGTG GGCATTCAAATGTATTACAGTGGG |
| 1890 | Table 3A | Hs.1602 | NM_000110 | 4557874 | dihydropyrimidine dehydrogenase (DPYD), mRNA /cds=(101,3178) | 1 | TGCACTTTTAGAAATGCATATTTGCCA AAAAACCTGTATTACTGAATAAT |
| 1891 | Table 3A | Hs.2985 | NM_000117 | 4557552 | emerin (Emery-Dreifuss muscular dystrophy) (EMD), mRNA /cds=(58,822) | 1 | GGGAGGGGATTAAACCAAGGCCACC CTGACTTTGTGTTTGTGGACACACA |
| 1892 | Table 3A | Hs.76753 | NM_000118 | 4557554 | endoglin (Osler-Rendu-Weber syndrome 1) (ENG), mRNA /cds=(350,2227) | 1 | GCCTGCCCTGTGTATTCACCACCAA TAAATCAGACCATGAACCTGAAA |
| 1893 | Table 3A | Hs.77929 | NM_000122 | 4557562 | excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing) (ERCC3), mRNA /cds=(95,2443) | 1 | AGGTGTATTTATGTTACCGTTCTGAAT AAACAGAATGGACATTGAACCA |
| 1894 | literature | Hs.48576 | NM_000123 | 4503600 | excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome)) (ERCC5), mRNA /cds=(197,3757) | 1 | TGTAATGAATTTGTCGCAAAGACGTA ATAAAATTAAGTGGTGGCAGCGTC |
| 1895 | literature | Hs.99924 | NM_000124 | 4557564 | excision repair cross-complementing rodent repair deficiency, complementation group 6 (ERCC6), mRNA /cds=(79,4580) | 1 | TGTCATGGAAGTTGGCTGCACTTGA TGTTTGTGTCATGATGTCTACCT |
| 1896 | db mining | Hs.1657 | NM_000125 | 4503602 | estrogen receptor 1 (ESR1), mRNA /cds=(360,2147) | 1 | TCGAGCACCTGTAACAATTTTCTCA ACCTATTTGATGTTCAAATAAAGA |
| 1897 | Table 3A | Hs.80424 | NM_000129 | 9961355 | coagulation factor XIII, A1 polypeptide (F13A1), mRNA /cds=(101,2299) | 1 | AACTTTACTAAGTAATCTCACAGCATT TGCCAAGTCTCCCAATATCCAAT |
| 1898 | literature | Hs.284153 | NM_000135 | 4503654 | Fanconi anemia, complementation group A (FANCA), mRNA /cds=(31,4398) | 1 | TAAGATCTTTAAACTGCTTTATACACT GTCACGTGGCTTCATCAGCTGTG |
| 1899 | literature | Hs.37953 | NM_000136 | 4557588 | Fanconi anemia, complementation group C (FANCC), mRNA /cds=(255,1928) | 1 | AAAACCACTACCTCAGAGAGAGCCA AAAATACAGAAGAGGCGGAGAGCG |
| 1900 | Table 3A | Hs.1437 | NM_000152 | 11496988 | glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II) (GAA), mRNA /cds=(441,3299) | 1 | CGAGCAAGCCTGGGAAGCTCAGGAAA ATTCACAGGACTTGGGAGATTCTAA |
| 1901 | Table 3A | Hs.273 | NM_000153 | 4557612 | galactosylceramidase (Krabbe disease) (GALC), mRNA /cds=(263,2272) | 1 | GGCTTAGCTACAGTGAAGTTTGCAT TGCTTTTGAAGACAAGAAAAGTGC |
| 1902 | Table 3A | Hs.86724 | NM_000161 | 4503948 | GTP cyclohydrolase 1 (dopa-responsive dystonia) (GCH1), mRNA /cds=(148,900) | 1 | ACTTCAAAATTACCTTTTCATATCCAT GATCTTGAGTCCATTTGGGGGAT |
| 1903 | Table 3A | Hs.1466 | NM_000167 | 4504006 | glycerol kinase (GK), mRNA /cds=(66,1640) | 1 | CAAACACTTTTGGGCCAGGATTTGAG TCTCTGCATGACATATACTTGATT |
| 1904 | Table 3A | Hs.1144 | NM_000174 | 4504076 | glycoprotein IX (platelet) (GP9), mRNA /cds=(222,755) | 1 | CAGACTCCACCAAGCCTGGTCAGCC CAAACCAACAGAGCCAGAAATAAA |
| 1905 | Table 3A | Hs.75772 | NM_000176 | 4504132 | nuclear receptor subfamily 3, group C, member 1 (NR3C1), mRNA /cds=(132,2465) | 1 | AGTGCAGAATCTCATAGTTGCCAAT AATACACTAATCTCTTCTATCCT |
| 1906 | literature | Hs.3248 | NM_000179 | 4504190 | mutS (E. coli) homolog 6 (MSH6), mRNA /cds=(87,4169) | 1 | AGACTGACTACATTGGAAGCTTTGAG TTGACTTCTGACCAAGGTGGTAA |
| 1907 | Table 3A | Hs.183868 | NM_000181 | 4504222 | glucuronidase, beta (GUSB), mRNA /cds=(26,1981) | 1 | CTGGGTTTGTGGTCATCTATTCTAG CAGGGAACACTAAAGGTGAAATA |
| 1908 | literature | Hs.75860 | NM_000182 | 4504324 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit (HADHA), mRNA /cds=(27,2318) | 1 | GTGGTGAGGGCAGTTCTGCACCCAG CCAAACACATAACAATAAAAACCAA |
| 1909 | Table 3A | Hs.146812 | NM_000183 | 4504326 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB), mRNA /cds=(46,1470) | 1 | TCTGTGTCCTAAAGATGTGTTCTCTAT AAAATACAAACCAACGTGCCTAA |
| 1910 | Table 3A | Hs.198427 | NM_000189 | 4504392 | hexokinase 2 (HK2), mRNA /cds=(1490,4243) | 1 | CTAGTCATAGAAATACCTCATTCGCC TGTGGGAAGAGAAGGGAAGCCTCT |
| 1911 | Table 3A | Hs.83951 | NM_000195 | 4504484 | Hermansky-Pudlak syndrome (HPS), mRNA /cds=(206,2308) | 1 | AGCAGCGGCTGGATGTGATATGTCTA GTTTAAACAGTCCCTTGATCTTT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|---|
| 1912 | Table 3A | Hs.168383 | NM_000201 | 4557877 | intercellular adhesion molecule 1 (CD54), rhinovirus receptor (ICAM1), mRNA /cds=(57,1655) | 1 | TATTGGAGGACTCCCTCCCAGCTTTG GAAGGTCATCCGCGTGTGTGTGT |
| 1913 | Table 3A | Hs.172458 | NM_000202 | 5360215 | iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA /cds=(331,1983) | 1 | ATACAAAGCAAACAACTCAAGTTAT GTCATACCTTTGGATACGAAGACC |
| 1914 | Table 3A | Hs.238893 | NM_000206 | 4557881 | od15g01.s1 cDNA /clone=IMAGE:1368048 | 1 | ATCTACCTCCGATTGTTCTCTGAACC GATGAGAAATAAAGTTTCTGTGTA |
| 1915 | Table 3A | Hs.83968 | NM_000211 | 4557885 | integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2), mRNA /cds=(72,2381) | 1 | CATGGAGACTTGAGGAGGGCTTGAG GTTGGTGAGGTTAGGTGCGTGTTTC |
| 1916 | literature | Hs.99877 | NM_000215 | 4557680 | Janus kinase 3 (a protein tyrosine kinase, leukocyte) (JAK3), mRNA /cds=(95,3469) | 1 | GCCCCAAGAAGCAAGGAACCAATTT AAGACTCTCGCATCTTCCCAACCC |
| 1917 | literature | Hs.1770 | NM_000234 | 4557718 | ligase I, DNA, ATP-dependent (LIG1), mRNA /cds=(120,2879) | 1 | CCGGAGTCTGGGATTTCATCCCGTCAT TTCTTTCAATAAATAATTATTGGA |
| 1918 | db mining | Hs.3076 | NM_000246 | 4557748 | MHC class II transactivator (MHC2TA), mRNA /cds=(138,3530) | 1 | GCAATGGCAGCCTTGGCAAACGCTA AATGAAAACTCGTGACAACACTTGTG |
| 1919 | literature | Hs.57301 | NM_000249 | 4557756 | mutL (E. coli) homolog 1 (colon cancer, nonpolyposis type 2) (MLH1), mRNA /cds=(21,2291) | 1 | AGTGTGGTAGCACTTAAGACTTATA CTTGCCTTCTGATAGTATTCCTTT |
| 1920 | literature | Hs.78934 | NM_000251 | 4557760 | mutS (E. coli) homolog 2 (colon cancer, nonpolyposis type 1) (MSH2), mRNA /cds=(68,2872) | 1 | AACTGAGGACTGTTTGCAATTGACAT AGGCAATAATAAGTGATGTGCTGA |
| 1921 | Table 3A | Hs.75514 | NM_000270 | 4557800 | nucleoside phosphorylase (NP), mRNA /cds=(109,978) | 1 | GGGCTCAGTTCTGCCTTATCTAAATC ACCAGAGACCAAACAGGACTAAT |
| 1922 | Table 3A | Hs.76918 | NM_000271 | 4557802 | Niemann-Pick disease, type C1 (NPC1), mRNA /cds=(123,3959) | 1 | GGCATGAAATGAGGGACAAAGAAAG CATCTCGTAGGTGTGTCTACTGGGT |
| 1923 | Table 3A | Hs.1023 | NM_000284 | 4505684 | pyruvate dehydrogenase (lipoamide) alpha 1 (PDHA1), mRNA /cds=(105,1277) | 1 | TCTTGGAACTTCCATTAAAGTGTGA GATTAGACAGGTGATTAATGTCATG |
| 1924 | Table 3A | Hs.78771 | NM_000291 | 4505762 | phosphoglycerate kinase 1 (PGK1), mRNA /cds=(79,1332) | 1 | ACTACTCAGCATGGAAACAAGATGAA ATTCCATTGTAGGTAGTGAGACA |
| 1925 | Table 3A | Hs.196177 | NM_000294 | 4505784 | phosphorylase kinase, gamma 2 (testis) (PHKG2), mRNA /cds=(93,1313) | 1 | CACATATGATCCTGCTACCCTCTTGA AGACCAGCCCGTACCTCTCTCCC |
| 1926 | Table 3A | Hs.169857 | NM_000305 | 4505952 | paraoxonase 2 (PON2), mRNA /cds=(32,1096) | 1 | GTGACCTCACTTCTGGCACTGTGACT ACTATGGCTGTTTGAAGTACTGA |
| 1927 | Table 3A | Hs.3873 | NM_000310 | 4506030 | palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile) (PPT1), mRNA /cds=(13,933) | 1 | AAGCCTTATTCTTCAACTAAAGATGA GGATTAAGAGCAAGAAGTTGGGG |
| 1928 | Table 3A | Hs.74621 | NM_000311 | 4506112 | prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia) (PRNP), mRNA /cds=(49,810) | 1 | GCACTGAATCGTTTCATGTAAGAATC CAAAGTGAGACCATTAACAGGTC |
| 1929 | Table 3A | Hs.288986 | NM_000344 | 13259515 | survival of motor neuron 1, telomeric (SMN1), transcript variant d, mRNA /cds=(163,1047) | 1 | GGTGCTCACATTCCTTAAATTAAGGA GAAATGCTGGCATAGAGCAGCACT |
| 1930 | Table 3A | Hs.2316 | NM_000346 | 4557852 | SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9) | 1 | CTTTTGTCTCTCCGTGAAACTTACCT TTCCCTTTTCTTCTCTTTTTT |
| 1931 | Table 3A | Hs.118787 | NM_000358 | 4507466 | transforming growth factor, beta-induced, 68kD (TGFB1), mRNA /cds=(47,2098) | 1 | TGGTATGTAGAGCTTAGATTTCCTA TTGTGACAGAGCCATGGTGTGTTT |
| 1932 | literature | Hs.2030 | NM_000361 | 4507482 | Thrombomodulin | 1 | TGGAGATAATCTAGAACACAGGCAAA ATCCTTGCTTATGACATCACTTGT |
| 1933 | Table 3A | Hs.83848 | NM_000365 | 4507644 | triosephosphate isomerase 1 (TPI1), mRNA /cds=(34,783) | 1 | GTGCCTCTGTGCTGTGTATGTGAACC ACCCATGTGAGGGAATAAACCTAG |
| 1934 | db mining | Hs.123078 | NM_000369 | 4507700 | thyroid stimulating hormone receptor (TSHR), mRNA /cds=(100,2394) | 1 | TGCAACCGGTTTTGTAAGTTAACA ACTACTACTACAATGGTAGGGGAA |
| 1935 | literature | Hs.75593 | NM_000375 | 4557872 | uroporphyrinogen III synthase (congenital erythropoietic porphyria) (UROS), mRNA /cds=(196,993) | 1 | CCTGTGCCAGCAGGAAGGAAGTCA AATAAACCACTGACTACCTGTGC |
| 1936 | db mining | Hs.2157 | NM_000377 | 4507908 | Wiskott-Aldrich syndrome (eczema-thrombocytopenia) (WAS), mRNA /cds=(34,1542) | 1 | CCCAACAATCCCAAGGCCCTTTTAT ACAAAAATCTCAGTTCTCTTCAC |
| 1937 | Table 3A | Hs.250 | NM_000379 | 9257259 | xanthine dehydrogenase (XDH), mRNA /cds=(81,4082) | 1 | TGTCTGTTTTAATCATGTATCTGGAAT AGGGTCGGGAAGGGTTTGTGCTA |
| 1938 | literature | Hs.192803 | NM_000380 | 4507936 | xeroderma pigmentosum, complementation group A (XPA), mRNA /cds=(26,847) | 1 | CACGATGGTGAAACAGTGGGGAAC TACTGCTGAAAAAGCCCTAATAGC |
| 1939 | Table 3A | Hs.179665 | NM_000389 | 11386202 | cyclin-dependent kinase inhibitor 1A (p21, Cip1) (CDKN1A), mRNA /cds=(75,569) | 1 | CCCTGGAGGCACTGAAGTGCTTAGT GTACTTGGAGTATTGGGGTCTGACC |
| 1940 | Table 3A | Hs.83942 | NM_000396 | 4503150 | cathepsin K (pseudosclerosis) (CTSK), mRNA /cds=(129,1118) | 1 | ACAAGTTTACATGATAAAAGAAATGT GATTGTCTTCCCTTCTTTCAC |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|---|
| 1941 | Table 3A | Hs.88974 | NM_000397 | 6996020 | cytochrome b-245, beta polypeptide (chronic granulomatous disease) (CYBB), mRNA /cds=(14,1726) | 1 | TTGTATGTGAATAATTCTAGCGGGG ACCTGGGAGATAATTCTACGGGGA |
| 1942 | Table 3A | Hs.1395 | NM_000399 | 9845523 | early growth response 2 (Krox-20 (Drosophila) homolog) (EGR2), mRNA /cds=(338,1768) | 1 | ATCTATTCTAACGCCAAACCACTAACT GAAGTTCAGATATAATGGATGGT |
| 1943 | Table 3A | Hs.180866 | NM_000416 | 4557879 | interferon gamma receptor 1 (IFNGR1), mRNA /cds=(43,1512) | 1 | GTAACGGAACATATCCAGTACTCCTG GTTCCCTAGGTGAGCAGGTGATGCC |
| 1944 | Table 3A | Hs.1724 | NM_000417 | 4557666 | interleukin 2 receptor, alpha (IL2RA), mRNA /cds=(159,977) | 1 | ACTAATTTGATGTTTACAGGTGGACA CACAAAGTGCCAAATCAATGCGTAC |
| 1945 | Table 3A | Hs.75545 | NM_000418 | 4557668 | interleukin 4 receptor (IL4R), mRNA /cds=(175,2652) | 1 | TGTGTGTTTTAGTTTCATCACCTGTTA TCTGTGTTTGCTGAGGAGAGTGG |
| 1946 | Table 3A | Hs.785 | NM_000419 | 6006009 | integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41B) (ITGA2B), mRNA /cds=(32,3151) | 1 | TTGGAGCTGTTCATTGGGTCTCTT GGTGTCGTTTCCCTCCCAACAGAG |
| 1947 | Table 3A | Hs.77318 | NM_000430 | 6031206 | platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit (45kD) (PAFAH1B1), mRNA /cds=(555,1787) | 1 | ATTTGTTGCTCTCAGACTGTGTA CAAAATTTATTTCATGTTTCTGCA |
| 1948 | Table 3A | Hs.949 | NM_000433 | 4557786 | neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2) (NCF2), mRNA /cds=(67,1647) | 1 | CTGAACCATTAAGTGAATTGGCTCTT AAGGCTTGAAGTAACCTTATAGGT |
| 1949 | Table 3A | Hs.78146 | NM_000442 | 4505706 | platelet/endothelial cell adhesion molecule (CD31 antigen) (PECAM1), mRNA /cds=(141,2357) | 1 | GCTAAGCTGCCGGTTCTTAAATCCAT CCTGCTAAGTTAATGTTGGGTAGA |
| 1950 | db mining | Hs.166891 | NM_000449 | 4557842 | regulatory factor X, 5 (influences HLA class II expression) (RFX5), mRNA /cds=(161,2011) | 1 | TGTAACCAATAAATCTGTAGTGACCT TACCTGTATTCCCTGTGCTATCCT |
| 1951 | Table 3A | Hs.75428 | NM_000454 | 4507148 | superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult)) (SOD1), mRNA /cds=(0,464) | 1 | ACATTCCCTTGATGTAGTCTGAGGC CCCTTAACCTCATCTGTTATCCTGC |
| 1952 | Table 3A | Hs.83918 | NM_000480 | 4502078 | adenosine monophosphate deaminase (isoform E) (AMPD3), mRNA /cds=(344,2674) | 1 | ATTTCTCCCTTATCTACTGTGATGACT TCAGAAGATACAATGGTCCCAGG |
| 1953 | Table 3A | Hs.88251 | NM_000487 | 7262293 | arylsulfatase A (ARSA), mRNA /cds=(375,1898) | 1 | TGTCTGGAGGGGGTTTGTCCTGATA ACGTAATAACACCACTGGAGACTT |
| 1954 | Table 3A | Hs.663 | NM_000492 | 6995995 | cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA /cds=(132,4574) | 1 | ACATGCGCTTCTCAACTCCAACTGA CTCTTAAGAAGACTGCATTATATT |
| 1955 | Table 3A | Hs.273385 | NM_000516 | 8659565 | guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1 (GNAS1), mRNA /cds=(68,1252) | 1 | AGATGTTCCAAATTTAGAAAGCTTAA GGCGGCCTACAGAAAAAGGAAAAA |
| 1956 | Table 3A | Hs.155376 | NM_000518 | 13788565 | hemoglobin, beta (HBB), mRNA /cds=(50,493) | 1 | AAGTCCAACCTACTAACTGGGGGATA TTATGAAGGGCCTTGAGCATCTGG |
| 1957 | Table 3A | Hs.119403 | NM_000520 | 13128865 | hexosaminidase A (alpha polypeptide) (HEXA), mRNA /cds=(26,1615) | 1 | ATCCAGCTCCCTCCCTAGAGCTATT CTCCTTTGGGTTTCTTGCTGCTGC |
| 1958 | Table 3A | Hs.51043 | NM_000521 | 13128866 | hexosaminidase B (beta polypeptide) (HEXB), mRNA /cds=(75,1745) | 1 | AAAAGGCCACAGCAATCTGTACTACA ATCAACTTTATTTTGAATCATGT |
| 1959 | literature | Hs.111749 | NM_000534 | 11496979 | postmeiotic segregation increased (S. cerevisiae) 1 (PMS1), mRNA /cds=(80,2878) | 1 | GATTAGTTACCATGAAATTGGTTCT GTCATAAAACAGCATGAGTCTGGT |
| 1960 | literature | Hs.177548 | NM_000535 | 11125773 | postmeiotic segregation increased (S. cerevisiae) 2 (PMS2), mRNA /cds=(24,2612) | 1 | AAAAATACACATCACACCCATTAAAA GTGATCTTGAGAACCCTTTTCAAA |
| 1961 | db mining | Hs.301461 | NM_000538 | 4506500 | 601845227F1 cDNA, 5' end /clone=IMAGE:4070407 /clone_end=5' | 1 | ACAGCAACAGCTATTAAATCAGCAAG TTTTGGAGCAAAAGACAACAGCAGT |
| 1962 | literature | Hs.150477 | NM_000553 | 5739523 | Werner syndrome (WRN), mRNA /cds=(231,4529) | 1 | TGACCAGGGCAGTGAAATGAACCC GCATTTTGGGTGCCATTAAATAGGG |
| 1963 | Table 3A | Hs.82212 | NM_000560 | 10834971 | CD53 antigen (CD53), mRNA /cds=(93,752) | 1 | CAATTTCTTTATTAGAGGGCCTTATTG ATGTGTTCTAAGTCTTTCCAGAA |
| 1964 | Table 3A | Hs.77424 | NM_000566 | 10835132 | Fc fragment of IgG, high affinity Ia, receptor for (CD64) (FCGR1A), mRNA /cds=(0,1124) | 1 | AGAGCTGAAATGTGAGGAACAAAAAG AAGAACAGCTGCAGGAAGGGGTGC |
| 1965 | literature | Hs.334687 | NM_000569 | 12056966 | Fc fragment of IgG, low affinity IIIa, receptor for (CD16) (FCGR3A), mRNA /cds=(33,797) | 1 | GGTAATAAGAGCAGTAGCAGCAGCAT CTCTGAACATTTCTCTGGATTGTC |
| 1966 | Table 3A | Hs.1369 | NM_000574 | 10835142 | decay accelerating factor for complement (CD55, Cromer blood group system) (DAF), mRNA /cds=(65,1210) | 1 | AGAGTTTGGAAAAAGCCTGTGAAAGG TGTCTTCTTTGACTTAATGTCTTT |
| 1967 | Table 3A | Hs.1722 | NM_000575 | 13236493 | interleukin 1, alpha (IL1A), mRNA /cds=(36,851) | 1 | GTATGGTAGATTCAAATGAACCACTG AAAAGGCATTTAGTTTCTTGTCCT |
| 1968 | Table 3A | Hs.126256 | NM_000576 | 10835144 | interleukin 1, beta (IL1B), mRNA /cds=(86,895) | 1 | AGCTATGGAATCAATTCAATTTGGAC TGGTGTGCTCTCTTAAATCAAGT |
| 1969 | literature | Hs.54443 | NM_000579 | 4502638 | chemokine (C-C motif) receptor 5 (CCR5), mRNA /cds=(357,1415) | 1 | GCTCTTAAGTTGTGAGAGTGCAACA GTAGCATAGGACCCTACCCTCTGG |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|--|
| 1970 | Table 3A | Hs.313 | NM_000582 | 4759165 | secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) (SPP1), mRNA /cds=(87,989) | 1 | GAATTTGGTGGTGTCAATTGCTTATTT GTTTCCACGGTTGTCCAGCAA |
| 1971 | Table 3A | Hs.624 | NM_000584 | 10834977 | interleukin 8 (IL8), mRNA /cds=(74,373) | 1 | AAAACAGCCAAAACCTCCACAGTCAAT ATTAGTAATTTCTTGCTGGTTGAA |
| 1972 | Table 3A | Hs.168132 | NM_000585 | 10835152 | interleukin 15 (IL15), mRNA /cds=(316,804) | 1 | TAGCATTGTTTAAAGGGTGATAGTCA AATTATGTATTGGTGGGGCTGGGT |
| 1973 | Table 3A | Hs.89679 | NM_000586 | 10835148 | interleukin 2 (IL2), mRNA /cds=(47,517) | 1 | GCAGATGAGACAGCAACCATTGTAGA ATTTCTGAACAGATGGATTACCTT |
| 1974 | Table 3A | Hs.694 | NM_000588 | 4504666 | interleukin 3 (colony-stimulating factor, multiple) (IL3), mRNA /cds=(9,467) | 1 | TCTAATTTCTGAAATGTGCAGCTCCC ATTTGGCCTGTGCGGTTGTGTTT |
| 1975 | literature | Hs.73917 | NM_000589 | 4504668 | interleukin 4 (IL4), mRNA /cds=(65,526) | 1 | ACCAGAGTACGTTGGAAAACCTTCTTG GAAAGGCTAAAGACGATCATGAGA |
| 1976 | Table 3A | Hs.75627 | NM_000591 | 4557416 | CD14 antigen (CD14), mRNA /cds=(119,1246) | 1 | TGAGGACTTTTCGACCAATTCACCCC TTGCCCCACCTTTATTAATAATCT |
| 1977 | Table 3A | Hs.158164 | NM_000593 | 9665247 | transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) (TAP1), mRNA /cds=(30,2456) | 1 | GCTGGCCCATAAACACCCTGTAGGTT CTTGATATTTATAATAAAATTGGT |
| 1978 | Table 3A | Hs.241570 | NM_000594 | 10835154 | tumor necrosis factor (TNF superfamily, member 2) (TNF), mRNA /cds=(85,786) | 1 | CCCAGGGAGTTGTGTCTGTAATCGG CCTACTATTCAGTGGCGAGAAATAA |
| 1979 | Table 3A | Hs.119663 | NM_000611 | 10835164 | CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) (CD59), mRNA /cds=(29,415) | 1 | TGATCTTGGCTGTATTTAATGGCATA GGCTGACTTTTGCAGATGGAGGAA |
| 1980 | Table 3A | Hs.856 | NM_000619 | 10835170 | interferon, gamma (IFNG), mRNA /cds=(108,608) | 1 | TTGTTGACAACTGTGACTGTACCCAA ATGGAAGTAACATCATTTGTTAAA |
| 1981 | Table 3A | Hs.172631 | NM_000632 | 6006013 | integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide) (ITGAM), mRNA /cds=(75,3533) | 1 | GTCAGATTGTGTTTTGAGGTTTCTT TCAGACAGATTCCAGCGCATGTGC |
| 1982 | Table 3A | Hs.194778 | NM_000634 | 4504680 | interleukin 8 receptor, alpha (IL8RA), mRNA /cds=(100,1152) | 1 | TCACCAGTCCCTCCCAAATGCTTTC CATGAGTTGCAGTTTTTCTAGT |
| 1983 | Table 3A | Hs.318885 | NM_000636 | 10835186 | superoxide dismutase 2, mitochondrial (SOD2), mRNA /cds=(4,672) | 1 | TACTTTGGGGACTTGTAGGGATGCCT TTCTAGTCCTATTCTATTGCAGTT |
| 1984 | Table 3A | Hs.2007 | NM_000639 | 4557328 | tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), mRNA /cds=(157,1002) | 1 | CCATCGGTGAAACTAACAGATAAGCA AGAGAGATGTTTTGGGGACTCATT |
| 1985 | Table 3A | Hs.82848 | NM_000655 | 5713320 | selectin L (lymphocyte adhesion molecule 1) (SELL), mRNA /cds=(88,1206) | 1 | AGCTCCTCTTCTGGCTTCTTACTGA AAGGTTACCTGTAAACATGCAATT |
| 1986 | Table 3A | Hs.1103 | NM_000660 | 10863872 | transforming growth factor, beta 1 (TGFB1), mRNA /cds=(841,2016) | 1 | CACCAGGAACCTGCTTTAGTGGGGG ATAGTGAAGAAGACAATAAAGATA |
| 1987 | Table 3A | Hs.157850 | NM_000661 | 4506664 | Homo sapiens, clone MGC:15545 IMAGE:3050745, mRNA, complete cds /cds=(1045,1623) | 1 | GGCTACAGAAAGAAGATGCCAGATG ACACCTTAAGACCTACTTGTGATATT |
| 1988 | Table 3A | Hs.89499 | NM_000698 | 4502056 | arachidonate 5-lipoxygenase (ALOX5), mRNA /cds=(44,2068) | 1 | GCATTTCCACACCAAGCAGCAACAGC AAATCACGACCACTGATAGATGTC |
| 1989 | Table 3A | Hs.78225 | NM_000700 | 4502100 | annexin A1 (ANXA1), mRNA /cds=(74,1114) | 1 | TCCCCAAACCATAAACCCATATACAA GTTGTTCTAGTAACAATACATGAG |
| 1990 | db mining | Hs.89485 | NM_000717 | 9951925 | carbonic anhydrase IV (CA4), mRNA /cds=(46,984) | 1 | GCTTCCGGTCTTAGCCTTCCCAGGT GGGACTTTAGGCATGATTAATAATA |
| 1991 | Table 3A | Hs.97087 | NM_000734 | 4557430 | CD3Z antigen, zeta polypeptide (TIT3 complex) (CD3Z), mRNA /cds=(178,669) | 1 | TGCTATTGCCCTTCTATTTTGCATAAT AAATGCTTCAGTGAAAATGCAGC |
| 1992 | db mining | Hs.28408 | NM_000752 | 4505032 | leukotriene b4 receptor (chemokine receptor-like 1) (LTB4R), mRNA /cds=(1717,2775) | 1 | GGAAGAAGAGGGAGAGATGGAGCAA AGTGAGGGCCGAGTGAGAGCGTGCT |
| 1993 | Table 3A | Hs.2175 | NM_000760 | 4503080 | colony stimulating factor 3 receptor (granulocyte) (CSF3R), mRNA /cds=(169,2679) | 1 | ATCCAGCCCCACCCAATGGCCTTTTG TGCTTGTTTCTATAACTTCAGTA |
| 1994 | literature | Hs.82568 | NM_000784 | 13904863 | cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1), mitochondrial protein encoded by nuclear gene, mRNA /cds=(201,1796) | 1 | CTCAGCTAAAAGGCCACCCCTTTATC GCATTGCTGTCTTGGGTAGAATA |
| 1995 | Table 3A | Hs.709 | NM_000788 | 4503268 | deoxycytidine kinase (DCK), mRNA /cds=(159,941) | 1 | ACCTTATGAACTACAGTGGAGCTACA CTCATTGAAATGTAATTTTCAGTTC |
| 1996 | Table 3A | Hs.150403 | NM_000790 | 4503280 | dopa decarboxylase (aromatic L-amino acid decarboxylase) (DDC), mRNA /cds=(69,1511) | 1 | TCCAGGGCAATCAATGTTTCACGCAAC TTGAAATTATATCTGTGGTCTTCA |
| 1997 | Table 3A | Hs.83765 | NM_000791 | 7262376 | dihydrofolate reductase (DHFR), mRNA /cds=(479,1042) | 1 | GCCAGATTTGGGGCATTTGGAAGAA GTTCATTGAAGATAAAGCAAAAGT |
| 1998 | Table 3A | Hs.179661 | NM_000801 | 4503724 | Homo sapiens, tubulin, beta 5, clone MGC:4029 IMAGE:3617988, mRNA, complete cds /cds=(1705,3039) | 1 | CTGCACCCTTCCCCCAGCACCATTATA TGAGTCTCAAGTTTTATTATTGCA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|--|
| 1999 | Table 3A | Hs.324784 | NM_000817 | 4503872 | glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD67, mRNA /cds=(550,2334) | 1 | TTTTGAAGAAGGGAAATTCACACTGT GCGTTTGTAGTATGCAAGAAGAAT |
| 2000 | Table 3A | Hs.11899 | NM_000859 | 4557642 | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMGCR), mRNA /cds=(50,2716) | 1 | TGTTGTGACTTTTGTAGCCAGTGACTTT TTCTGAGCTTTTCATGGGAAGTGG |
| 2001 | literature | Hs.1570 | NM_000861 | 13435403 | histamine receptor H1 (HRH1), mRNA /cds=(178,1641) | 1 | ACTTCACACAGACAAGTGGCTAAGTG TCCATTATTTACCTTGAAACATCA |
| 2002 | Table 3A | Hs.83733 | NM_000873 | 10433041 | cDNA FLJ11724 fis, clone HEMBA1005331 /cds=UNKNOWN | 1 | ACAGCCAACTGGAAGATATAAAAGT TTGGGTCTGTCTCCTCTCCTTCAG |
| 2003 | Table 3A | Hs.82112 | NM_000877 | 4504658 | interleukin 1 receptor, type I (IL1R1), mRNA /cds=(82,1791) | 1 | ATTAAAGCACCAAAATTCATGTACAGC ATGCATCACGGATCAATAGACTGT |
| 2004 | Table 3A | Hs.75596 | NM_000878 | 4504664 | interleukin 2 receptor, beta (IL2RB), mRNA /cds=(131,1786) | 1 | ATGGAAATGTATTTCCTTCTCCACT TTGGGAGGCTCCCACCTTCTTGGG |
| 2005 | Table 3A | Hs.2247 | NM_000879 | 4504670 | interleukin 5 (colony-stimulating factor, eosinophil) (IL5), mRNA /cds=(44,448) | 1 | TCAGAGGGAAAGTAAATATTTCAGGC ATACTGACACTTTGCCAGAAAGCA |
| 2006 | db mining | Hs.72927 | NM_000880 | 4504676 | interleukin 7 (IL7), mRNA /cds=(384,917) | 1 | GTGTAACACAGTGCCTTCAATAAATG GTATAGCAAATGTTTTCACATGAA |
| 2007 | literature | Hs.673 | NM_000882 | 4504638 | interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35) (IL12A), mRNA /cds=(169,828) | 1 | TGGGACTATTACATCCACATGATACC TCTGATCAAGTATTTTGACATTT |
| 2008 | Table 3A | Hs.75432 | NM_000884 | 4504688 | IMP (inosine monophosphate) dehydrogenase 2 (IMPDH2), mRNA /cds=(47,1591) | 1 | CATTGCTATGAGAAGCGGCTTTTCTG AAAAGGGATCCAGCACACCTCCTC |
| 2009 | Table 3A | Hs.40034 | NM_000885 | 6006032 | integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) (ITGA4), mRNA /cds=(1151,4267) | 1 | CTTCAGACTGAACATGTACACTGGTT TGAGCTTAGTGAAATGACTTCCGG |
| 2010 | Table 3A | Hs.51077 | NM_000887 | 6006014 | integrin, alpha X (antigen CD11C (p150), alpha polypeptide) (ITGAX), mRNA /cds=(58,3549) | 1 | TTTAAATGTTTGTGTTAATACACATTA AAACATCGCACAAAAACGATGCA |
| 2011 | Table 3A | Hs.1741 | NM_000889 | 4504776 | integrin, beta 7 (ITGB7), mRNA /cds=(151,2547) | 1 | GCAACCTTGCATCCATCTGGGCTACC CCACCCAAGTATACAATAAAGTCT |
| 2012 | Table 3A | Hs.81118 | NM_000895 | 4505028 | leukotriene A4 hydrolase (LTA4H), mRNA /cds=(68,1903) | 1 | TGCTGGTGGGGAAGACTTAAAGATG GATTAAAGACCTGCGTATTGATGA |
| 2013 | literature | Hs.456 | NM_000897 | 4505040 | leukotriene C4 synthase (LTC4S), mRNA /cds=(96,548) | 1 | AGGGGCGCTCGCTTCCGCATCCTAG TCTCTATCATTAAGTTCTAGTGAC |
| 2014 | Table 3A | Hs.171880 | NM_000937 | 14589948 | polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A), mRNA /cds=(386,6298) | 1 | AGCTGATCCTCGGAAGAACAAGCT AAAGCTGCCTTTTGTCTGTTATTT |
| 2015 | Table 3A | Hs.183842 | NM_000942 | 4758949 | ubiquitin B (UBB), mRNA /cds=(94,783) | 1 | CACAGGCCCATGGACTCACTTTTGTA ACAACTCCTACCAACACTGACCA |
| 2016 | Table 3A | Hs.74519 | NM_000947 | 4506052 | primase, polypeptide 2A (58kD) (PRIM2A), mRNA /cds=(87,1616) | 1 | AGGAGGAGTTTCTATTAAATCTGTCT ACTTGAGTGATGCTATTTAAGTCC |
| 2017 | Table 3A | Hs.199248 | NM_000958 | 4506258 | prostaglandin E receptor 4 (subtype EP4) (PTGER4), mRNA /cds=(388,1854) | 1 | CCTGTGCAATAGACACATACATGTCA CATTTAGCTGTGCTCAGAAGGGCT |
| 2018 | Table 3A | Hs.199248 | NM_000958 | 4506258 | prostaglandin E receptor 4 (subtype EP4) (PTGER4), mRNA /cds=(388,1854) | 1 | CCTGTGCAATAGACACATACATGTCA CATTTAGCTGTGCTCAGAAGGGCT |
| 2019 | Table 3A | Hs.250505 | NM_000964 | 4506418 | retinoic acid receptor, alpha (RARA), mRNA /cds=(102,1490) | 1 | TGCACCTGTTACTGTTGGGCTTTCCA CTGAGATCTACTGGATAAAGAATA |
| 2020 | Table 3A | Hs.119598 | NM_000967 | 4506648 | ribosomal protein L3 (RPL3), mRNA /cds=(6,1217) | 1 | AAGAAGGAGCTTAATGCCAGGAACA GATTTTGCAGTTGGTGGGGTCTCAA |
| 2021 | Table 3A | Hs.174131 | NM_000970 | 4506656 | ribosomal protein L6 (RPL6), mRNA /cds=(26,892) | 1 | AGGGCTACCTGCGATCTGTGTTTGTCT CTGACGAATGGAATTTATCCTCAC |
| 2022 | Table 3A | Hs.153 | NM_000971 | 4506658 | ribosomal protein L7 (RPL7), mRNA /cds=(10,756) | 1 | CCATGATTATTTTCTAAGCTGGTTG GTTAATAAACAGTACCTCTCTCA |
| 2023 | Table 3A | Hs.99858 | NM_000972 | 4506660 | ribosomal protein L7a (RPL7A), mRNA /cds=(31,831) | 1 | AAAGGCTAAGAGACTTGCCACTAAAC TGGGTTAAATGTACACTGTTGAGT |
| 2024 | Table 3A | Hs.178551 | NM_000973 | 4506662 | ribosomal protein L8 (RPL8), mRNA /cds=(43,816) | 1 | GGAACCAAGACTGTGCAGGAGAAAG AGAACTAGTGCTGAGGGCCTCAATA |
| 2025 | Table 3A | Hs.179943 | NM_000975 | 4506594 | ribosomal protein L11 (RPL11), mRNA /cds=(0,536) | 1 | TGGTTCCAGCAGAAGTATGATGGGAT CATCCTTCTGCGCAAATAAATTC |
| 2026 | Table 3A | Hs.180842 | NM_000977 | 4506598 | ribosomal protein L13 (RPL13), mRNA /cds=(51,686) | 1 | TTGGTTGTTTGGTTAGTGACTGATGT AAAACGGTTTTCTGTGGGGAGGT |
| 2027 | Table 3A | Hs.234518 | NM_000978 | 14591907 | ribosomal protein L23 (RPL23) | 1 | ATGCTGGCAGCATTGCATGATTCTCC AGTATATTTGTAAAAAATAAAAAA |
| 2028 | Table 3A | Hs.75458 | NM_000979 | 4506606 | ribosomal protein L18 (RPL18), mRNA /cds=(15,581) | 1 | CGGGCCAGCCGAGGCTACAAAAACT AACCCTGGATCCTACTCTCTTATTA |
| 2029 | Table 3A | Hs.272822 | NM_000981 | 4506608 | RuvB (E coli homolog)-like 1 (RUVBL1), mRNA /cds=(76,1446) | 1 | ACCTCCCACCTTTGTCTGTACATACG GCCTCTGTGATTACATAGATCAGC |
| 2030 | Table 3A | Hs.184108 | NM_000982 | 4506610 | ribosomal protein L21 (gene or pseudogene) (RPL21), mRNA /cds=(33,515) | 1 | TTCAACTAAAGCGCCACCTGCTCCAC CCAGAGAAGCACACTTTGTGAGAA |
| 2031 | Table 3A | Hs.326249 | NM_000983 | 4506612 | ribosomal protein L22 (RPL22), mRNA /cds=(51,437) | 1 | TTGGAAATCATAGTCAAAGGGCTTCC TTGGTTCGCCACTCATTTATTTGT |
| 2032 | Table 3A | Hs.326249 | NM_000983 | 4506612 | ribosomal protein L22 (RPL22), mRNA /cds=(51,437) | 1 | TTGGAAATCATAGTCAAAGGGCTTCC TTGGTTCGCCACTCATTTATTTGT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|-----------------------------|
| 2033 | Table 3A | Hs.184776 | NM_000984 | 4506614 | ribosomal protein L23a (RPL23A), mRNA /cds=(23,493) | 1 | CCTGATGGAGAGAAGAAGGCATATGT |
| 2034 | Table 3A | Hs.82202 | NM_000985 | 14591906 | ribosomal protein L17 (RPL17), mRNA /cds=(286,840) | 1 | TCGACTGGCTCTGATTACGATGC |
| 2035 | Table 3A | Hs.184582 | NM_000986 | 4506618 | ribosomal protein L24 (RPL24), mRNA /cds=(39,512) | 1 | CAGAAGAACTGAAGAAAACAAAACT |
| 2036 | Table 3A | Hs.192760 | NM_000987 | 4506620 | kinesin family member 5A (KIF5A), mRNA /cds=(148,3246) | 1 | TATGGCACGGGAGTAAATTCAGCA |
| 2037 | Table 3A | Hs.111611 | NM_000988 | 4506622 | ribosomal protein L27 (RPL27), mRNA /cds=(17,427) | 1 | GTTCAGCTCCCCGAGTTGGTGAAAA |
| 2038 | Table 3A | Hs.76064 | NM_000990 | 14141189 | ribosomal protein L27a (RPL27A), mRNA /cds=(22,468) | 1 | ACGCTAAACTGGCAGATTAGATTC |
| 2039 | Table 3A | Hs.184014 | NM_000993 | 4506632 | ribosomal protein L31 (RPL31), mRNA /cds=(7,384) | 1 | CTCCTGTTGGGTAAAGGTGTTGAGTG |
| 2040 | Table 3A | Hs.169793 | NM_000994 | 4506634 | ribosomal protein L32 (RPL32), mRNA /cds=(34,441) | 1 | TGACTTGTGCTGAAAACCTGGTTC |
| 2041 | Table 3A | Hs.289093 | NM_000996 | 4506638 | cDNA FLJ11509 fis, clone HEMBA1002166 /cds=UNKNOWN | 1 | GAACAAGTGGTCTCTCCAGAACTGC |
| 2042 | Table 3A | Hs.179779 | NM_000997 | 4506640 | ribosomal protein L37 (RPL37), mRNA /cds=(28,321) | 1 | GGTTTTAGATGCTTTGTTTGATC |
| 2043 | Table 3A | Hs.5566 | NM_000998 | 4506642 | ribosomal protein L37a (RPL37A), mRNA /cds=(17,295) | 1 | GGCTTGAAGCCACATGGAGGGAGTT |
| 2044 | Table 3A | Hs.300141 | NM_001000 | 4506646 | cDNA FLJ14163 fis, clone NT2RP100409 /cds=UNKNOWN | 1 | TCATTAATGCTAACTACTTTTAAA |
| 2045 | Table 3A | Hs.119500 | NM_001004 | 4506670 | ribosomal protein, large P2 (RPLP2), mRNA /cds=(74,421) | 1 | ATCTACAGACAGTCAATGTGGAGAG |
| 2046 | Table 3A | Hs.155101 | NM_001006 | 4506722 | mRNA for KIAA1578 protein, partial cds /cds=(0,3608) | 1 | AACTAATCGCTGATCAAATAACGT |
| 2047 | Table 3A | Hs.180911 | NM_001008 | 4506726 | ribosomal protein S4, Y-linked (RPS4Y), mRNA /cds=(12,803) | 1 | GCGCAGTGAAGAAAATGAGTAGGCA |
| 2048 | Table 3A | Hs.76194 | NM_001009 | 13904869 | ribosomal protein S5 (RPS5), mRNA /cds=(53,667) | 1 | GCTCATGTGCACGTTTTCTGTTTAA |
| 2049 | Table 3A | Hs.301547 | NM_001011 | 4506740 | ribosomal protein S7 (RPS7), mRNA /cds=(81,665) | 1 | CAATCTTCTGCTAAGCCATTGGAC |
| 2050 | Table 3A | Hs.182740 | NM_001015 | 14277698 | ribosomal protein S11 (RPS11), mRNA /cds=(33,509) | 1 | ACAGAATCCGAGTGATGCTGTACC |
| 2051 | Table 3A | Hs.165590 | NM_001017 | 14591910 | ribosomal protein S13 (RPS13), mRNA /cds=(32,487) | 1 | GGCAGCTGTTGCAGCATCCAGTTCAT |
| 2052 | Table 3A | Hs.80617 | NM_001020 | 14591912 | ribosomal protein S16 (RPS16), mRNA /cds=(52,492) | 1 | CTTAAGAATGTCAACGATTATGCA |
| 2053 | Table 3A | Hs.5174 | NM_001021 | 14591913 | ribosomal protein S17 (RPS17), mRNA /cds=(25,432) | 1 | AGACGCTCCTCTACTCTTTGGAGACA |
| 2054 | Table 3A | Hs.298262 | NM_001022 | 14591914 | ribosomal protein S19 (RPS19), mRNA /cds=(69,506) | 1 | TCACTGGCCATATAATAATGGGTT |
| 2055 | Table 3A | Hs.182979 | NM_001024 | 14670385 | cDNA: FLJ22838 fis, clone KAIA4494, highly similar to HUML12A ribosomal protein L12 mRNA /cds=UNKNOWN | 1 | TCTGTTATGAACACGTTGGTTGGCTG |
| 2056 | Table 3A | Hs.182979 | NM_001024 | 14670385 | cDNA: FLJ22838 fis, clone KAIA4494, highly similar to HUML12A ribosomal protein L12 mRNA /cds=UNKNOWN | 1 | GATTACAGTAATAATATGAAGGC |
| 2057 | Table 3A | Hs.251664 | NM_001025 | 14790142 | DNA for insulin-like growth factor II (IGF-2); exon 7 and additional ORF /cds=(0,233) | 1 | TGAGAAGAAGGAGGAGTCTGAAGAG |
| 2058 | Table 3A | Hs.180450 | NM_001026 | 14916502 | ribosomal protein S24 (RPS24), transcript variant 1, mRNA /cds=(37,429) | 1 | TCAGATGATGACATGGGATTGGCC |
| 2059 | Table 3A | Hs.113029 | NM_001028 | 14591916 | ribosomal protein S25 (RPS25), mRNA /cds=(63,440) | 1 | GCTAAAGTTGAACGAGCTGATGGATA |
| 2060 | Table 3A | Hs.539 | NM_001032 | 13904868 | ribosomal protein S29 (RPS29), mRNA /cds=(30,200) | 1 | TGAACCACCAAGTCCAGAATCTGT |
| 2061 | Table 3A | Hs.2934 | NM_001033 | 4506748 | ribonucleotide reductase M1 polypeptide (RRM1), mRNA /cds=(187,2565) | 1 | GCTGGCCACCAACAGAGCAGTGGC |
| 2062 | Table 3A | Hs.172129 | NM_001046 | 4506974 | cDNA: FLJ21409 fis, clone COL03924 /cds=UNKNOWN | 1 | TAAATTGCAGTAGCAGCATATCTTT |
| 2063 | Table 3A | Hs.256278 | NM_001066 | 4507576 | tumor necrosis factor receptor superfamily, member 1B (TNFRSF1B), mRNA /cds=(89,1474) | 1 | GCCAAAGTCCAACCGCTGATTTTCCA |
| 2064 | literature | Hs.156346 | NM_001067 | 4507632 | topoisomerase (DNA) II alpha (170kD) (TOP2A), mRNA /cds=(36,4631) | 1 | GCTGCTGCCCAATAAACCTGTCTG |
| 2065 | Table 3A | Hs.75248 | NM_001068 | 11225253 | topoisomerase (DNA) II beta (180kD) (TOP2B), mRNA /cds=(0,4865) | 1 | CTCGGGACCTGTGTTGAATTTTTTCT |
| 2066 | Table 3A | Hs.174140 | NM_001096 | 4501864 | ATP citrate lyase (ACLY), mRNA /cds=(84,3401) | 1 | GATGTGCTGTATTATTTTCAATAA |
| 2067 | Table 3A | Hs.288061 | NM_001101 | 5016088 | actin, beta (ACTB), mRNA /cds=(73,1200) | 1 | GCTGCCAACAGAAGCATAGAACAA |
| 2068 | db mining | Hs.150402 | NM_001105 | 10862690 | activin A receptor, type I (ACVR1), mRNA /cds=(340,1869) | 1 | ACCATGCTGGGTTAATAAATGGCC |
| | | | | | | 1 | GATGGCATCGTCTCAAAGAAGCTTTTG |
| | | | | | | 1 | ACTGGAGAGAATCACAGATGTGGA |
| | | | | | | 1 | CCAATGTTTCTCTTTTGGCCCTATACA |
| | | | | | | 1 | AAGGCAAGAAGGAAAGACCAAGA |
| | | | | | | 1 | CTGGCAAAAAGCCGAAGGAGTAAAG |
| | | | | | | 1 | GTGCTGCAATGATGTTAGCTGTGGC |
| | | | | | | 1 | TGGTGAAGATGCATGAATAGGTCCAA |
| | | | | | | 1 | CCAGCTGTACATTTGGAAAAATAA |
| | | | | | | 1 | GCCAGTGTTCCTGTCAGTACGCGAA |
| | | | | | | 1 | GGATATCGGTTTCAATTAAGTTGGAC |
| | | | | | | 1 | GAGTGATACTCATGAGAAGTACTGA |
| | | | | | | 1 | TAGGACCTTTATCTGGATATGGTC |
| | | | | | | 1 | GGTGATTCTTCTCTGTTGAAGTGAAG |
| | | | | | | 1 | TTTGTGAGAGTAGTTTTCTTTGTC |
| | | | | | | 1 | TGTGTGTTGATCCCAAGACAATGAAA |
| | | | | | | 1 | GTTTGCATGTATGCTGGACGGCA |
| | | | | | | 1 | GGGGAAGGTGTTTTAGTACAAGACA |
| | | | | | | 1 | TCAAAGTGAAGTAAAGCCCAAGTG |
| | | | | | | 1 | AGGAAACATCCAAACAACAAGCAA |
| | | | | | | 1 | GAAACCGAAGAAGACATCTTTTGA |
| | | | | | | 1 | AGCTGCCACCTCAGTCTCTTCTGT |
| | | | | | | 1 | ATTATCATAGTCTGGTTTAAATAA |
| | | | | | | 1 | GGAGGACGCCAGGGCTTACCTGTAC |
| | | | | | | 1 | ACTGACTTGAGACCAAGTTGAATAA |
| | | | | | | 1 | AGCAAAGATTTCAGTAGAATTGTAGT |
| | | | | | | 1 | CCTGAACGCTACGGGAAAAATGCA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|--|
| 2069 | Table 3A | Hs.172028 | NM_001110 | 4557250 | a disintegrin and metalloproteinase domain 10 (ADAM10), mRNA /cds=(469,2715) | 1 | TGGTGGTATTTCAGTGGTCCAGGATTC TGTAATGCTTTACACAGGCAGTTT |
| 2070 | Table 3A | Hs.7957 | NM_001111 | 7669471 | adenosine deaminase, RNA-specific (ADAR), transcript variant ADAR-a, mRNA /cds=(187,3867) | 1 | TGCTTTTATGTGTCCCTTGATAACAGT GACTTAACAAATATACATTCTCTCA |
| 2071 | Table 3A | Hs.172199 | NM_001114 | 4557254 | adenylate cyclase 7 (ADCY7), mRNA /cds=(265,3507) | 1 | TTGTTTCAAAATGCTGTTTCATTTTTTA TAAAGTACCAGTGTTTAGCTGCT |
| 2072 | Table 3A | Hs.3416 | NM_001122 | 4557260 | adipose differentiation-related protein (ADFP), mRNA /cds=(0,1313) | 1 | AGAGATGGACAAGAGCAGCCAGGAG ACCCAGCGATCTGAGCATAAACTC |
| 2073 | literature | Hs.394 | NM_001124 | 4501944 | adrenomedullin (ADM), mRNA /cds=(156,713) | 1 | TGAAAGAGAAAGACTGATTACCTCCT GTGTGGAAGAAGGAAACACCGAGT |
| 2074 | literature | Hs.278398 | NM_001151 | 4502096 | DNA sequence from clone RP1-202D23 on chromosome 6q14.1-15 Contains part of the gene for N-acetylglucosamine-phosphate mutase, part of a gene for a novel protein, ESTs, STSs and GSSs /cds=(0,5916) | 1 | GGAATACCTCAGAAAGAGATGCTTCAT TGAGTGTTCAATTAACACACATG |
| 2075 | Table 3A | Hs.300711 | NM_001154 | 4809273 | annexin A5 (ANXA5), mRNA /cds=(192,1154) | 1 | ACCATGATACTTTAATTAGAAGCTTAG CCTTGAAATTGTGAACCTTGGA |
| 2076 | Table 3A | Hs.300711 | NM_001154 | 4809273 | annexin A5 (ANXA5), mRNA /cds=(192,1154) | 1 | ACCATGATACTTTAATTAGAAGCTTAG CCTTGAAATTGTGAACCTTGGA |
| 2077 | Table 3A | Hs.118796 | NM_001155 | 4809274 | annexin A6 (ANXA6), transcript variant 1, mRNA /cds=(170,2191) | 1 | GCCTCTGCCCTGGTTTGGCTATGTCA GATCCAATAAACATCCTGAACCTC |
| 2078 | Table 3A | Hs.75510 | NM_001157 | 4557316 | annexin A11 (ANXA11), mRNA /cds=(178,1695) | 1 | TGCCTTTTCTACCCCATCCCTCAGAG CCTCTTGCTGTGCTAAATAGATGTT |
| 2079 | Table 3A | Hs.14142 | NM_001161 | 4502124 | nudix (nucleoside diphosphate linked moiety X)-type motif 2 (NUDT2), mRNA /cds=(174,617) | 1 | GGCCAGGCCCAAGTAAGTGACCTT GTACTTTATAATAAACCTCAAGCA |
| 2080 | Table 3A | Hs.289107 | NM_001166 | 10880127 | baculoviral IAP repeat-containing 2 (BIRC2), mRNA /cds=(1159,3015) | 1 | GCCGAATTGTCTTTGGTGCTTTTCAC TTGTGTTTTAAATAAGGATTTTT |
| 2081 | Table 3A | Hs.83656 | NM_001175 | 10835001 | Rho GDP dissociation inhibitor (GDI) beta (ARHGDIB), mRNA /cds=(152,757) | 1 | CCCCTGCCAGAGGGAGTTCTTCTTTT GTGAGAGACACTGTAAACGACACA |
| 2082 | Table 3A | Hs.74515 | NM_001178 | 4502232 | aryl hydrocarbon receptor nuclear translocator-like (ARNTL), mRNA /cds=(145,1896) | 1 | AGAAGTCCCCCATGTGGATATTTCTT ATACTAATTGTATCATAAAGCCGT |
| 2083 | Table 3A | Hs.6551 | NM_001183 | 4557340 | ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump), subunit 1 (ATP6S1), mRNA /cds=(1353,2198) | 1 | GGGCAGGAGCATGGGGTGCTTGGTT GTTTCCTTCTAATAAAATAAACGC |
| 2084 | literature | Hs.77613 | NM_001184 | 4502324 | ataxia telangiectasia and Rad3 related (ATR), mRNA /cds=(79,8013) | 1 | ATGCATTTGGTATGAATCTGTGGTTG TATCTGTTCAATTCTAAAGTACAA |
| 2085 | literature | Hs.2556 | NM_001192 | 4507572 | tumor necrosis factor receptor superfamily, member 17 (TNFRSF17), mRNA /cds=(218,772) | 1 | TTCTCTAGGTTACTGTGGGAGCTTA ATGGTAGAAACTTCTTGGTTTCA |
| 2086 | literature | Hs.158303 | NM_001198 | 4557362 | PR domain containing 1, with ZNF domain (PRDM1), mRNA /cds=(223,2592) | 1 | CCTCCCAGCAACCCACTACCTCTGGT ACCTGTAAGGTCAAACAAGAAAC |
| 2087 | db mining | Hs.87223 | NM_001203 | 4502430 | bone morphogenetic protein receptor, type IB (BMPRI1B), mRNA /cds=(273,1781) | 1 | CCGTGTCTGTTTGATAGGCGGAGAAAC CGTTGGGTAACTTGTTCAGATAT |
| 2088 | Table 3A | Hs.53250 | NM_001204 | 4755129 | bone morphogenetic protein receptor, type II (serine/threonine kinase) (BMPRII), mRNA /cds=(408,3524) | 1 | TGAGGGTGAGGGCAGGCTGAGGCAA CGAGTGGGAGGTTCAAACAGAGTG |
| 2089 | Table 3A | Hs.101025 | NM_001207 | 4502464 | basic transcription factor 3 (BTF3), mRNA /cds=(0,476) | 1 | CCCAACAATCTGTGGATGGAAAAGC ACCACTTGCTACTGGAGAGGATGA |
| 2090 | Table 3A | Hs.321247 | NM_001225 | 4502576 | mRNA; cDNA DKFZp586A181 (from clone DKFZp586A181); partial cds /cds=(0,314) | 1 | AATCAACTTCAAGGAGACCTTCATT AGTACAGCTTGTCATATTTAACATT |
| 2091 | db mining | Hs.19949 | NM_001228 | 4502582 | mRNA for MACH-alpha-1 protein /cds=(291,1730) | 1 | AGGCGATGATATTCTCACCATCCTGA CTGAAGTGAATGAAAGTAAGCA |
| 2092 | literature | Hs.514 | NM_001239 | 4502622 | cyclin H (CCNH), mRNA /cds=(60,1031) | 1 | TGACGACCTGGTAGAATCTCTCTAAC CATTGGAAGTTGATTTCTCAATGC |
| 2093 | Table 3A | Hs.180841 | NM_001242 | 4507586 | tumor necrosis factor receptor superfamily, member 7 (TNFRSF7), mRNA /cds=(100,882) | 1 | GCTGCGAAAGACCCACATGCTACAA GACGGGCAAAATAAAGTGACAGATG |
| 2094 | Table 3A | Hs.1314 | NM_001243 | 4507588 | tumor necrosis factor receptor superfamily, member 8 (TNFRSF8), mRNA /cds=(222,2009) | 1 | CGCCCATGATGGGAGGGATTGACAT GTTTCAACAAAATAATGCACCTCCT |
| 2095 | literature | Hs.1313 | NM_001244 | 4507606 | tumor necrosis factor (ligand) superfamily, member 8 (TNFSF8), mRNA /cds=(114,818) | 1 | TCTTTCAGATAGCAGGCAGGGAAGCA ATGTAGTGTGGTGGGAGAGCCCC |
| 2096 | db mining | Hs.25648 | NM_001250 | 4507580 | tumor necrosis factor receptor superfamily, member 5 (TNFRSF5), mRNA /cds=(47,880) | 1 | CAGGAGGATGGCAAAGAGAGTCGCA TCTCAGTGCAGGAGAGACAGTGAGG |
| 2097 | Table 3A | Hs.99899 | NM_001252 | 4507604 | tumor necrosis factor (ligand) superfamily, member 7 (TNFSF7), mRNA /cds=(137,718) | 1 | GGGGGTAGTGGTGGCAGGACAAGAG AAGGCATTGAGCTTTTCTTTTCATT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|---|
| 2098 | db mining | Hs.76688 | NM_001266 | 7262373 | carboxylesterase 1 (monocyte/macrophage serine esterase 1) (CES1), mRNA /cds=(67,1767) | 1 | GCCATGAAGGAGCAAGTTTTGTATTT GTGACCTCAGCTTTGGGAATAAAG |
| 2099 | Table 3A | Hs.22670 | NM_001270 | 4557446 | chromodomain helicase DNA binding protein 1 (CHD1), mRNA /cds=(163,5292) | 1 | GCTACTTGTTTACATTGTACACTGCG ACCACCTTGCCGCTTTTCATCACA |
| 2100 | literature | Hs.20295 | NM_001274 | 4502802 | CHK1 (checkpoint, S.pombe) homolog (CHEK1), mRNA /cds=(34,1464) | 1 | ACCAAGTTTCAGGGGACATGAGTTTT CCAGCTTTTATACACAGTATCTC |
| 2101 | db mining | Hs.306440 | NM_001278 | 4502842 | mRNA; cDNA DKFZp566L084 (from clone DKFZp566L084) /cds=UNKNOWN | 1 | GGCAAATGAGGAACAGGGCAATAGT ATGATGAATCTTGATTGGAGTTGGT |
| 2102 | Table 3A | Hs.301921 | NM_001295 | 4502630 | chemokine (C-C motif) receptor 1 (CCR1), mRNA /cds=(62,1129) | 1 | TGTTCTTCATCTAAGCCTTCTGGTTTT ATGGGTGACAGATTCGACTGCCA |
| 2103 | Table 3A | Hs.285313 | NM_001300 | 9961346 | core promoter element binding protein (COPEB) | 1 | TATACCATGAGATGAGATGACCACCA ATCATTTTCTTGGGGGAGGGGGT |
| 2104 | Table 3A | Hs.90073 | NM_001316 | 4503072 | chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA /cds=(123,3038) | 1 | CCTAGGAAATCACAGGCTTCTGAGCA CAGCTGCATTAACAAAGGAAGT |
| 2105 | Table 3A | Hs.82890 | NM_001344 | 4503252 | defender against cell death 1 (DAD1), mRNA /cds=(66,407) | 1 | AAATGTAACCTTTTGCTTTCCAAATTA AAGAACTCCATGCCACTCTCAA |
| 2106 | Table 3A | Hs.172690 | NM_001345 | 11415023 | diacylglycerol kinase, alpha (80kD) (DGKA), mRNA /cds=(103,2310) | 1 | ACACACATACACACACCCCAAAACAC ATACATTGAAAGTGCCTCATCTGA |
| 2107 | Table 3A | Hs.301305 | NM_001352 | 4503262 | Homo sapiens, clone MGC:13202 IMAGE:3677636, mRNA, complete cds /cds=(366,2330) | 1 | GACCCATCTCCACCGCTCCGCTT AACACGATCTGAATAAATCTTGA |
| 2108 | Table 3A | Hs.306098 | NM_001353 | 5453542 | aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase) (AKR1C1), mRNA /cds=(6,977) | 1 | ACAGCAAAGCCCATTGGCCAGAAAG GAAAGACAATAATTTTGTTTTTCA |
| 2109 | Table 3A | Hs.74578 | NM_001357 | 13514819 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; leukophysin) (DDX9), transcript variant 1, mRNA /cds=(80,3919) | 1 | AAGGAGTAAAGATTGCCTTTAAATA ACTTGGTATTTTCTGGCTTTCGT |
| 2110 | Table 3A | Hs.4747 | NM_001363 | 4503336 | dyskeratosis congenita 1, dyskerin (DKC1), mRNA /cds=(92,1636) | 1 | GGCCTCGTTTACTTTTTAAAAATGAAA TTGTTTCATTGCTGGGAGAGAAT |
| 2111 | Table 3A | Hs.77462 | NM_001379 | 4503350 | DNA (cytosine-5-)-methyltransferase 1 (DNMT1), mRNA /cds=(237,5087) | 1 | TCAACTAATGATTAGTGATCAAATTG TGCAGTACTTTGTGCACTCTGGA |
| 2112 | Table 3A | Hs.154210 | NM_001400 | 13027635 | endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA /cds=(243,1391) | 1 | TAGGTTTCTGACTTTTGTGGATCATTT TGCACATAGCTTTATCAACTTTT |
| 2113 | Table 3A | Hs.274466 | NM_001403 | 4503472 | eukaryotic translation elongation factor 1 alpha 1-like 14 (EEF1A1L14), mRNA /cds=(620,1816) | 1 | AAATCAGTACTTTTTAATGGAACAAC TTGACCCCCAAATTTGTCACAGA |
| 2114 | Table 3A | Hs.2186 | NM_001404 | 4503480 | Homo sapiens, eukaryotic translation elongation factor 1 gamma, clone MGC:4501 IMAGE:2964623, mRNA, complete cds /cds=(2278,3231) | 1 | AGATCTTCAAGTGAACATCTCTTGCC ATCACCTAGCTGCCTGCACCTGCC |
| 2115 | Table 3A | Hs.129673 | NM_001416 | 4503528 | eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1), mRNA /cds=(16,1236) | 1 | CAGGAGGGGGGAGGGAAGGGAGCC AAGGGATGGACATCTTGTCATTTTT |
| 2116 | Table 3A | Hs.93379 | NM_001417 | 4503532 | eukaryotic translation initiation factor 4B (EIF4B), mRNA /cds=(0,1835) | 1 | GCAAGTATGCTGCTCTCTGTGTGAT GGTGAAGATGAAAATGAGGGAGAA |
| 2117 | Table 3A | Hs.183684 | NM_001418 | 4503538 | eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2), mRNA /cds=(306,3029) | 1 | TTGTGGGTGTGAAACAAATGGTGAGA ATTTGAATTGGTCCCTCCTATTAT |
| 2118 | Table 3A | Hs.229533 | NM_001420 | 5231299 | ol06d12.s1 cDNA, 3' end /clone=IMAGE:1522679 /clone_end=3' | 1 | AAAGGGAAAAAGACCTCGTGGAGAAT TTTTACTGGGGATTCTTGAACCTG |
| 2119 | Table 3A | Hs.151139 | NM_001421 | 4503554 | E74-like factor 4 (ets domain transcription factor) (ELF4), mRNA /cds=(382,2373) | 1 | AAATGATTTTACTATGCGTGTTCAG CAGTTGGCATTAAGTGCCTTTT |
| 2120 | Table 3A | Hs.79368 | NM_001423 | 4503558 | epithelial membrane protein 1 (EMP1), mRNA /cds=(218,691) | 1 | ATTTGCACTACTCTGGTGGATTGTTCT AGTACTGTATTGGGCTTCTTCGT |
| 2121 | Table 3A | Hs.9999 | NM_001425 | 4503562 | epithelial membrane protein 3 (EMP3), mRNA /cds=(241,732) | 1 | GAGGAGGTCTCTTCTATGCCACCGG CCTCTGCCAGCTTTGCACCAGCGTG |
| 2122 | Table 3A | Hs.254105 | NM_001428 | 4503570 | enolase 1, (alpha) (ENO1), mRNA /cds=(94,1398) | 1 | GCTAGATCCCCGGTGGTTTTGTGCTC AAAATAAAAGCCTCAGTGACCCA |
| 2123 | Table 3A | Hs.115263 | NM_001432 | 4557566 | epiregulin (EREG), mRNA /cds=(166,675) | 1 | TTTGAAGAGCCATTTTGGTAAACGGT TTTTATTAAAGATGCTATGGAACA |
| 2124 | Table 3A | Hs.99853 | NM_001436 | 12056464 | fibrillarin (FBL), mRNA /cds=(59,1024) | 1 | GTCAGGATTGCGAGAGATGTGTGTTG ATACTGTTGCACGTGTGTTTTCT |
| 2125 | Table 3A | Hs.153179 | NM_001444 | 4557580 | fatty acid binding protein 5 (psoriasis-associated) (FABP5), mRNA /cds=(48,455) | 1 | CATGCAGCTATTTCAAAGTGTGTTGG ATTAATTAGGATCATCCCTTTGGT |
| 2126 | Table 3A | Hs.14845 | NM_001455 | 4503738 | forkhead box O3A (FOXO3A), mRNA /cds=(924,2945) | 1 | TAATGGCCCCCTTACCCTGGGTGAAGC ACTTACCTTGGAACAGAACTCTA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|---|
| 2127 | Table 3A | Hs.428 | NM_001459 | 4503750 | fms-related tyrosine kinase 3 ligand (FLT3LG), mRNA /cds=(92,799) | 1 | AAGGCCTCATCCTGGGGAGGATACG TAGGCACACAGAGGGGAGTCACCAG |
| 2128 | Table 3A | Hs.99855 | NM_001462 | 4503780 | formyl peptide receptor-like 1 (FPR1), mRNA /cds=(772,1827) | 1 | TGGGGTAAGTGGAGTTGGGAAATAC AAGAAGAGAAAGACCAGTGGGGATT |
| 2129 | Table 3A | Hs.58435 | NM_001465 | 4503820 | FYN-binding protein (FYB-120/130) (FYB), mRNA /cds=(30,2381) | 1 | ACCTAGCGGACAATGATGGAGAGAT CTATGATGATATTGCTGATGGCTGC |
| 2130 | Table 3A | Hs.197345 | NM_001469 | 4503840 | thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA /cds=(17,1846) | 1 | GTGATGGTGTAGCCCTCCCACTTTGC TGTTCTTACTTTACTGCCTGAAT |
| 2131 | Table 3A | Hs.56845 | NM_001494 | 6598322 | GDP dissociation inhibitor 2 (GDI2), mRNA /cds=(152,1489) | 1 | GCCTCTACTTCTGTCTCAAAATGGCT CCAAATGATTCTGTACTGCAAAA |
| 2132 | Table 3A | Hs.272529 | NM_001503 | 4504088 | glycosylphosphatidylinositol specific phospholipase D1 (GPLD1), mRNA /cds=(32,2557) | 1 | TCTCCTTCCACAGTTTATTTCTCGCT TCCTTTCATCTAAACCTTTCTT |
| 2133 | literature | Hs.191356 | NM_001515 | 6681761 | general transcription factor IIH, polypeptide 2 (44kD subunit) (GTF2H2), mRNA /cds=(0,1187) | 1 | ACACTGTTGCCCTGGCTGTATTCTATA AGATTCCAGCTCCTTCAGGTGTTT |
| 2134 | literature | Hs.90304 | NM_001516 | 4504198 | general transcription factor IIH, polypeptide 3 (34kD subunit) (GTF2H3), mRNA /cds=(0,911) | 1 | GTCAATATTCTGCAATTTTCAGCCCCA TTTGTAATACGTGCGAGACAGCCT |
| 2135 | literature | Hs.102910 | NM_001517 | 4504200 | general transcription factor IIH, polypeptide 4 (52kD subunit) (GTF2H4), mRNA /cds=(127,1515) | 1 | GGCGGGAGCTGGCGGGGGCGGGGCA TCAGAACTCAGGTGTTTTTATTAC |
| 2136 | Table 3A | Hs.197540 | NM_001530 | 4504384 | hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) (HIF1A), mRNA /cds=(264,2744) | 1 | TTCCTTTTGTCTTTTGTGGTGGATCT AACACTAACTGATTGTTTTGTT |
| 2137 | Table 3A | Hs.235887 | NM_001535 | 4504494 | HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 1 (HRMT1L1), mRNA /cds=(165,1466) | 1 | ACGTCCTCCAAATAAATTATGTGTTG GTGCCATCGACATGCTCAATAAA |
| 2138 | Table 3A | Hs.94 | NM_001539 | 4504510 | heat shock protein, DNAJ-like 2 (HSJ2), mRNA /cds=(82,1275) | 1 | AGGTGGTGTTCAGTGTGACACCTCTT AATGGCCAGTGAATAACACTCACT |
| 2139 | Table 3A | Hs.20315 | NM_001548 | 4504584 | interferon-induced protein with tetratricopeptide repeats 1 (IFIT1), mRNA /cds=(64,1500) | 1 | CTGAGACTGGCTGCTGACTTTGAGAA CTCTGTGAGACAAGGTCCTTAGGC |
| 2140 | Table 3A | Hs.181874 | NM_001549 | 4504586 | interferon-induced protein with tetratricopeptide repeats 4 (IFIT4), mRNA /cds=(61,1533) | 1 | GCAGGGAAGCTTTCATGTTGCTCTA AGGTACATTTTTAAAGAGTTGTTT |
| 2141 | Table 3A | Hs.7879 | NM_001550 | 4504606 | interferon-related developmental regulator 1 (IFRD1), mRNA /cds=(219,1580) | 1 | CGAACCAAGCTAGAAGCAAATGTCCG AGATAAGAGAGCAGATGTTGGAGA |
| 2142 | Table 3A | Hs.239189 | NM_001551 | 4557662 | glutaminase (GLS), mRNA /cds=(19,2028) | 1 | GGAAGGAAAAGAGTGCTGAGAAATG GCTCTGTATAATCTATGGCTATCCG |
| 2143 | db mining | Hs.846 | NM_001557 | 4504682 | interleukin 8 receptor, beta (IL8RB), mRNA /cds=(408,1490) | 1 | ACCAAGGCTAGAACACCTGCCCTATA TTTTTTGTTAAATGATTTTCATTCA |
| 2144 | Table 3A | Hs.327 | NM_001558 | 4504632 | interleukin 10 receptor, alpha (IL10RA), mRNA /cds=(61,1797) | 1 | CCTCTGCCAAAGTACTCTTAGGTGCC AGTCTGGTAAGTGAAGTCCCTCTG |
| 2145 | literature | Hs.73895 | NM_001561 | 5730094 | tumor necrosis factor receptor superfamily, member 9 (TNFRSF9), mRNA /cds=(139,906) | 1 | AAAATAATGCACCACTTTTAACAGAA CAGACAGATGAGGACAGAGCTGGT |
| 2146 | Table 3A | Hs.83077 | NM_001562 | 4504652 | interleukin 18 (interferon-gamma-inducing factor) (IL18), mRNA /cds=(177,758) | 1 | GAATTGGGGGATAGATCTATAATGTT CACTGTTCAAAACGAAGACTAGCT |
| 2147 | Table 3A | Hs.107153 | NM_001564 | 4504694 | inhibitor of growth family, member 1-like (ING1L), mRNA /cds=(91,933) | 1 | CCGTTTGCTTTTCAGAAAATGTTTATG GGTAAATGCATAAGACTATGCAAT |
| 2148 | Table 3A | Hs.2248 | NM_001565 | 4504700 | small inducible cytokine subfamily B (Cys-X-Cys), member 10 (SCYB10), mRNA /cds=(66,362) | 1 | CCCAAATCTTTTCAGTGGCTACCTTAC ATACAATCCAAACACATACAGGA |
| 2149 | Table 3A | Hs.32944 | NM_001566 | 4504704 | inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), transcript variant b, mRNA /cds=(294,3158) | 1 | AAATTAATAAGTCACAAGAAAAACAAA AGTGCCAGAAGATGTCCAGCCAC |
| 2150 | Table 3A | Hs.106673 | NM_001568 | 4503520 | eukaryotic translation initiation factor 3, subunit 6 (48kD) (EIF3S6), mRNA /cds=(22,1359) | 1 | AGAGGCTCCTAACTGGGCAACTCAA GATTCTGGCTTCTACTGAAGAACCA |
| 2151 | Table 3A | Hs.14376 | NM_001614 | 11038618 | actin, gamma 1 (ACTG1), mRNA /cds=(74,1201) | 1 | GGTTTTCTACTGTTATGTGAGAACATT AGGCCCCAGCAACACGTCATTGT |
| 2152 | Table 3A | Hs.83636 | NM_001619 | 6138971 | adrenergic, beta, receptor kinase 1 (ADRBK1), mRNA /cds=(85,2154) | 1 | CAGCTTCTGCCACTTCCCAGGTAAGC AGGAGGAGGTGCCAACAGTGTTAG |
| 2153 | Table 3A | Hs.170087 | NM_001621 | 5016091 | aryl hydrocarbon receptor (AHR), mRNA /cds=(643,3189) | 1 | ACCATTTTTGTACTCTCTCCACATG TACTGGATAAATGTTTAGTGG |
| 2154 | Table 3A | Hs.75313 | NM_001628 | 4502048 | aldo-keto reductase family 1, member B1 (aldose reductase) (AKR1B1), mRNA /cds=(45,995) | 1 | GTGCCACTAACGGTTGAGTTTTGACT GCTTGGAACTGGAATCCTTTCAGC |
| 2155 | Table 3A | Hs.100194 | NM_001629 | 4502058 | arachidonate 5-lipoxygenase-activating protein (ALOX5AP), mRNA /cds=(30,515) | 1 | TCTCCACCACCATCTCCCTCTACTT CTCATTTCTAACTCTCTGCTGAA |
| 2156 | Table 3A | Hs.262476 | NM_001634 | 5209326 | S-adenosylmethionine decarboxylase 1 (AMD1), mRNA /cds=(320,1324) | 1 | GGTGTGGACTTAAATCAGTTGAAAT GTATTTCTGTACCAAAATTTACCC |
| 2157 | Table 3A | Hs.82542 | NM_001637 | 4502114 | acyloxyacyl hydrolase (neutrophil) (AOAH), mRNA /cds=(274,2001) | 1 | CCCTTCCGCTGTTCTGAAATAACCT TTCATAAAGTGCTTTGGGTGCCAT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|--|
| 2158 | Table 3A | Hs.73722 | NM_001641 | 4502136 | APEX nuclease (multifunctional DNA repair enzyme) (APEX), mRNA /cds=(205,1161) | 1 | TTCTCATGTATAAACTAGGAATCCTC CAACCAGGCTCCTGTGATAGAGT |
| 2159 | literature | Hs.288650 | NM_001650 | 4755123 | aquaporin 4 (AQP4), transcript variant a, mRNA /cds=(39,1010) | 1 | AGACACGCTATCAGCTTATTCCTTC TCTACTGGAATATTGGTATAGTCA |
| 2160 | Table 3A | Hs.792 | NM_001656 | 4502196 | ADP-ribosylation factor domain protein 1, 64kD (ARFD1), mRNA /cds=(22,1746) | 1 | TGCTCTGGTAACAAGATGTGACTTTTT GGTAGCACTGTTGTGTTTCATTCT |
| 2161 | Table 3A | Hs.270833 | NM_001657 | 4502198 | amphiregulin (schwannoma-derived growth factor) (AREG), mRNA /cds=(209,967) | 1 | TCCTCTTCCAGTGGATCATAAGACA ATGGACCCCTTTTGTATGATGGT |
| 2162 | literature | Hs.74571 | NM_001658 | 6995997 | ADP-ribosylation factor 1 (ARF1), mRNA /cds=(75,620) | 1 | ACTGTTTTGTATACCTGTTTTTCAGTTT TCATTTTCGACAAACAAGCACTGT |
| 2163 | literature | Hs.183153 | NM_001661 | 4502206 | ADP-ribosylation factor 4-like (ARF4L), mRNA /cds=(156,761) | 1 | ACATAGTTTTTATTTTTGTCTGTGA AAGTGCCAAGAACCCTCCCCAC |
| 2164 | Table 3A | Hs.77273 | NM_001664 | 10835048 | ras homolog gene family, member A (ARHA), mRNA /cds=(151,732) | 1 | TCACCTGGACTTAAGCCTCTGGCTCT AATTCACAGTGTCTTTCTCCTCA |
| 2165 | Table 3A | Hs.3109 | NM_001666 | 11386132 | Rho GTPase activating protein 4 (ARHGAP4), mRNA /cds=(42,2882) | 1 | AGATGCCTGGCAGGGCTGGTGGCG ATTCTAAAGACCTCGTGTGTGATTC |
| 2166 | Table 3A | Hs.181243 | NM_001675 | 4502264 | activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4), mRNA /cds=(881,1936) | 1 | GGATAGTCAGGAGCGCTCAATGTGCTT GTACATAGAGTGTCTAGCTGTGT |
| 2167 | Table 3A | Hs.76941 | NM_001679 | 4502280 | ATPase, Na+/K+ transporting, beta 3 polypeptide (ATP1B3), mRNA /cds=(0,839) | 1 | TTGTGAAATATCTTGTACTGCTTTTA TTTAGCAGACTGTGGACTGTAAT |
| 2168 | Table 3A | Hs.73851 | NM_001685 | 4502292 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6 (ATP5J), mRNA /cds=(1,327) | 1 | CTGGAGGACCTGTTGATGCTAGTTCA GAGTATCACCAAGAGCTGGAGAGG |
| 2169 | Table 3A | Hs.8110 | NM_001686 | 4502294 | L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain (HADHSC), mRNA /cds=(87,1031) | 1 | GCTGCACAAGAGCCTTGATTGAAGAT ATATTCTTTCTGAACAGTATTTAA |
| 2170 | Table 3A | Hs.81634 | NM_001688 | 4502298 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1), mRNA /cds=(32,802) | 1 | TTGCCTTTATAAAAACTTGCTGCCTG ACTAAAGATTAAACAGTTATAGTT |
| 2171 | Table 3A | Hs.1697 | NM_001693 | 4502310 | ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2 (ATP6B2), mRNA /cds=(25,1560) | 1 | TGGTCTGCTTTTTGACCTCTCTCTAC CTTTTCAGGGTAATCTTTGTGGC |
| 2172 | Table 3A | Hs.86905 | NM_001695 | 4502314 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42kD (ATP6C), mRNA /cds=(166,1314) | 1 | CCTGTCTTGTGTTTGTGTGTGCTAA CAGAAATAAGTTGCAGTATGGTCG |
| 2173 | Table 3A | Hs.76572 | NM_001697 | 4502302 | ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O), mRNA /cds=(36,677) | 1 | AAAAGTGTGGTTTTCTGCCATCAGT GAAAATTCTTAAACTTGAGCAAC |
| 2174 | db mining | Hs.155024 | NM_001706 | 4502382 | B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6), mRNA /cds=(327,2447) | 1 | AGGGTTTGGCTGTGTCTAACTGCAT TACCGCGTTGTAAAAATAGCTGT |
| 2175 | literature | Hs.2243 | NM_001715 | 4502412 | B lymphoid tyrosine kinase (BLK), mRNA /cds=(222,1739) | 1 | CCTAGGCTGCCTCCAGCACTGCGG GGCTTTTCTGCAATAAAGTCACGAG |
| 2176 | literature | Hs.113916 | NM_001716 | 14589867 | Burkitt lymphoma receptor 1, GTP-binding protein (BLR1), transcript variant 2, mRNA /cds=(288,1271) | 1 | GGCAGCACAGAGACCCTCGGAACAA GCCTAAAAATTGTTCAAATAAAAA |
| 2177 | Table 3A | Hs.77054 | NM_001731 | 4502472 | B-cell translocation gene 1, anti-proliferative (BTG1), mRNA /cds=(308,823) | 1 | AAGCTTTTCCACAAACCACCATCTAT TTTGTGAACCTTGTGTAGTCATCT |
| 2178 | db mining | Hs.263812 | NM_001736 | 4502508 | nuclear distribution gene C (A.nidulans) homolog (NUDC), mRNA /cds=(90,1085) | 1 | TGGCAAGTTGGAAAATATGTAAGTGG AATCTCAAAGTCTTTGGGACAA |
| 2179 | Table 3A | Hs.182278 | NM_001743 | 4502548 | Homo sapiens, calmodulin 2 (phosphorylase kinase, delta), clone MGC:1447 IMAGE:3504793, mRNA, complete cds /cds=(93,542) | 1 | TCTGCTTATGGCACAATTTGCCTCAA ATCCATTCAAAGTTGTATATTTGT |
| 2180 | Table 3A | Hs.155560 | NM_001746 | 10716562 | calnexin (CANX), mRNA /cds=(89,1867) | 1 | CCATTGTTGTCAAATGCCAGTGTCC ATCAGATGTGTTCTCCTATTTTCT |
| 2181 | Table 3A | Hs.76288 | NM_001748 | 12408645 | calpain 2, (mII) large subunit (CAPN2), mRNA /cds=(142,2244) | 1 | GCTGCCTCTGTAATTCATGTATTCA AAGGAAAAGACACCTTGCCCTATAA |
| 2182 | Table 3A | Hs.279607 | NM_001750 | 5729759 | calpastatin (CAST), mRNA /cds=(66,1358) | 1 | TCAAGTCAGCAACAGAGCAAAATAAA GGTTAGATAAGTCCTTGTGTAGCA |
| 2183 | Table 3A | Hs.179881 | NM_001755 | 13124872 | core-binding factor, beta subunit (CBFB), transcript variant 2, mRNA /cds=(11,559) | 1 | CTTGCCCTAAGCTACCAGATTGCTTT TGCCACCATTGGCCATACTGTGTG |
| 2184 | Table 3A | Hs.75586 | NM_001759 | 4502616 | cyclin D2 (CCND2), mRNA /cds=(269,1138) | 1 | TGGTTTTGAATGCAATTAGGTTATGC TATTTGGACAATAAACTACCTTG |
| 2185 | Table 3A | Hs.83173 | NM_001760 | 4502618 | cyclin D3 (CCND3), mRNA /cds=(165,1043) | 1 | TGCAAGGTTTAGGCTGGTGGCCAG GACCATCATCTACTGTAAATAAAGA |
| 2186 | Table 3A | Hs.1973 | NM_001761 | 4502620 | cyclin F (CCNF), mRNA /cds=(43,2403) | 1 | GTGTGGTCGGGGTGAGAACCAAGC GTTGGAAGCTGAGACCCGCTCTGTC |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|---|
| 2187 | literature | Hs.343474 | NM_001762 | 4502642 | 601885667F1 cDNA, 5' end /clone=IMAGE:4104184 /clone_end=5' | 1 | AGCAGCAGTGACATAAAATTCATGT TAGATAAGCATATGTTACTTACCT |
| 2188 | Table 3A | Hs.66052 | NM_001775 | 4502664 | CD38 antigen (p45) (CD38), mRNA /cds=(69,971) | 1 | CTCCACAATAAGGTCAATGCCAGAGA CGGAAGCCTTTTTCCCAAAGTCT |
| 2189 | literature | Hs.205353 | NM_001776 | 4502666 | ectonucleoside triphosphate diphosphohydrolase 1 (ENTPD1), mRNA /cds=(67,1599) | 1 | TGGAGGTATTCAATATCCTTTGCCTC AAGGACTTCGGCAGATGCTCTC |
| 2190 | Table 3A | Hs.901 | NM_001778 | 4502674 | CD48 antigen (B-cell membrane protein) (CD48), mRNA /cds=(36,767) | 1 | GGTGGCCCAACATTCTGGCCTGTTAC TTACCTGAGATGAGCTCTTTTAACT |
| 2191 | Table 3A | Hs.287995 | NM_001779 | 4502676 | cDNA: FLJ23181 fis, clone LNG11094 /cds=UNKNOWN | 1 | TTAAGAAAGAAATACCCACTAACAAAG ACAAGCATTAGTTTTGGCTGTCA |
| 2192 | Table 3A | Hs.82401 | NM_001781 | 4502680 | CD69 antigen (p60, early T-cell activation antigen) (CD69), mRNA /cds=(81,680) | 1 | GCAAGACATAGAATAGTGTGGAAAA TGTGCAATATGTGATGTGGCAAAAT |
| 2193 | Table 3A | Hs.116481 | NM_001782 | 4502682 | CD72 antigen (CD72), mRNA /cds=(108,1187) | 1 | GGGCGGCCCCGGAGCCAGCCAGGCA GTTTTATTGAAATCTTTTTAAATAAT |
| 2194 | Table 3A | Hs.79630 | NM_001783 | 4502684 | CD79A antigen (immunoglobulin- associated alpha) (CD79A), transcript variant 1, mRNA /cds=(36,716) | 1 | CTGATTGTAGCAGCCTCGTTAGTGTG ACCCCTCTCCTGATCTGTCTCAG |
| 2195 | literature | Hs.184298 | NM_001799 | 4502742 | cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase) (CDK7), mRNA /cds=(34,1074) | 1 | AGAGAACTGAGACAACATTTTACTA CTGAGGGAATAGCCAAAAGGCA |
| 2196 | Table 3A | Hs.276770 | NM_001803 | 4502760 | CDW52 antigen (CAMPATH-1 antigen) (CDW52), mRNA /cds=(24,209) | 1 | CATGGGGGCAACAGCCAAAATAGGG GGGTAATGATGTAGGGGCCAAGCAG |
| 2197 | Table 3A | Hs.10029 | NM_001814 | 4503140 | cathepsin C (CTSC), mRNA /cds=(33,1424) | 1 | TTCTGGAAGATGGTCAGCTATGAAGT AATAGAGTTTGCTTAATCATTTGT |
| 2198 | literature | Hs.41 | NM_001816 | 4502794 | carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8), mRNA /cds=(32,1081) | 1 | GGGTGGCTCTGATATAGTAGCTCTGG TGATGTTCTGCATTTCAAGAAGA |
| 2199 | Table 3A | Hs.83758 | NM_001827 | 4502858 | CDC28 protein kinase 2 (CKS2), mRNA /cds=(95,334) | 1 | TTCCAGTCAGTTTTTCTCTTAAGTGCC TGTTTGAGTTTACTGAAACAGTT |
| 2200 | literature | Hs.158324 | NM_001837 | 4502636 | chemokine (C-C motif) receptor 3 (CCR3), mRNA /cds=(31,1098) | 1 | AAGGACCAAGGAGATGAAGCAAAACA CATTAAGCCTTCCACACTCACCTCT |
| 2201 | Table 3A | Hs.3462 | NM_001867 | 4502992 | cytochrome c oxidase subunit VIIc (COX7C), mRNA /cds=(18,209) | 1 | AGGTGCAGCCTCTGGAAGTGGATCA AACTAGAACTCATATGCCATACTAGT |
| 2202 | Table 3A | Hs.75360 | NM_001873 | 4503008 | carboxypeptidase E (CPE), mRNA /cds=(290,1720) | 1 | ACTTAAAGTTTAGGGTTTCTCTTGG TTGTAGAGTGGCCAGAAATTGCA |
| 2203 | Table 3A | Hs.1940 | NM_001885 | 4503056 | crystallin, alpha B (CRYAB), mRNA /cds=(25,552) | 1 | GTCTTGTAAGTGTGCTGAAGCTTAT TAATGCTAAGGGCAGGCCAAAT |
| 2204 | Table 3A | Hs.19904 | NM_001902 | 4503124 | cystathionase (cystathionine gamma- lyase) (CTH), mRNA /cds=(33,1250) | 1 | CCAGAGCTGCTATTAGAAGCTGCTTC CTGTGAAGATCAATCTTCTGAGT |
| 2205 | literature | Hs.178452 | NM_001903 | 4503126 | catenin (cadherin-associated protein), alpha 1 (102kD) (CTNNA1), mRNA /cds=(4,2727) | 1 | TCCTCTTCTCCAGCTTCAAATGCA CAATTCATCATTTGGGCTCACTTCT |
| 2206 | Table 3A | Hs.297939 | NM_001908 | 4503138 | cathepsin B (CTSB), mRNA /cds=(177,1196) | 1 | CAGCTTCACCTGTCAAGTTAACAAG GAATGCCTGTGCCAATAAAGGTT |
| 2207 | Table 3A | Hs.78056 | NM_001912 | 4503154 | cathepsin L (CTSL), mRNA /cds=(288,1289) | 1 | CTCGAATCATTTGAAGATCCGAGTGTG ATTTGAATTTCTGTGATATTTTAC |
| 2208 | literature | Hs.289271 | NM_001916 | 4503184 | cytochrome c-1 (CYC1), mRNA /cds=(8,985) | 1 | CTTCATCTGGAAGAAGAGGCAAGGG GGCAGGAGACCTACCGCTCTAGCTG |
| 2209 | Table 3A | Hs.77494 | NM_001929 | 4503318 | deoxyguanosine kinase (DGUOK), mRNA /cds=(11,793) | 1 | AGACTTTGCCATTGTTGCCATTGTTTT CTTTTGACCTGAAGCATTTTGA |
| 2210 | db mining | Hs.334626 | NM_032332 | 14150113 | hypothetical protein MGC4238 (MGC4238), mRNA /cds=(30,977) | 1 | AAAAGTAGGGGAGGGGCTGGGTCTG CAAAATTAATAAATAGAAGAGGGGGT |
| 2211 | Table 3A | Hs.180383 | NM_001946 | 4503418 | dual specificity phosphatase 6 (DUSP6), transcript variant 1, mRNA /cds=(351,1496) | 1 | GTCGCAAGGGGATAATCTGGGAAA GACACCAAATCATGGGCTCACTTTA |
| 2212 | Table 3A | Hs.82113 | NM_001948 | 4503422 | dUTP pyrophosphatase (DUT), mRNA /cds=(29,523) | 1 | TCAGTAAACAAATTTCTTTCACAAGGTA CAAAATCTTGCTAAGCTGAAGT |
| 2213 | Table 3A | Hs.42287 | NM_001952 | 12669917 | E2F transcription factor 6 (E2F6), mRNA /cds=(0,845) | 1 | GTTTTACTTAGGACAAGTTGTACCTT GCCCTCTCTCCAGCTCTGCTCCCA |
| 2214 | literature | Hs.2271 | NM_001955 | 4503460 | endothelin 1 (EDN1), mRNA /cds=(336,974) | 1 | ACTGGCTTCCATCAGTGGTAAGTGCT TTGGTCTCTTCTTTCATCTGGGGA |
| 2215 | Table 3A | Hs.275959 | NM_001959 | 4503476 | eukaryotic translation elongation factor 1 beta 2 (EEF1B2), mRNA /cds=(235,912) | 1 | TGGATGTGGCTGCTTTCAACAAGATC TAAATCCATCCTGGATCATGGCA |
| 2216 | Table 3A | Hs.326035 | NM_001964 | 4503492 | early growth response 1 (EGR1), mRNA /cds=(270,1901) | 1 | TGTGTTGTATATCCTTCCAAAAAATTA AAACGAAAATAAAGTAGTGCGA |
| 2217 | Table 3A | Hs.79306 | NM_001968 | 4503534 | eukaryotic translation initiation factor 4E (EIF4E), mRNA /cds=(18,671) | 1 | GTCTTCCATGTGAACAGCATAAGTTT GGAGCACTAGTTTGTATTATTATGT |
| 2218 | literature | Hs.99863 | NM_001972 | 4503548 | elastase 2, neutrophil (ELA2), mRNA /cds=(38,841) | 1 | GCCCACACCCACACTCTCCAGCATCT GGCACAATAAACATTCTCTGTTTT |
| 2219 | db mining | Hs.211956 | NM_012099 | 6912245 | CD3-epsilon-associated protein; antisense to ERCC-1 (ASE-1), mRNA /cds=(488,2020) | 1 | AGCTGTTTCTGGGTAATCTAGAGT GGGTTTGGTTCTTTATTTTCCC |
| 2220 | Table 3A | Hs.62192 | NM_001993 | 10518499 | coagulation factor III (thromboplastin, tissue factor) (F3), mRNA /cds=(123,1010) | 1 | GCAGGAGACATTGGTATTCTGGGCA GCTTCTAATATGCTTTACAATCTG |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|---|
| 2221 | Table 3A | Hs.278333 | NM_001995 | 4503650 | fatty-acid-Coenzyme A ligase, long-chain 1 (FACL1), nuclear gene encoding mitochondrial protein, mRNA /cds=(73,2172) | 1 | TGGTTTTCATATCAAAAGATCATGTTG GGATTAACCTTGCCCTTTTCCCCA |
| 2222 | Table 3A | Hs.77393 | NM_002004 | 4503684 | farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDPS), mRNA /cds=(114,1373) | 1 | ATCTACAAGCGGAGAAAGTGACCTAG AGATTGCAAGGGCGGGGAGAGGAG |
| 2223 | Table 3A | Hs.170133 | NM_002015 | 9257221 | forkhead box O1A (rhabdomyosarcoma) (FOXO1A), mRNA /cds=(385,2352) | 1 | TGTTTAAATGGCTTGGTGTCTTTCTTT TCTAATTATGCAGAATAAGCTCT |
| 2224 | Table 3A | Hs.89764 | NM_002024 | 4503764 | fragile X mental retardation 1 (FMR1), mRNA /cds=(219,2117) | 1 | AAAAGTGTACTTTTGATTCACATGTTTT CAAAATGGAGTTGGAGTTTCATTCA |
| 2225 | Table 3A | Hs.138381 | NM_002027 | 4503770 | farnesyltransferase, CAAX box, alpha (FNTA), mRNA /cds=(6,1145) | 1 | TCCATCAGAGCTGGTCTGCACACTCA CATTATCTTGCTATCACTGTAACC |
| 2226 | Table 3A | Hs.753 | NM_002029 | 4503778 | formyl peptide receptor 1 (FPR1), mRNA /cds=(61,1113) | 1 | GACACTTTCGAGCTCCAGCTCCAGC TTCGTCTCACCTTGAGTTAGGCTG |
| 2227 | Table 3A | Hs.62954 | NM_002032 | 4503794 | ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(91,663) | 1 | TGTTGGGGTTTCTTTACCTTTTCTAT AAGTTGTACCAAAACATCCACTT |
| 2228 | Table 3A | Hs.278238 | NM_002041 | 8051596 | GA-binding protein transcription factor, beta subunit 2 (47kD) (GABPB2), transcript variant gamma, mRNA /cds=(169,1251) | 1 | AGGAGTCTTTTACCCGGTGTGCTTTG CCGCAGTCATCCAAAATAAATCA |
| 2229 | Table 3A | Hs.169476 | NM_002046 | 7669491 | Homo sapiens, glyceraldehyde-3-phosphate dehydrogenase, clone MGC:10926 IMAGE:3628129, mRNA, complete cds /cds=(2306,3313) | 1 | TAGGGAGCCGCACCTTGTCTGTATACC ATCAATAAAGTACCCTGTGCTCAA |
| 2230 | db mining | Hs.334695 | NM_002050 | 4503926 | GATA-binding protein 2 (GATA2), mRNA /cds=(193,1617) | 1 | GCTGTATATAAAGCTGTCCCGAGCTT AGATTCTGTATCGGGTACGGCGG |
| 2231 | Table 3A | Hs.62661 | NM_002053 | 4503938 | guanylate binding protein 1, interferon-inducible, 67kD (GBP1), mRNA /cds=(68,1846) | 1 | TGCTTATGTGTCAAAGTCCCTAGGA AAGTGGTTGATGTTCTTATAGCA |
| 2232 | Table 3A | Hs.1674 | NM_002056 | 4503980 | glutamine-fructose-6-phosphate transaminase 1 (GFPT1), mRNA /cds=(122,2167) | 1 | GCTGAATGACATATTTTATCTTGTCT TTAAATCACAACACAGAGCTGC |
| 2233 | Table 3A | Hs.296261 | NM_002072 | 4504044 | guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA /cds=(220,1299) | 1 | TGTCTCTCTCTCTTTTCTTTCTATG GAGCAAAACAAAGCTGATTTCCC |
| 2234 | Table 3A | Hs.215595 | NM_002074 | 11321584 | guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA /cds=(280,1302) | 1 | CAGTGTACTGCAAGGAAGCTGGATG CAAGATAGATACTATATAAAGTGT |
| 2235 | Table 3A | Hs.183773 | NM_002078 | 6715599 | golgi autoantigen, golgin subfamily a, 4 (GOLGA4), mRNA /cds=(285,6977) | 1 | TGTATTGTATGCAAACTGTGATTGTT GGCAGTGTCTCTCTGAGAAACA |
| 2236 | Table 3A | Hs.180577 | NM_002087 | 4504150 | granulin (GRN), mRNA /cds=(62,1843) | 1 | GGGGTGTGTTGTGTGTGCGCGTGT GCGTTTCAATAAAGTTGTACACTT |
| 2237 | Table 3A | Hs.2707 | NM_002094 | 4504166 | G1 to S phase transition 1 (GSPT1), mRNA /cds=(648,2147) | 1 | TTTAGTATTTTTCCCCAGGCCAGAT CATTCGTGAGTGTGCGAGTGTGTG |
| 2238 | Table 3A | Hs.75113 | NM_002097 | 4753158 | general transcription factor IIIA (GTF3A), mRNA /cds=(19,1290) | 1 | TGCTTTGTTTAAAGGACTGCAGACCA AGGAGTCGAGCTTTCTCTCAGAGC |
| 2239 | Table 3A | Hs.119192 | NM_002106 | 4504254 | H2A histone family, member Z (H2AFZ), mRNA /cds=(106,492) | 1 | ACCTTATTTCCACTCTGGTGGATAAG TTCAATAAAGGTCATATCCAAAC |
| 2240 | Table 3A | Hs.181307 | NM_002107 | 4504278 | H3 histone, family 3A (H3F3A), mRNA /cds=(374,784) | 1 | AATGTTGTCTGTCTTCTGTGCTGTT CTGTAAGTTTGTCTATTAATAATACA |
| 2241 | Table 3A | Hs.263435 | NM_002108 | 4809282 | histidine ammonia-lyase (HAL), mRNA /cds=(297,2270) | 1 | ACCTTCCTCATTTACAGATAAGGAA TCTTTGGGGATTAACCAACCTCCT |
| 2242 | literature | Hs.77798 | NM_002109 | 6996013 | histidyl-tRNA synthetase (HARS), mRNA /cds=(455,1984) | 1 | AGATACCTCCCAACCAACCAATTGCCA AAGGTCGAATAAAATGCCTCAACC |
| 2243 | Table 3A | Hs.89555 | NM_002110 | 4504356 | hemopoietic cell kinase (HCK), mRNA /cds=(168,1685) | 1 | GCAATCCACAATCTGACATTCTCAGG AAGCCCCCAAGTTGATATTTCTAT |
| 2244 | db mining | Hs.277477 | NM_002117 | 11321588 | major histocompatibility complex, class I, C (HLA-C), mRNA /cds=(0,1100) | 1 | TCTCAGGCTGCGTGACGAACAGTG CCCAAGGCTCTGATGAGTCTCTCAT |
| 2245 | Table 3A | Hs.814 | NM_002121 | 4504404 | major histocompatibility complex, class II, DP beta 1 (HLA-DPB1), mRNA /cds=(19,795) | 1 | GCCTCCAACCATGTTCCCTTCTTCTT AGCACCACAATAATCAAAACCCA |
| 2246 | Table 3A | Hs.308026 | NM_002125 | 4504412 | major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), mRNA /cds=(29,829) | 1 | CTCATCTTCAACTTTTGTGCTCCCTT TGCCATAACCCTATGGCCTCCTG |
| 2247 | Table 3A | Hs.324278 | NM_002128 | 4504424 | mRNA; cDNA DKFZp566M063 (from clone DKFZp566M063) /cds=UNKNOWN | 1 | TGGGGGTTGTAAATTGGCATGGAAT TTAAAGCAGGTTCTTGTGGTGCA |
| 2248 | Table 3A | Hs.80684 | NM_002129 | 14141173 | high-mobility group (nonhistone chromosomal) protein 2 (HMG2), mRNA /cds=(190,819) | 1 | TGTGTGTATGGTAGCACAGCAAACCT GTAGGAATTAGTATCAATAGTAAA |
| 2249 | Table 3A | Hs.1119 | NM_002135 | 4504440 | nuclear receptor subfamily 4, group A, member 1 (NR4A1), mRNA /cds=(110,1906) | 1 | CCTGCCTGGCTCTCTTCTTCTACCCT CCTTCCACATGTACATAAAGTGTG |
| 2250 | Table 3A | Hs.249495 | NM_002136 | 4504444 | heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 2, mRNA /cds=(104,1222) | 1 | AGATGGGAATGAAGCTTGTGTATCCA TTATCATGTGTAATCAATAAACGA |

Table 8

| | | | | | | | |
|------|-----------|-----------|-----------|----------|---|---|---|
| 2251 | Table 3A | Hs.232400 | NM_002137 | 14043073 | heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1), transcript variant B1, mRNA /cds=(169,1230) | 1 | TTAAGATTTTCTCAAAGTTTGA GCTATTAGCCAGGATCATGGTGT |
| 2252 | Table 3A | Hs.303627 | NM_002138 | 14110413 | heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA-binding protein 1, 37kD) (HNRPD), transcript variant 1, mRNA /cds=(285,1352) | 1 | TGCGGCTAGTTCAGAGAGATTTT AGCTGTGGTGGACTTCATAGATGA |
| 2253 | Table 3A | Hs.146381 | NM_002139 | 4504450 | RNA binding motif protein, X chromosome (RBMX), mRNA /cds=(11,1186) | 1 | GCATTTTGCCTTTCTGACATTTCTTG GGAATCTGCAAGAACCTCCCCTT |
| 2254 | Table 3A | Hs.2733 | NM_002145 | 4504464 | homeo box B2 (HOXB2), mRNA /cds=(78,1148) | 1 | TTCCGTTTGGTAGACTCCTTCCAATG AAATCTCAGGAATAATTAACTCT |
| 2255 | Table 3A | Hs.3268 | NM_002155 | 4504514 | heat shock 70kD protein 6 (HSP70B') (HSPA6), mRNA /cds=(0,1931) | 1 | GGCAGAGAAGGAGGAGTATGAGCAT CAGAAGAGGGAGCTGGAGCAAATCT |
| 2256 | Table 3A | Hs.79037 | NM_002156 | 4504520 | Homo sapiens, heat shock 60kD protein 1 (chaperonin), clone MGC:19755 IMAGE:3630225, mRNA, complete cds /cds=(1705,3396) | 1 | AGCAGCCTTTCTGTGGAGAGTGAGAA TAATTGTGTACAAAGTAGAGAAGT |
| 2257 | Table 3A | Hs.1197 | NM_002157 | 4504522 | heat shock 10kD protein 1 (chaperonin 10) (HSP10), mRNA /cds=(41,349) | 1 | AATGATAACTAATGACATCCAGTGTC TCCAAATTTGTTCTGTACTGA |
| 2258 | db mining | Hs.93177 | NM_002176 | 4504602 | interferon, beta 1, fibroblast (IFNB1), mRNA /cds=(0,563) | 1 | TCCCTCTGGGACTGGACAATTGCTTC AAGCATTCTTCAACCAGCAGATGC |
| 2259 | Table 3A | Hs.82065 | NM_002184 | 4504674 | interleukin 6 signal transducer (gp130, oncostatin M receptor) (IL6ST), mRNA /cds=(255,3011) | 1 | CGGCTACATGCCTCAGTGAAGGACTA GTAGTTCTGCTACAACCTTCAGCA |
| 2260 | Table 3A | Hs.237868 | NM_002185 | 4504678 | interleukin 7 receptor (IL7R), mRNA /cds=(22,1401) | 1 | CATGAGTCAAGAGCATCCTGCTCTA CCATGTGGATTGGTCACAAGGTT |
| 2261 | db mining | Hs.1702 | NM_002186 | 4504684 | interleukin 9 receptor precursor (IL9R) gene, complete cds /cds=(214,1779) | 1 | GTGAGAGTCTGTCTGGATGGAGG CTGGAGGCTCCCCCTCAACCCCTC |
| 2262 | db mining | Hs.674 | NM_002187 | 4504640 | interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), mRNA /cds=(13,999) | 1 | CCTGATACACAATTATGACCAGAAAA TATGGCTCCATGAAGGTGCTACTT |
| 2263 | Table 3A | Hs.41724 | NM_002190 | 4504650 | interleukin 17 (cytotoxic T-lymphocyte-associated serine esterase 8) (IL17), mRNA /cds=(53,520) | 1 | ATTCAATTCAGAGTAGTTTCAAGTTT CACATCGTAACCATTTTCGCCCCG |
| 2264 | Table 3A | Hs.80645 | NM_002198 | 4504720 | interferon regulatory factor 1 (IRF1), mRNA /cds=(197,1174) | 1 | TGGAAATGTCATCTAACCATTAAAGTC ATGTGTGAACACATAAGGACGTGT |
| 2265 | Table 3A | Hs.83795 | NM_002199 | 4755144 | interferon regulatory factor 2 (IRF2), mRNA /cds=(177,1226) | 1 | AATTTCCAGATTTGAAGACAAAAATA CTCTAATTCTAACCCAGAGCAAGCT |
| 2266 | Table 3A | Hs.334450 | NM_002200 | 4504726 | interferon regulatory factor 5 (IRF5), transcript variant 1, mRNA /cds=(102,1616) | 1 | TGGCAGCTACCCCTTCTTGAGAGTC CAAGAACCTGGAGCAGAAATAATT |
| 2267 | Table 3A | Hs.241545 | NM_002208 | 6007850 | Homo sapiens, Similar to hypothetical protein, clone MGC:1824 IMAGE:3509518, mRNA, complete cds /cds=(533,1504) | 1 | TTCCTTCAGGATGATCTAGAGCAGCA TGGAGCTGTTGGTAGAATATTAGT |
| 2268 | Table 3A | Hs.174103 | NM_002209 | 4504756 | integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL), mRNA /cds=(88,3600) | 1 | TGCCAAGCACAGTGCCTGCATGTATT TATCCAATAAATGTGAAATTTCTGT |
| 2269 | Table 3A | Hs.287797 | NM_002211 | 4504766 | mRNA for FLJ00043 protein, partial cds /cds=(0,4248) | 1 | ACCACTGTATGTTTACTTCTCACCATT TGAGTTGCCCATCTGTTTTCACA |
| 2270 | Table 3A | Hs.5215 | NM_002212 | 4504770 | integrin beta 4 binding protein (ITGB4BP), mRNA /cds=(70,807) | 1 | GGCTGAGGGTTCTGCTGTCTGTGC CACCCCATTAAGTGCAGTTCCTCC |
| 2271 | Table 3A | Hs.50651 | NM_002227 | 4504802 | Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA /cds=(75,3503) | 1 | ACCATCCAATCGGACAAGCTTTTCAGA ACCTTATTGAAGGATTGAAGCAC |
| 2272 | Table 3A | Hs.198951 | NM_002229 | 4504808 | jun B proto-oncogene (JUNB) | 1 | AGTCTCTAAAGAGTTTATTTAAGACG TGTTTGTGTTTGTGTGTTTGT |
| 2273 | Table 3A | Hs.3886 | NM_002267 | 4504898 | karyopherin alpha 3 (importin alpha 4) (KPNA3), mRNA /cds=(91,1656) | 1 | TGGAAGACTAAAGAGGTGCAATGTGA TCTGAGCCTCCATCATTGTCCTCC |
| 2274 | Table 3A | Hs.74011 | NM_002286 | 11693297 | lymphocyte-activation gene 3 (LAG3), mRNA /cds=(349,1938) | 1 | GCAGCCAGCAGATCTCAGCAGCCCA GTCCAAATAAACGTCCTGTCTAGCA |
| 2275 | Table 3A | Hs.334822 | NM_002295 | 9845501 | Homo sapiens, Similar to ribosomal protein L4, clone MGC:2966 IMAGE:3139805, mRNA, complete cds /cds=(1616,2617) | 1 | GGTAGGAGCAACCACTGACTGGTCTT AAGCTGTTCTTCATAGGCTCTTA |
| 2276 | Table 3A | Hs.152931 | NM_002296 | 4504960 | lamin B receptor (LBR), mRNA /cds=(75,1922) | 1 | TCAGCTACACTTTGTTTTAAGTTTGT TTTTGACATGTTTATTTGGCAAA |
| 2277 | Table 3A | Hs.76506 | NM_002298 | 7382490 | lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA /cds=(173,2056) | 1 | TCCCCCTCCGCTCCCAAGGAAGAA AGAATGTTACTGCCTTAATAAAAAA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|--|
| 2278 | Table 3A | Hs.234489 | NM_002300 | 4557031 | Homo sapiens, lactate dehydrogenase B, clone MGC:3600 IMAGE:3028947, mRNA, complete cds /cds=(1745,2749) | 1 | GTGAATTTGGGCTCACAGAATCAAAG CCTATGCTTGGTAGCTCTTGAACA |
| 2279 | Table 3A | Hs.2250 | NM_002309 | 6006018 | leukemia inhibitory factor (cholinergic differentiation factor) (LIF), mRNA /cds=(64,672) | 1 | TCCTTCCTTTCCACTGAAAAGCACAT GGCCTTGGGTGACAAATTCCTCTT |
| 2280 | Table 3A | Hs.2798 | NM_002310 | 6042197 | leukemia inhibitory factor receptor (LIFR), mRNA /cds=(153,3446) | 1 | AGAAATGTTTCAGTAATGAAAAATATA TCCAATCAGAGCCATCCCGAAAA |
| 2281 | literature | Hs.166091 | NM_002312 | 4504996 | ligase IV, DNA, ATP-dependent (LIG4), mRNA /cds=(474,3008) | 1 | TTTTAACTTTTAAAGGTTGAAAAGACAA TAGCCCAAAGCCAAAGAAAGAAAA |
| 2282 | Table 3A | Hs.158203 | NM_002313 | 6006043 | actin binding LIM protein 1 (ABLM), transcript variant ABLIM-I, mRNA /cds=(99,2435) | 1 | GCACTCCTTTGTATATACTCTGCAT CACTGTCTACTACAACTTCGTG |
| 2283 | Table 3A | Hs.890 | NM_002341 | 4505034 | lymphotoxin beta (TNF superfamily, member 3) (LTB), transcript variant 1, mRNA /cds=(8,742) | 1 | TGGCAGTGGGAAAAATGTAGGAGAC TGTTTGGAAATTGATTTTGAACCTG |
| 2284 | literature | Hs.1116 | NM_002342 | 4505038 | lymphotoxin beta receptor (TNFR superfamily, member 3) (LTBR), mRNA /cds=(168,1475) | 1 | CATGCAAATAAAAAGATGGGACCTA AACTCGTGCCGCTCGTGCCGAATT |
| 2285 | Table 3A | Hs.105938 | NM_002343 | 4505042 | lactotransferrin (LTF), mRNA /cds=(294,2429) | 1 | GGATTGCCCATCCATCTGCTTACAAT TCCCTGCTGTCGCTTAGCAAGAA |
| 2286 | Table 3A | Hs.210 | NM_002344 | 4505044 | leukocyte tyrosine kinase (LTK), mRNA /cds=(170,2581) | 1 | GAGCACTGGATTGCTTCCCATATTAG AGCGTCCTTCATCTGGCGAGACCC |
| 2287 | Table 3A | Hs.80887 | NM_002350 | 4505054 | v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), mRNA /cds=(297,1835) | 1 | AACCGCATATATACATAGCATGACAT TTCTTTGTGCTTTGGCTTACTTGT |
| 2288 | Table 3A | Hs.75709 | NM_002355 | 10947032 | mannose-6-phosphate receptor (cation dependent) (M6PR), mRNA /cds=(170,1003) | 1 | ATTTGTTTGCATCCCTCCCCACACC CTGGTGTTTTAAATGAAGAAAAA |
| 2289 | Table 3A | Hs.330716 | NM_002356 | 11125771 | cDNA FLJ14368 fis, clone HEMBA1001122 /cds=UNKNOWN | 1 | AAACTCCTGCTTAAGGTGTTCTAATTT TCTGTGAGCACACTAAAAGCGAA |
| 2290 | Table 3A | Hs.69547 | NM_002385 | 4505122 | myelin basic protein (MBP), mRNA /cds=(10,570) | 1 | GACATGCGGGCTGGGCAGCTGTAG AGTCCAACGTGGGGCAGCACAGAGA |
| 2291 | Table 3A | Hs.172195 | NM_002408 | 6031183 | mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT2), mRNA /cds=(489,1832) | 1 | ACCAAAATTCAGTGAAGGCATTCTAC AAGTTTTGAGTTAGCATTACATTT |
| 2292 | literature | Hs.1384 | NM_002412 | 4505176 | O-6-methylguanine-DNA methyltransferase (MGMT), mRNA /cds=(40,663) | 1 | TAACACTGCATCGGATGCGGGGCGT GGAGGACCCGCTGTATTAAAGGAAG |
| 2293 | Table 3A | Hs.177543 | NM_002414 | 4505182 | antigen identified by monoclonal antibodies 12E7, F21 and O13 (MIC2), mRNA /cds=(123,680) | 1 | TCCATCGAGCACGTCTGAAACCCCTG GTAGCCCCGACTTCTTTTAATTA |
| 2294 | db mining | Hs.83169 | NM_002421 | 13027798 | matrix metalloproteinase 1 (interstitial collagenase) (MMP1), mRNA /cds=(71,1480) | 1 | CAGTCACTGGTGTCAACCCTGGATAG GCAAGGGATAACTCTTCAACACAA |
| 2295 | db mining | Hs.83326 | NM_002422 | 13027803 | matrix metalloproteinase 3 (stromelysin 1, progelatinase) (MMP3), mRNA /cds=(63,1496) | 1 | GGGAAGCACTCGTGTCAACAGACA AGTGACTGTATCTGTGTAGACTATT |
| 2296 | db mining | Hs.2256 | NM_002423 | 13027804 | matrix metalloproteinase 7 (matrilysin, uterine) (MMP7), mRNA /cds=(47,850) | 1 | TCTATGAGCTTTGTCACTGCGCGTAG ATGTCAAATAAATGTTACATACACA |
| 2297 | db mining | Hs.73862 | NM_002424 | 4505220 | matrix metalloproteinase 8 (neutrophil collagenase) (MMP8), mRNA /cds=(71,1474) | 1 | ATATGGTGCTGTTTTCTACCCTTGG AAGAAATGTAGATGATGTTTCG |
| 2298 | db mining | Hs.2258 | NM_002425 | 4505204 | matrix metalloproteinase 10 (stromelysin 2) (MMP10), mRNA /cds=(22,1452) | 1 | TTGCTAGGCGAGATAGGGGGAAGAC AGATATGGGTGTTTTAATAATCT |
| 2299 | db mining | Hs.1695 | NM_002426 | 4505206 | matrix metalloproteinase 12 (macrophage elastase) (MMP12), mRNA /cds=(12,1424) | 1 | AAGTTGCTTCTTAACATCCTTGGACT GAGAAATTACTTACTTCTGGCA |
| 2300 | db mining | Hs.2936 | NM_002427 | 13027796 | matrix metalloproteinase 13 (collagenase 3) (MMP13), mRNA /cds=(28,1443) | 1 | CTCAGGCAAAGAAAAATGAAATGCATA TTTGCAAAGTGATTAGGAAGTGT |
| 2301 | literature | Hs.82380 | NM_002431 | 4505224 | menage a trois 1 (CAK assembly factor) (MNAT1), mRNA /cds=(34,963) | 1 | TGGAAGAGAGGAATAAATAATTCACC TATATGTGTTTGAAGTTGTGACAG |
| 2302 | literature | Hs.79396 | NM_002434 | 4505232 | N-methylpurine-DNA glycosylase (MPG), mRNA /cds=(146,1042) | 1 | GCCTGAGCAAAGGGCCTGCCAGAC AAGATTTTTTAATTGTTAAAAACC |
| 2303 | Table 3A | Hs.1861 | NM_002436 | 6006024 | membrane protein, palmitoylated 1 (55kD) (MPP1), mRNA /cds=(115,1515) | 1 | AAATGACACATCTGTGCAATAGAATG ATGCTGCTCTAGGGAAACCTTCA |
| 2304 | literature | Hs.42674 | NM_002439 | 4505248 | mutS (E. coli) homolog 3 (MSH3), mRNA /cds=(16,3402) | 1 | ATATTTTTATTGTTTTCAGTTTCAGATA ATTGGCACTGGGTGAATCTGGC |
| 2305 | literature | Hs.115246 | NM_002440 | 4505250 | mutS (E. coli) homolog 4 (MSH4), mRNA /cds=(41,2851) | 1 | TTCCAGGACCGAACAAGTTCAGAA AAGACTGAAGAATAATCACAATTC |
| 2306 | literature | Hs.112193 | NM_002441 | 4505252 | mRNA for G7 protein (G7 gene located in the class III region of the major histocompatibility complex /cds=(56,2611) | 1 | TTCTTATCTCCCTCAGACGCAGAGT TTTTAGTTTCTCTAGAAATTTTGT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|---|
| 2307 | Table 3A | Hs.288742 | NM_002444 | 4505256 | cDNA: FLJ22712 fis, clone HSI13435 /cds=UNKNOWN | 1 | TTTTGGAGGGGTTTATGCTCAATCCA TGTTCTATTTCAGTGCCAAATAAAA |
| 2308 | literature | Hs.388 | NM_002452 | 4505274 | nudix (nucleoside diphosphate linked moiety X)-type motif 1 (NUDT1), mRNA /cds=(26,496) | 1 | CATTGATGGCGCAGAGCCGGGTTT CATCTGGAATTAACCTGGATGGAAGG |
| 2309 | Table 3A | Hs.82132 | NM_002460 | 4505286 | interferon regulatory factor 4 (IRF4), mRNA /cds=(105,1460) | 1 | TGGAAATCCCGTGTGCTTCAAACCT GAGACAGATGGGACTTAACAGGCA |
| 2310 | Table 3A | Hs.82132 | NM_002460 | 4505286 | interferon regulatory factor 4 (IRF4), mRNA /cds=(105,1460) | 1 | TGGAAATCCCGTGTGCTTCAAACCT GAGACAGATGGGACTTAACAGGCA |
| 2311 | Table 3A | Hs.76391 | NM_002462 | 4505290 | myxovirus (influenza) resistance 1, homolog of murine (interferon-inducible protein p78) (MX1), mRNA /cds=(345,2333) | 1 | CGTCCTGCGGAGCCCTGTCTCCTCT CTCTGTAATAAACTCATTTCTAGCC |
| 2312 | Table 3A | Hs.926 | NM_002463 | 11342663 | myxovirus (influenza) resistance 2, homolog of murine (MX2), mRNA /cds=(104,2251) | 1 | TTTCCCTGATTATGATGAGCTTCCATT GTTCTGTTAAGTCTTGAGAGGA |
| 2313 | Table 3A | Hs.79070 | NM_002467 | 12962934 | v-myc avian myelocytomatosis viral oncogene homolog (MYC), mRNA /cds=(558,1877) | 1 | CAAATGCAACCTCACACCTTGGCTG AGTCTTGAGACTGAAAGATTAGC |
| 2314 | Table 3A | Hs.243886 | NM_002482 | 4505332 | nuclear autoantigenic sperm protein (histone-binding) (NASP), mRNA /cds=(85,2448) | 1 | GGGACACTGGAGGCTGGAGCTACAG TTGAAAGCACTGCATGTTAAGAGGG |
| 2315 | Table 3A | Hs.25812 | NM_002485 | 6996019 | Nijmegen breakage syndrome 1 (nibrin) (NBS1), mRNA /cds=(52,2316) | 1 | TCTGTCATGCCACAAATCCCTTTCTA AGGAAGACTGCCCTACTATAGCAG |
| 2316 | Table 3A | Hs.19236 | NM_002492 | 4505362 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SGDH) (NDUFB5), mRNA /cds=(6,575) | 1 | GGAGAAATAGGAATTTGTGAACCCCT AAAATTGTAGCAACTTTGAAAGGT |
| 2317 | Table 3A | Hs.10758 | NM_002495 | 4505368 | NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase) (NDUFS4), mRNA /cds=(8,535) | 1 | ACAAGAGTATCCACAAAATAGGTTGG CACTGACTATATCTCTGCTTGACT |
| 2318 | literature | Hs.1827 | NM_002507 | 4505392 | nerve growth factor receptor (TNFR superfamily, member 16) (NGFR), mRNA /cds=(113,1396) | 1 | GCCCTCCTGAACTTACACACAAAAC GTTAAGTGATGAACATTAATATAGC |
| 2319 | Table 3A | Hs.82226 | NM_002510 | 4505404 | glycoprotein (transmembrane) nmb (GPNMB), mRNA /cds=(91,1773) | 1 | AAACCATCTACTATATGTTAGACATGA CATTCTTTTCTCTCCTTCTCTGA |
| 2320 | Table 3A | Hs.214 | NM_002515 | 4505424 | neuro-oncological ventral antigen 1 (NOVA1), transcript variant 1, mRNA /cds=(60,1592) | 1 | GTGATCTCGTGGAATCAGTGGTTAG CATTGCCGCTATTATATTTACTCA |
| 2321 | Table 3A | Hs.89385 | NM_002519 | 4505430 | nuclear protein, ataxia-telangiectasia locus (NPAT), mRNA /cds=(34,4317) | 1 | TTGTGATGTTAAGAAATTTGTATGGT GTGGCAGTGGTCTATTCTTAAGGA |
| 2322 | Table 3A | Hs.9614 | NM_002520 | 10835062 | nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), mRNA /cds=(0,884) | 1 | CGGATGACTGACCAAGAGGCTATTCA AGATCTCTGGCAGTGGAGGAAGTC |
| 2323 | Table 3A | Hs.153952 | NM_002526 | 4505466 | 5' nucleotidase (CD73) (NT5), mRNA /cds=(49,1773) | 1 | CCTAAATCTGTGTGTATTGTGAAG TGGTATAAGAAATGACTTTGAACC |
| 2324 | Table 3A | Hs.66196 | NM_002528 | 6224977 | nth (E.coli endonuclease III)-like 1 (NTHL1), mRNA /cds=(0,938) | 1 | CAGGCTGAGGTGGACCAAGAAGGCA ACCAAGTCCCGAGAGGAGACCCGCG |
| 2325 | Table 3A | Hs.264981 | NM_002535 | 4505484 | 2'-5'-oligoadenylate synthetase 2 (69-71 kD) (OAS2), transcript variant 2, mRNA /cds=(19,2082) | 1 | GAATGTAGGGAAGAGGTGCCAAGCC AACCGTGGGGTTAGCTCTAATTATT |
| 2326 | Table 3A | Hs.74563 | NM_002537 | 9845506 | ornithine decarboxylase antizyme 2 (OAZ2), mRNA /cds=UNKNOWN | 1 | ACGGGGATGTCAGGGAGGCAAGTGT GTTGTGTTACTGTGTCAATAAACTG |
| 2327 | Table 3A | Hs.75212 | NM_002539 | 4505488 | ornithine decarboxylase 1 (ODC1) mRNA /cds=(334,1719) | 1 | GGCAGAAATGGGCCAAAAGCTTAGTG TTGTGACCTGTTTTTAAATAAAGT |
| 2328 | literature | Hs.96398 | NM_002542 | 7949101 | 8-oxoguanine DNA glycosylase (OGG1), nuclear gene encoding mitochondrial protein, transcript variant 1b, mRNA /cds=(1266,2240) | 1 | CAAGATGGGGTGGGGGATATTGAGG GAGACAGCGCTAAGGATGGTTTTAT |
| 2329 | Table 3A | Hs.77729 | NM_002543 | 4505500 | oxidised low density lipoprotein (lectin-like) receptor 1 (OLR1), mRNA /cds=(61,882) | 1 | TAGGCTTCTATTTCTTTCCACCCACT CTTCACAGGCTATTCTACTTTAA |
| 2330 | literature | Hs.81791 | NM_002546 | 4507566 | tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), mRNA /cds=(94,1299) | 1 | GGTAACCAGGTCCAATCAGTAAAAAT AAGCTGCTTATAACTGGAATGGC |
| 2331 | Table 3A | Hs.172182 | NM_002568 | 4505574 | poly(A)-binding protein, cytoplasmic 1 (PABPC1), mRNA /cds=(502,2403) | 1 | TCTGTTTTAAGTAACAGAATTGATAAC TGAGCAAGGAAACGTAATTTGGA |
| 2332 | Table 3A | Hs.75716 | NM_002575 | 4505594 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2 (SERPINB2), mRNA /cds=(72,1319) | 1 | TGCCCTTAATTGTTCTCATAATGAAGA ATAAGTAGGTACCCTCCATGCC |
| 2333 | Table 3A | Hs.188 | NM_002600 | 4505662 | phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4) (PDE4B), mRNA /cds=(765,2459) | 1 | TGCCATTAAGCAGGAATGTCATGTTT CAGTTCATTACAAAAGAAAACAAT |
| 2334 | literature | Hs.37040 | NM_002607 | 4505678 | platelet-derived growth factor alpha polypeptide (PDGFA), mRNA /cds=(403,993) | 1 | ACCTGTTTTGTATACCTGAGAGCCTG CTATGTTCTTCTTTGTGATCCA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|---|
| 2335 | literature | Hs.1976 | NM_002608 | 4505680 | platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog) (PDGFB), mRNA /cds=(1022,1747) | 1 | CTGCTTCCTTCAGTTTGTAAAGTCGG TGATTATATTTTGGGGGCTTTCC |
| 2336 | literature | Hs.81564 | NM_002619 | 4505732 | platelet factor 4 (PF4), mRNA /cds=(7,312) | 1 | AGCATACTTCTTTTTCCAGTTTCAAT CTAACTGTGAAAGAACTTCTGA |
| 2337 | Table 3A | Hs.53155 | NM_002621 | 4505736 | properdin P factor, complement (PFC), mRNA /cds=(242,1651) | 1 | GAACCTCTAACACTTCTCTCCTCCACT CTGAGCCCCCTGACCTTCCAAACC |
| 2338 | literature | Hs.99910 | NM_002627 | 11321600 | phosphofructokinase, platelet (PFKP), mRNA /cds=(33,2387) | 1 | CCAGTGCGTGCTGTCTGTGGAGTGT GTCTCATGCTTTCAGATGTCATAT |
| 2339 | Table 3A | Hs.181013 | NM_002629 | 4505752 | phosphoglycerate mutase 1 (brain) (PGAM1), mRNA /cds=(31,795) | 1 | CCCTGCCACATGGGTCAGTGTTCAT CTGAGCATAACTGTACTAAATCCT |
| 2340 | Table 3A | Hs.78713 | NM_002635 | 4505774 | solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 (SLC25A3), nuclear gene encoding mitochondrial protein, transcript variant 1b, mRNA /cds=(48,1133) | 1 | TGCTTAAGGCAAGAGTTTCAGATTTA CTGTTGAAATAAACCAACTGTTC |
| 2341 | Table 3A | Hs.166204 | NM_002636 | 13435395 | PHD finger protein 1 (PHF1), transcript variant 2, mRNA /cds=(215,1918) | 1 | CCTGACCCCTCCCATCCTTCCCATT CCTTTGATGTTATTTTGTACAGC |
| 2342 | Table 3A | Hs.112341 | NM_002638 | 4505786 | protease inhibitor 3, skin-derived (SKALP) (PI3), mRNA /cds=(119,472) | 1 | TAAGTCCCTGCTGCCCTTCCCCTTCC CACACTGTCCATTCTTCTCCCAT |
| 2343 | Table 3A | Hs.250697 | NM_002643 | 4505796 | ras-like protein (TC10), mRNA /cds=(0,641) | 1 | TGATGTGATTGTAGCTTTTAAACTAT GAAACCCCTGAGAGATTGTACCT |
| 2344 | db mining | Hs.32942 | NM_002649 | 4505802 | phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), mRNA /cds=(323,3628) | 1 | CCCAAGGTTCTTAAGCCTGGCTGCA AAGAAGAATCAACAGGGACACTTT |
| 2345 | Table 3A | Hs.154846 | NM_002651 | 4505808 | phosphatidylinositol 4-kinase, catalytic, beta polypeptide (PIK4CB), mRNA /cds=(69,2555) | 1 | TAGAAGTTTGCTTTTTCCCTGCCTGT CTTGGTCACTACCACCTTCTCCCT |
| 2346 | Table 3A | Hs.77274 | NM_002658 | 4505862 | plasminogen activator, urokinase (PLAU), mRNA /cds=(76,1371) | 1 | TGACCAGCACTGTCTCAGTTTCACTT TCACATAGATGCCCTTTCTTGGC |
| 2347 | Table 3A | Hs.179657 | NM_002659 | 4505864 | plasminogen activator, urokinase receptor (PLAUR), mRNA /cds=(426,1433) | 1 | CTGCCCATCTCAGCTCACCATCACC CTGCTAATGACTGCCAGACTGTGG |
| 2348 | Table 3A | Hs.77436 | NM_002664 | 4505878 | pleckstrin (PLEK), mRNA /cds=(60,1112) | 1 | TTCTGGAAGCTGTTCCCACTCCAGAG TGTTTTATCAATAGCCTAGAGGT |
| 2349 | Table 3A | Hs.44499 | NM_002687 | 4505922 | pinin, desmosome associated protein (PNN), mRNA /cds=(30,2261) | 1 | GGATTACCTTTCTTGTAAAGAGGAT GCTGCCCTAAGAATTGCATGTTGT |
| 2350 | Table 3A | Hs.180107 | NM_002690 | 4505930 | polymerase (DNA directed), beta (POLB), mRNA /cds=(113,1120) | 1 | GGGTCTTTGGTGTTTTTAAATGATTGT TTCTTCTTCATGCTTTTGCTTGC |
| 2351 | literature | Hs.99890 | NM_002691 | 4505932 | polymerase (DNA directed), delta 1, catalytic subunit (125kD) (POLD1), mRNA /cds=(53,3376) | 1 | CATGGGGCGGGGCGGGACCAAGGG AGAATTAATAAAGTTCTGGACTTTTG |
| 2352 | Table 3A | Hs.334828 | AB058697 | 14017804 | mRNA for KIAA1794 protein, partial cds /cds=(1592,4000) | 1 | ATTTAAAGCACAGTTTGTTTTTCTGTG ACCTATAGAGTGCAAGAATGCAC |
| 2353 | Table 3A | Hs.79402 | NM_002694 | 14702172 | polymerase (RNA) II (DNA directed) polypeptide C (33kD) (POLR2C), transcript variant gamma, mRNA /cds=(57,884) | 1 | CAGCACTGTCTCCAGATAGGAACATG CACAAGCAGTTAATTAGGCAGCC |
| 2354 | Table 3A | Hs.1101 | NM_002698 | 4505958 | POU domain, class 2, transcription factor 2 (POU2F2), mRNA /cds=(54,1445) | 1 | CTCCCTCCCATTCCTCTGGTCCCTG CCTTGGTCCCTTGCTGGGAAGAG |
| 2355 | Table 3A | Hs.2164 | NM_002704 | 4505980 | pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP), mRNA /cds=(66,452) | 1 | AAGGTTGGTTAAAGATGGCAGAAAG AAGATGAAATAAATAAGCCTGGT |
| 2356 | Table 3A | Hs.17883 | NM_002707 | 4505998 | protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform (PPM1G), mRNA /cds=(24,1664) | 1 | CTCATCACCGTTCTGTGCCTGTGCT CTGTTGTGTTGGAGGGAAGGACTG |
| 2357 | Table 3A | Hs.77876 | NM_002709 | 4506004 | Homo sapiens, Similar to RIKEN cDNA 2410153K17 gene, clone MGC:19595 IMAGE:3840843, mRNA, complete cds /cds=(469,1899) | 1 | TTTGCTTGGAACACGACTTGAAATA AATAAACTTTGTTTCTTAGGAGA |
| 2358 | Table 3A | Hs.79081 | NM_002710 | 4506006 | protein phosphatase 1, catalytic subunit, gamma isoform (PPP1CC), mRNA /cds=(154,1125) | 1 | AAAAGAACTGTGTTTCAACAGATGAC CGTGTAACATACCGTGTGGTGAAG |
| 2359 | Table 3A | Hs.36587 | NM_002712 | 4506012 | protein phosphatase 1, regulatory subunit 7 (PPP1R7), mRNA /cds=(15,1097) | 1 | GACGCCACACACCATTTTTCAGATGCC GTTGCAATTAATCTTGCCACACT |
| 2360 | Table 3A | Hs.179574 | NM_002717 | 4506018 | protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform (PPP2R2A), mRNA /cds=(105,1448) | 1 | ATGTTTTAGTAACAGTTGGCTGTAAT CACTCCTCGCGGTGTCTGGCACTG |
| 2361 | Table 3A | Hs.171734 | NM_002719 | 4506022 | protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C), mRNA /cds=(88,1632) | 1 | AGTTCTGCGTTTGGCATCTTCACTCT TTCCAAAATGTATCTGTACATCAG |
| 2362 | Table 3A | Hs.1908 | NM_002727 | 4506044 | proteoglycan 1, secretory granule (PRG1), mRNA /cds=(24,500) | 1 | TGTGTTTGAGAGCTAGTGGATGTGT TTGCTACAAGTATGATTGCTGTT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|---------|---|---|---|
| 2363 | Table 3A | Hs.183037 | NM_002734 | 4506062 | protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) (PRKAR1A), mRNA /cds=(87,1232) | 1 | AAATCTGGGGAAGAGGTTTTATTTAC ATTTTAGGGTGGGTAAGAAAGCCA |
| 2364 | Table 3A | Hs.2499 | NM_002741 | 4506072 | protein kinase C-like 1 (PRKCL1), mRNA /cds=(84,2912) | 1 | CAGAGCGGAGGCTGGGATCTAGCGA GAGAGATGCAGAAGATGTGAAGAAA |
| 2365 | literature | Hs.324473 | NM_002745 | 4506086 | 40 kDa protein kinase related to rat ERK2 /cds=(134,1180) | 1 | CGTTTGGAGGGGCGGTTTCTGGTAG TTGTGGCTTTTATGCTTTCAAAGAA |
| 2366 | literature | Hs.267445 | NM_002750 | 4506094 | mRNA; cDNA DKFZp434B231 (from clone DKFZp434B231) /cds=UNKNOWN | 1 | GGGGTGGGAGGGATGGGGAGTCGG TTAGTCATTGATAGAAGTACTTTTGAA |
| 2367 | literature | Hs.274382 | NM_002759 | 4506102 | protein kinase, interferon-inducible double stranded RNA dependent (PRKR), mRNA /cds=(435,2090) | 1 | TGCAGAAACAGAAAGGTTTTCTTCTT TTTGCTTCAAAAACATTCTTACAT |
| 2368 | db mining | Hs.56 | NM_002764 | 4506126 | phosphoribosyl pyrophosphate synthetase 1 (PRPS1), mRNA /cds=(66,1022) | 1 | AGATTAAGTCTGGACCTCCTACCTG CATTATCTCATTCTGGCTTCCTTG |
| 2369 | Table 3A | Hs.82159 | NM_002786 | 4506178 | proteasome (prosome, macropain) subunit, alpha type, 1 (PSMA1), mRNA /cds=(105,896) | 1 | CTTTGTGGTTTTAAAGACAACTGTGA AATAAAATGTTTTCACCGCTGGT |
| 2370 | Table 3A | Hs.167106 | NM_002788 | 4506182 | proteasome (prosome, macropain) subunit, alpha type, 3 (PSMA3), mRNA /cds=(5,772) | 1 | GAAGTCAGCTGGGTTGGTGAATTAAC TAATGGAAGACATGAAATTGTTCC |
| 2371 | Table 3A | Hs.251531 | NM_002789 | 4506184 | proteasome (prosome, macropain) subunit, alpha type, 4 (PSMA4), mRNA /cds=(59,844) | 1 | ACGATGATGGTTACCCCTTCATGGACG TCTTAATCTCCACACACATCCCC |
| 2372 | Table 3A | Hs.76913 | NM_002790 | 4506186 | proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA /cds=(21,746) | 1 | TTCAGTTCTAATAATGCTCTTAATTT TATTTCCAGCTCCTGTTCTCTGG |
| 2373 | Table 3A | Hs.233952 | NM_002792 | 4506188 | proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7), mRNA /cds=(24,770) | 1 | GCCTTTCCATTCCATTTATTCACACTG AGTGCTCTACAATAAACTTCCGT |
| 2374 | Table 3A | Hs.89545 | NM_002796 | 4506198 | proteasome (prosome, macropain) subunit, beta type, 4 (PSMB4), mRNA /cds=(23,817) | 1 | TGCATTATCCAGAACTGAAGTTGCC TACTTTTAACTTTGAAGTTGGCTA |
| 2375 | Table 3A | Hs.118065 | NM_002799 | 4506202 | proteasome (prosome, macropain) subunit, beta type, 7 (PSMB7), mRNA /cds=(14,847) | 1 | GCCCAGTAAGACACTCATGTGGCTAG TGTTTGCCGAATGAACTCAACTC |
| 2376 | Table 3A | Hs.61153 | NM_002803 | 4506208 | proteasome (prosome, macropain) 26S subunit, ATPase, 2 (PSMC2), mRNA /cds=(66,1367) | 1 | TAAGTCTTATGCCAAATTCAGTGCTA CTCCTCGTTACATGACATACAACT |
| 2377 | Table 3A | Hs.79387 | NM_002805 | 4506212 | proteasome (prosome, macropain) 26S subunit, ATPase, 5 (PSMC5), mRNA /cds=(0,1220) | 1 | AAGTGAGTGGACAGCCTTTGTGTGTA TCTCTCCAATAAAGCTCTGTGGGC |
| 2378 | Table 3A | Hs.341867 | NM_002807 | 4506224 | z172b08.r1 cDNA, 5' end /clone=IMAGE:727863 /clone_end=5' | 1 | TCTCCAAGTCTTTGGTTGAAGAGAAG ATATATGACTGTTGAGTGTGCTCT |
| 2379 | Table 3A | Hs.74619 | NM_002808 | 4506226 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 (PSMD2), mRNA /cds=(112,2673) | 1 | GGGGAATGTCGCCTCCTGCTCTTTT GTTACTGAGTGAGATAAGGTTGTT |
| 2380 | Table 3A | Hs.155543 | NM_002811 | 4506230 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) (PSMD7), mRNA /cds=(83,1057) | 1 | TGGCATCCTCAGGGGTTGTGATCCA GCTCCATATATTGTTACCTTCAAA |
| 2381 | Table 3A | Hs.78466 | NM_002812 | 4506232 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 8 (PSMD8), mRNA /cds=(70,843) | 1 | CGGGCACTGGGTGGGGCAGGGCAC GAGTTATTTAAAACAGTTACACTGCA |
| 2382 | Table 3A | Hs.306328 | NM_002817 | 4506222 | mRNA activated in tumor suppression, clone TSAP13 extended /cds=UNKNOWN | 1 | CGGACATCTTTCCGTTGCGGTTTGA GAATGTTCTATAATAAACCCCTC |
| 2383 | Table 3A | Hs.250655 | NM_002823 | 4506276 | prothymosin, alpha (gene sequence 28) (PTMA), mRNA /cds=(155,487) | 1 | TTTGGCCTGTTTGTATGTGTGA AACAATGTTGCCAACAATAACA |
| 2384 | Table 3A | Hs.155894 | NM_002827 | 4506288 | protein tyrosine phosphatase, non-receptor type 1 (PTPN1), mRNA /cds=(72,1379) | 1 | AGCGAGCTGCTCTGCTATGCTCTTAA GCCAATATTTACTCATCAGGTCAT |
| 2385 | Table 3A | Hs.82829 | NM_002828 | 4506290 | protein tyrosine phosphatase, non-receptor type 2 (PTPN2), mRNA /cds=(60,1307) | 1 | TGTAGTTGGGGTAGATTATGATTTAG GAAGCAAAAGTAAGAAGCAGCATT |
| 2386 | Table 3A | Hs.63489 | NM_002831 | 4506296 | protein tyrosine phosphatase, non-receptor type 6 (PTPN6), mRNA /cds=(144,1931) | 1 | GCGATGGACAGACTCACAACCTGAA CCTAGGAGTGCCCCATTCTTTGTGA |
| 2387 | Table 3A | Hs.35 | NM_002832 | 4506298 | protein tyrosine phosphatase, non-receptor type 7 (PTPN7), mRNA /cds=(155,1174) | 1 | GCTCAGGAGGGTACAAGCTCCAGAA CAGTAACCAAGTGGGAAAATAAGA |
| 2388 | Table 3A | Hs.62 | NM_002835 | 4506286 | protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA /cds=(19,2361) | 1 | CTGGATTCATGCAGCCAGCTTTGCAG GTTATCAGAGATCAAAGATTGTAA |
| 2389 | Table 3A | Hs.26045 | NM_002836 | 4506302 | protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA /cds=(695,3103) | 1 | TATCATGGGGAGTAATAGGACCAGAG CGGTATCTCTGGCACCACACTAGC |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|---|
| 2390 | Table 3A | Hs.170121 | NM_002838 | 4506306 | protein tyrosine phosphatase, receptor type, C (PTPRC), mRNA /cds=(86,4000) | 1 | CTGTGGAAAAATATTTAAGATAGTTTT GCCAGAACAGTTTGACAGACGT |
| 2391 | Table 3A | Hs.2050 | NM_002852 | 4506332 | pentaxin-related gene, rapidly induced by IL-1 beta (PTX3), mRNA /cds=(67,1212) | 1 | ACTCTCAAATAATTAAGGACTGTA TTGTTGAACAGAGGGACAATTGT |
| 2392 | literature | Hs.7179 | NM_002853 | 4506384 | RAD1 (S. pombe) homolog (RAD1), mRNA /cds=(437,1285) | 1 | AACATCATGGGAATAATTGTGAGTCAG CGTAACATTTCAAGAGCTAAAGG |
| 2393 | Table 3A | Hs.151536 | NM_002870 | 4506362 | RAB13, member RAS oncogene family (RAB13), mRNA /cds=(139,750) | 1 | TGCTCCTGTTCTGTCACTTGTCTATGG TCTTTCTTGGATTAAAGGCCACC |
| 2394 | literature | Hs.16184 | NM_002873 | 4506382 | RAD17 (S. pombe) homolog (RAD17), mRNA /cds=(642,2654) | 1 | GGGGTTGTAAATATCAACTATTCAAC AGTTTAGGATGCAATTACGAGTGT |
| 2395 | literature | Hs.23044 | NM_002875 | 4506388 | Homo sapiens, Similar to RIKEN cDNA 2610036L13 gene, clone MGC:16386 IMAGE:3938081, mRNA, complete cds /cds=(82,840) | 1 | AATCTTATGTTTTCCAAGAGAACTAAA GCTGGAGAGACCTGACCCTTCTCT |
| 2396 | literature | Hs.11393 | NM_002876 | 4506390 | RAD51 (S. cerevisiae) homolog C (RAD51C), mRNA /cds=(16,423) | 1 | TGCACCAGGTGTTGGAAAAACACAAT TATGGTAAAAATAAGTGTCTCCT |
| 2397 | literature | Hs.100669 | NM_002877 | 10835028 | RAD51 (S. cerevisiae)-like 1 (RAD51L1), mRNA /cds=(70,1122) | 1 | AATGGGCACACAGGGAACAGGAAAT GGGAATGAGAGCAAGGGTTGGGTTG |
| 2398 | literature | Hs.125244 | NM_002878 | 4506392 | RAD51 (S. cerevisiae)-like 3 (RAD51L3), mRNA /cds=(124,993) | 1 | TCTTCTTCATCTCTGTTTTGCTCTTAA AAATATAAAAAGGCAATTCCCGG |
| 2399 | literature | Hs.89571 | NM_002879 | 4506394 | RAD52 (S. cerevisiae) homolog (RAD52), mRNA /cds=(31,1290) | 1 | AGATGTAACCCACCTTGACCATAAAT TGGCTTTTCATAGTGCTCAGATGT |
| 2400 | Table 3A | Hs.279474 | NM_002880 | 8850222 | HSPC070 protein (HSPC070), mRNA /cds=(331,1581) | 1 | CTAGGCTCTGGGCACATTTCTGTTC TTGAATTCTGCTCCTGAAGAGGGT |
| 2401 | Table 3A | Hs.24763 | NM_002882 | 6382077 | RAN binding protein 1 (RANBP1) | 1 | TACCCTGCCCTCTTTTTCGGTTTGT TTTTATTCTTTCATTTTTACAAGG |
| 2402 | Table 3A | Hs.758 | NM_002890 | 4506430 | RAS p21 protein activator (GTPase activating protein) 1 (RASA1), transcript variant 1, mRNA /cds=(118,3261) | 1 | GCTGCCTAECTTATCCATCTTTGAAC TTCTGACTACTTGTGTATCTGCT |
| 2403 | Table 3A | Hs.29287 | NM_002894 | 4506440 | retinoblastoma-binding protein 8 (RBBP8), mRNA /cds=(298,2991) | 1 | CCTTTAAACAATAAGGCGCTTTCATT TTGCACTCTAACTTAAGAGTTTT |
| 2404 | Table 3A | Hs.6106 | NM_002896 | 4506444 | RNA binding motif protein 4 (RBM4), mRNA /cds=(55,1155) | 1 | TCCTGCCTCCTGCGGCTGTTGGATTT GGGAATGACCTTGGTGAGAGTCTC |
| 2405 | Table 3A | Hs.167791 | NM_002901 | 4506454 | reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA /cds=(52,1047) | 1 | ATACTCTGAGCTGTGGACTGAACCTGG CAGACACAACCTGTACAGATTGAA |
| 2406 | literature | Hs.115521 | NM_002912 | 4506482 | REV3 (yeast homolog)-like, catalytic subunit of DNA polymerase zeta (REV3L), mRNA /cds=(822,9980) | 1 | AAGGAATTATGTGGTCAGTGCATTGT TTTTTAACTGGAATCATTTTGT |
| 2407 | Table 3A | Hs.75256 | NM_002922 | 4506514 | regulator of G-protein signalling 1 (RGS1), mRNA /cds=(14,604) | 1 | TGCTCTTAAACCAGGGAGTCAGATA TATTTGAAGGTTAAATCATTTGGT |
| 2408 | Table 3A | Hs.78944 | NM_002923 | 4506516 | regulator of G-protein signalling 2, 24kD (RGS2), mRNA /cds=(32,667) | 1 | GCCAAAAATCTGTCTGAAGGCAGCT ACACTTTGAAGTGTCTTTGAATA |
| 2409 | Table 3A | Hs.82280 | NM_002925 | 11184225 | regulator of G-protein signalling 10 (RGS10), mRNA /cds=(43,546) | 1 | CCTCTCAGGACGTGCCGGGTTTATCA TTGCTTTGTTATTTTGAAGGACTG |
| 2410 | Table 3A | Hs.1010 | NM_002932 | 4506544 | regulator of mitotic spindle assembly 1 (RMSA1), mRNA /cds=(774,2030) | 1 | TGACTATCTGTAATGGATCAATTTTG GATATGACTTTGGGTGGGGGTAAA |
| 2411 | Table 3A | Hs.84318 | NM_002945 | 4506582 | replication protein A1 (70kD) (RPA1), mRNA /cds=(69,1919) | 1 | CGAGCTGAGAAAGCGGTCATGAGCAC CTGGGGATTTTAGTAAGTGTGTCTT |
| 2412 | Table 3A | Hs.79411 | NM_002946 | 4506584 | replication protein A2 (32kD) (RPA2), mRNA /cds=(77,889) | 1 | GGTAGTGCCCTCCAGGGGCAGAGGAA AAGAAGAAGTGTTACTGCATTTTGT |
| 2413 | literature | Hs.1608 | NM_002947 | 4506586 | replication protein A3 (14kD) (RPA3), mRNA /cds=(30,395) | 1 | ATGGTCAGATTAGATGCAAGAATAAA GCAGTTGTCCGAGTCTAAGTTTCT |
| 2414 | Table 3A | Hs.2280 | NM_002950 | 4506674 | ribophorin I (RPN1), mRNA /cds=(137,1960) | 1 | TGGTATTCTGTTCTGAAGTCTAGGAT ATTTTTCAGCCTATAAAGCCCCCT |
| 2415 | Table 3A | Hs.169476 | NM_002951 | 4506676 | Homo sapiens, glyceraldehyde-3-phosphate dehydrogenase, clone MGC:10926 IMAGE:3628129, mRNA, complete cds /cds=(2306,3313) | 1 | ACTTACCAGATGTTGCTTTTGA AAA GTTGAAATGTGTAATTGTTTTGGA |
| 2416 | Table 3A | Hs.182426 | NM_002952 | 4506718 | ribosomal protein S2 (RPS2), mRNA /cds=(11,892) | 1 | AGCGGACTCAGGCTCCAGCTGTGGC TACAACATAGGGTTTTATACAGA |
| 2417 | Table 3A | Hs.3297 | NM_002954 | 4506712 | ribosomal protein S27a (RPS27A), mRNA /cds=(38,508) | 1 | TTATTGTGGCAAATGTTGTCTGACTTA CTGTTTCAACAAACAGAGACA |
| 2418 | db mining | Hs.20084 | NM_002957 | 10862707 | retinoid X receptor, alpha (RXRA), mRNA /cds=(75,1463) | 1 | TGGACAGTAGCATTAGAATTGTGGAA AAGGAACACGCAAGGGAGAGTG |
| 2419 | Table 3A | Hs.79350 | NM_002958 | 11863158 | RYK receptor-like tyrosine kinase (RYK), mRNA /cds=(103,1917) | 1 | CTGGTAAATTTTGTGCTTATCTTCAAG GCTGGCTTAAGTATAAAATTGTT |
| 2420 | Table 3A | Hs.81256 | NM_002961 | 9845514 | S100 calcium-binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog) (S100A4), transcript variant 1, mRNA /cds=(69,374) | 1 | CCCTGGCTCCTTCAGACACGTGCTTG ATGCTGAGCAAGTTCAATAAAGAT |
| 2421 | Table 3A | Hs.100000 | NM_002964 | 9845519 | S100 calcium-binding protein A8 (calgranulin A) (S100A8), mRNA /cds=(55,339) | 1 | GTTAACTTCCAGGAGTTCCTCATTCT GGTGATAAGATGGGCTGGCAGCC |
| 2422 | Table 3A | Hs.23978 | NM_002967 | 4506778 | scaffold attachment factor B (SAFB), mRNA /cds=(53,2800) | 1 | CCTGTCTCGTGGCAACAAGGCTATGT TCTGTTAGGAGTTACCTTAAACTG |

Table 8

| | | | | | | | |
|------|-----------------|-----------|-----------|---------|---|---|---|
| 2423 | Table 3A | Hs.28491 | NM_002970 | 4506788 | spermidine/spermine N1-acetyltransferase (SAT), mRNA /cds=(165,680) | 1 | AGTCAGATCTTTCTCCTTGAATATCTT TCGATAAACAAACAGGTGGTGTG |
| 2424 | Table 3A | Hs.74592 | NM_002971 | 4506790 | special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's) (SATB1), mRNA /cds=(214,2505) | 1 | TCCTATAATTATTTCTGTAGCACTCCA CACTGATCTTTGGAACTTGCCC |
| 2425 | Table 3A | Hs.112842 | NM_002978 | 4506818 | sodium channel, nonvoltage-gated 1, delta (SCNN1D), mRNA /cds=(0,1916) | 1 | CCACGGGTGATGCTTCCAGGGGTTTC TGGCGGGAGTCTCAGCCGAAGAGAG |
| 2426 | Table 3A | Hs.303649 | NM_002982 | 4506840 | small inducible cytokine A2 (monocyte chemotactic protein 1, homologous to mouse Sig-je) (SCYA2), mRNA /cds=(53,352) | 1 | GAAATTGCTTTTCTCTTGAACCACA GTTCTACCCCTGGGATGTTTTGAG |
| 2427 | Table 3A | Hs.73817 | NM_002983 | 4506842 | small inducible cytokine A3 (homologous to mouse Mip-1a) (SCYA3), mRNA /cds=(83,361) | 1 | ACCAGACTGACAAATGTGTATCGGAT GCTTTTGTTCAGGGCTGTGATCGG |
| 2428 | Table 3A | Hs.75703 | NM_002984 | 4506844 | small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA /cds=(108,386) | 1 | CCACTGTCACTGTTTCTCTGCTGTTG CAAATACATGGATAACACATTTGA |
| 2429 | db mining | Hs.66742 | NM_002987 | 4506828 | small inducible cytokine subfamily A (Cys-Cys), member 17 (SCYA17), mRNA /cds=(52,336) | 1 | CGAAGAAGAGCCACAGTGAGGGAGA TCCCATCCCCTGTCTGAACTGGAG |
| 2430 | cytokine arrays | Hs.57907 | NM_002989 | 4506834 | small inducible cytokine subfamily A (Cys-Cys), member 21 (SCYA21), mRNA /cds=(58,462) | 1 | GACCTGATACGGCTCCCCAGTACAC CCCACCTCTCTCTGTAAATATGAT |
| 2431 | Table 3A | Hs.97203 | NM_002990 | 4506836 | small inducible cytokine subfamily A (Cys-Cys), member 22 (SCYA22), mRNA /cds=(19,300) | 1 | CTCAAGCGTCTCTGGGATCTCCTTCTC CCTCTGTCTGTCTTGCCCTC |
| 2432 | Table 3A | Hs.247838 | NM_002991 | 4506838 | small inducible cytokine subfamily A (Cys-Cys), member 24 (SCYA24), mRNA /cds=(0,359) | 1 | CCTCAAGGGAGGAGTGATCTTCACCA CCAAGAAGGGCCAGCAGTTCTGTG |
| 2433 | Table 3A | Hs.164021 | NM_002993 | 4506850 | small inducible cytokine subfamily B (Cys-X-Cys), member 6 (granulocyte chemotactic protein 2) (SCYB6), mRNA /cds=(63,407) | 1 | TCCTGTGTGTCATGTTGGTTTTGGT ACTTGTATTGTCATTTGGAGAAAC |
| 2434 | Table 3A | Hs.89714 | NM_002994 | 4506848 | small inducible cytokine subfamily B (Cys-X-Cys), member 5 (epithelial-derived neutrophil-activating peptide 78) (SCYB5), mRNA /cds=(106,450) | 1 | TCCTGTGATGGAAATACAACCTGGTAT CTTCACTTTTTAGGAATTGGGAA |
| 2435 | Table 3A | Hs.3195 | NM_002995 | 4506852 | small inducible cytokine subfamily C, member 1 (lymphotactin) (SCYC1), mRNA /cds=(20,364) | 1 | AATTTGCAGTAAACTTTTAATTAATG CTCATCTGGTAACTCAACACCCC |
| 2436 | Table 3A | Hs.3577 | NM_003001 | 9257243 | succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC), nuclear gene encoding mitochondrial protein, mRNA /cds=(26,535) | 1 | GCTGCTTTTGAGGAGAAAATATATAG CTTTGGACACGAGGAAGATCTAGA |
| 2437 | Table 3A | Hs.168289 | NM_003002 | 4506864 | succinate dehydrogenase complex, subunit D, integral membrane protein (SDHD), nuclear gene encoding mitochondrial protein, mRNA /cds=(11,490) | 1 | AAACGCTTGGAGTGCTTCTGAATATA CAGAAGTTCCATTTAAGGGCAAGT |
| 2438 | Table 3A | Hs.75232 | NM_003003 | 4506866 | SEC14 (S. cerevisiae)-like 1 (SEC14L1), mRNA /cds=(303,2450) | 1 | TGCATCGTGTCTTCTACCTTTAGTACCT TGCCACTCTTTTAAACGCTGCT |
| 2439 | Table 3A | Hs.73800 | NM_003005 | 6031196 | selectin P (granule membrane protein 140kD, antigen CD62) (SELP), mRNA /cds=(95,2587) | 1 | GACCTTCCTGCCACCAGTCACTGTCC CTCAAATGACCCAAAGACCAATAT |
| 2440 | Table 3A | Hs.79283 | NM_003006 | 6031197 | selectin P ligand (SELPLG), mRNA /cds=(59,1267) | 1 | AGACCTTTCTTTGGGACTGTGTGGAC CAAGGAGCTTCCATCTAGTGACAA |
| 2441 | Table 3A | Hs.75217 | NM_003010 | 4506888 | mitogen-activated protein kinase kinase 4 (MAP2K4), mRNA /cds=(9,1208) | 1 | GCTCAGTAACATAACTGCTTCTTGGA GCTTTGGAATATTTATCCTGTAT |
| 2442 | Table 3A | Hs.145279 | NM_003011 | 4506890 | SET translocation (myeloid leukemia-associated) (SET), mRNA /cds=(3,836) | 1 | TTCTGCACAGGTCTCTGTTTAGTAAA TACATCACTGTATACCGATCAGGA |
| 2443 | Table 3A | Hs.73965 | NM_003016 | 4506898 | splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(155,820) | 1 | CGGGCCTTGCAATAAATAACGGAGC ATACAGTGAGCACATCTAGCTGAT |
| 2444 | Table 3A | Hs.14368 | NM_003022 | 4506924 | SH3 domain binding glutamic acid-rich protein like (SH3BGR1), mRNA /cds=(78,422) | 1 | AGAGATGCCTTTGTTGATGAGATTC AAACTTGATGCTATGCTTTAAAT |
| 2445 | Table 3A | Hs.2554 | NM_003032 | 4506948 | sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) (SIAT1), mRNA /cds=(310,1530) | 1 | AGTCCCATTCTCTCTTTCAATACCTA CCCCAAATCTTCTCCTAACCT |
| 2446 | Table 3A | Hs.323032 | NM_003035 | 4506958 | TAL1 (SCL) interrupting locus (SIL), mRNA /cds=(380,4243) | 1 | TGTCACACTGGCTATCAAAGAATAAG AAAATTATTGAGTATGAGTGTGTT |
| 2447 | Table 3A | Hs.32970 | NM_003037 | 4506968 | signaling lymphocytic activation molecule (SLAM), mRNA /cds=(133,1140) | 1 | GCAAAACCCAGAAGCTAAAAAGTCAA TAAACAGAAAGAATGATTTTGAGA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|---|
| 2448 | Table 3A | Hs.198296 | NM_003070 | 4507068 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), mRNA /cds=(297,5015) | 1 | TTGTGACCAAAATGGGCCTCAAAGATT CAGATTGAAACAAACAAAAGCTT |
| 2449 | Table 3A | Hs.236030 | NM_003075 | 4507080 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2 (SMARCC2), mRNA /cds=(22,3663) | 1 | AAGGTTCTATTAACCACTTCTAAGGG TACACCTCCCTCCAACTACTGCA |
| 2450 | Table 3A | Hs.79335 | NM_003076 | 4507082 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1 (SMARCD1), mRNA /cds=(265,1572) | 1 | GTTGTATCACCCCGAGTTAGCATAT CCCAGGCTCGCAGACTCAACACAG |
| 2451 | Table 3A | Hs.174051 | NM_003089 | 4507118 | small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen) (SNRP70), mRNA /cds=(680,2524) | 1 | CCACTTGAGTTTGTCTCCAAGGGTA GGTGTCTCATTTGTTCTGGCCCCCT |
| 2452 | Table 3A | Hs.31121 | NM_003098 | 4507136 | syntrophin, alpha 1 (dystrophin-associated protein A1, 59kD, acidic component) (SNTA1), mRNA /cds=(37,1554) | 1 | TCCTGTCTCTCTCTCTTACTCTTG GATAAATAAACAGCCTGTGAGCAC |
| 2453 | Table 3A | Hs.11183 | NM_003100 | 4507140 | sorting nexin 2 (SNX2), mRNA /cds=(29,1588) | 1 | CCTGACCCTCTTTGAATTAAGTGGAC TGTGGCATGACATTTCTGCAATACT |
| 2454 | Table 3A | Hs.92909 | NM_003103 | 4507152 | NREBP mRNA, complete cds /cds=(49,7209) | 1 | TCTAAACCTTTATTTTCAAAGCTTAAG GCCCAAATACAACTTCTCTGGA |
| 2455 | Table 3A | Hs.278571 | NM_003105 | 6325473 | sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA /cds=(197,6841) | 1 | CATGGTGATAGCCTGAAAGAGCTTTC CTCACTAGAAACCAATGGTGTA |
| 2456 | Table 3A | Hs.21293 | NM_003115 | 4507758 | UDP-N-acetylglucosamine pyrophosphorylase 1 (UAP1), mRNA /cds=(0,1517) | 1 | GGAGAAGGATTAGAAAGTTATGTGGC AGATAAAGAATCCATGCACCTCT |
| 2457 | Table 3A | Hs.71465 | NM_003129 | 6806899 | squalene epoxidase (SQLE), mRNA /cds=(214,1938) | 1 | ACAGTTTTTCTTTGAATTTAGTATTT GAGATGAGTTGTTGGGACATGCA |
| 2458 | Table 3A | Hs.300741 | NM_003130 | 4507206 | sorcin (SRI), mRNA /cds=(12,608) | 1 | GATCTAGTCTGTTACACCATTTAGAA CTTTCCTCAGCCATTATCAGTCAT |
| 2459 | Table 3A | Hs.75975 | NM_003133 | 4507216 | signal recognition particle 9kD (SRP9), mRNA /cds=(106,366) | 1 | AGCATGGTAAGTTCCTTAGCTATAT GAATTTTGGCATGTTTCAGAGAGA |
| 2460 | Table 3A | Hs.75761 | NM_003137 | 4507218 | SFRS protein kinase 1 (SRPK1), mRNA /cds=(108,2075) | 1 | ACATTTTATTTCTTTCTACTGAGGGCA TTGTCTGTTTTCTTTGTAATGC |
| 2461 | Table 3A | Hs.83715 | NM_003142 | 10835066 | Sjogren syndrome antigen B (autoantigen La) (SSB), mRNA /cds=(72,1298) | 1 | AAAAGGAAACCGAATTAGGTCCTACT TCAATGTCCACCTGTGAGAAAGGA |
| 2462 | Table 3A | Hs.250773 | NM_003144 | 6552340 | signal sequence receptor, alpha (translocon-associated protein alpha) (SSR1), mRNA /cds=(111,971) | 1 | CCTATCCCCGGATGTGTGAGAATAAT GTGTTCATAAAGCATGGATCTCGT |
| 2463 | Table 3A | Hs.74564 | NM_003145 | 6552341 | signal sequence receptor, beta (translocon-associated protein beta) (SSR2), mRNA /cds=(50,601) | 1 | CCAGTGCTCTATTCTGGGTTAGAGAAG TGCTTACTAAGGGGTTTTCTAATA |
| 2464 | Table 3A | Hs.321677 | NM_003150 | 4507252 | signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3), mRNA /cds=(220,2532) | 1 | GGGTGATCTGCTTTTATCTAAATGCA AATAAGGATGTGTTCTCTGAGACC |
| 2465 | Table 3A | Hs.80642 | NM_003151 | 4507254 | signal transducer and activator of transcription 4 (STAT4), mRNA /cds=(81,2327) | 1 | GGGAGTGTGTGACTGAAATGCTTGA AACCAAAGCTTCAGATAAAGCTTGC |
| 2466 | literature | Hs.251664 | NM_003153 | 4507258 | DNA for insulin-like growth factor II (IGF-2); exon 7 and additional ORF /cds=(0,233) | 1 | GAGCCAACTCCACTCCTTCTTTCTAT CATTCCTCGCCACCTCCTCCA |
| 2467 | Table 3A | Hs.70186 | NM_003169 | 4507312 | suppressor of Ty (S.cerevisiae) 5 homolog (SUPT5H), mRNA /cds=(48,3311) | 1 | CTTCCTGTACCTCCTCCCCACAGCTT GCTTTTGTGTACCGTCTTTCAAT |
| 2468 | Table 3A | Hs.12303 | NM_003170 | 11321572 | suppressor of Ty (S.cerevisiae) 6 homolog (SUPT6H), mRNA /cds=(1164,5975) | 1 | GCTGCTGCCACCGCTTCTGCCTGT CATTTGAATAAACAGTGTTCATT |
| 2469 | Table 3A | Hs.106469 | NM_003171 | 4507314 | suppressor of var1 (S.cerevisiae) 3-like 1 (SUPV3L1), mRNA /cds=(0,2360) | 1 | TGGGACTCATCCAAAGGGACGAGA AGAAAGAAGAAGAACCTGATTCGG |
| 2470 | Table 3A | Hs.3196 | NM_003172 | 4507318 | surfeit 1 (SURF1), mRNA /cds=(14,916) | 1 | TCAAGACTGCCTTTATGCTGGATCAT GTGCTACTGGTATAAAGTTCTGGC |
| 2471 | Table 3A | Hs.37936 | NM_003173 | 4507320 | suppressor of variegation 3-9 (Drosophila) homolog 1 (SUV39H1), mRNA /cds=(45,1283) | 1 | GTACACCCCTCAACCCTATGCAGCCT GGAGTGGGCATCAATAAATGAAC |
| 2472 | literature | Hs.74101 | NM_003177 | 4507328 | spleen tyrosine kinase (SYK), mRNA /cds=(148,1986) | 1 | CCATGAGACTGATCCCTGGCCACTGA AAAGCTTTCTGACAATAAAAAATG |
| 2473 | Table 3A | Hs.32675 | NM_003193 | 6006029 | tubulin-specific chaperone e (TBCE), mRNA /cds=(80,1663) | 1 | TTGGGAAGTGACCATTTCTAGGCTTA TACATAATAGCAATAATAAAGGCT |
| 2474 | Table 3A | Hs.171626 | NM_003197 | 6006030 | transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L), mRNA /cds=(101,592) | 1 | ATGTGGTAAACCCAGAAAGCATCCA TCATGAATGCAAGATACTTTCAAT |
| 2475 | Table 3A | Hs.75133 | NM_003201 | 4507400 | transcription factor 6-like 1 (mitochondrial transcription factor 1-like) (TCF6L1), mRNA /cds=(132,872) | 1 | TTCACATTGTATTTCAGAGTTGATGGTT GTACATATAAGTGATTGCTGGTT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|---|
| 2476 | Table 3A | Hs.169294 | NM_003202 | 4507402 | transcription factor 7 (T-cell specific, HMG-box) (TCF7), mRNA /cds=(79,885) | 1 | GCCACTGGTTTCTCAGAATCCAAAGA TCACATATTCTAGTGTAACTGCG |
| 2477 | Table 3A | Hs.74637 | NM_003217 | 4507432 | testis enhanced gene transcript (TEGT), mRNA /cds=(40,753) | 1 | CTGTGCTTTTTGCTTGGGATAATGGA GTTTTTCTTTAGAAACAGTGCCAA |
| 2478 | Table 3A | Hs.77356 | NM_003234 | 4507456 | transferrin receptor (p90, CD71) (TFRC), mRNA /cds=(263,2545) | 1 | TATCAGACTAGTGACAAGCTCCTGGT CTTGAGATGTCTTCTCGTTAAGGA |
| 2479 | Table 3A | Hs.79059 | NM_003243 | 4507470 | transforming growth factor, beta receptor III (betaglycan, 300kD) (TGFB3), mRNA /cds=(348,2897) | 1 | AGGGCTTGAGGTGAATTTTCATTAAT GGAATAATATGATGCCACTTTGCA |
| 2480 | Table 3A | Hs.87409 | NM_003246 | 4507484 | thrombospondin 1 (THBS1), mRNA /cds=(111,3623) | 1 | TTGACCTCCCATTTTTACTATTTGCCA ATACCTTTTTCTAGGAATGTGCT |
| 2481 | Table 3A | Hs.63668 | NM_003264 | 4507528 | toll-like receptor 2 (TLR2), mRNA /cds=(129,2483) | 1 | AGCGGGAAGGATTTTGGGTAATCTG AGAGCTGCCATAAAGTCTTAGGTT |
| 2482 | Table 3A | Hs.159239 | NM_003266 | 4507532 | toll-like receptor 4 (TLR4), mRNA /cds=(284,2683) | 1 | TGATGTTTGATGGACCTATGAATCTA TTTAGGGAGACACAGATGGCTGGG |
| 2483 | Table 3A | Hs.31130 | NM_003273 | 4507546 | transmembrane 7 superfamily member 2 (TM7SF2), mRNA /cds=(254,2023) | 1 | AGCCCTGAGGATGAACAACCTCAGA GAAGAGGTGGTTTAGAGCAAGGAAA |
| 2484 | Table 3A | Hs.1117 | NM_003291 | 4507656 | tripeptidyl peptidase II (TPP2), mRNA /cds=(23,3772) | 1 | AATAAATTTGCCAAACCAAGATCACA GTACACCATATGCACTCTGGTACC |
| 2485 | Table 3A | Hs.326456 | NM_003295 | 4507668 | hypothetical protein FLJ20030 (FLJ20030), mRNA /cds=(1,1239) | 1 | TTTGGAGTGGAGGCATTGTTTTAAG AAAAACATGTCTATGTAGTTGTCT |
| 2486 | Table 3A | Hs.5542 | NM_003315 | 4507712 | tetratricopeptide repeat domain 2 (TTC2), mRNA /cds=(26,1480) | 1 | GCGGGGTGGACAGGGAGGCAGCTT GTGAATTTTGTCTTACTGTTTAACT |
| 2487 | Table 3A | Hs.178551 | NM_003316 | 10835036 | ribosomal protein L8 (RPL8), mRNA /cds=(43,816) | 1 | AACCTTCAGATACTTGTGAACATGCC TATATTTGTCCAACTGTCCAGA |
| 2488 | Table 3A | Hs.274401 | NM_003321 | 4507732 | mRNA; cDNA DKFZp434P086 (from clone DKFZp434P086); partial cds /cds=(798,1574) | 1 | GAAGCTTGAGGCTGGCTGGCTGGGG AGGTCAGTAACTTTGAATAGTAAG |
| 2489 | literature | Hs.129780 | NM_003327 | 4507578 | tumor necrosis factor receptor superfamily, member 4 (TNFRSF4), mRNA /cds=(5,838) | 1 | AAGATGTACCCTTCAGGTGAACCTGG TATCAGACCCACAGTACTTGCTGT |
| 2490 | Table 3A | Hs.29877 | NM_003328 | 4507742 | TXK tyrosine kinase (TXK), mRNA /cds=(86,1669) | 1 | AGCAAGATAGCCAAATGTGACATCAA GCTCCATTGTTTCGGAAATCCAGG |
| 2491 | Table 3A | Hs.13046 | NM_003330 | 4507746 | thioredoxin reductase 1 (TXNRD1), mRNA /cds=(439,1932) | 1 | AGTGGAATGTTCTATCCCCACAAGAA GGATTATATCTTATGAGCTTGCT |
| 2492 | Table 3A | Hs.5308 | NM_003333 | 4507760 | ubiquitin A-52 residue ribosomal protein fusion product 1 (UBA52), mRNA /cds=(37,423) | 1 | CCCGTGGCCCTGGAGCCTCAATAAA GTGTCCCTTTCATTGACTGGAGCAG |
| 2493 | Table 3A | Hs.80612 | NM_003336 | 4507768 | ubiquitin-conjugating enzyme E2A (RAD6 homolog) (UBE2A), mRNA /cds=(120,578) | 1 | TTATGCATTTATCACTTCCAAATCTAA CTTTGCACAAGTAACCCATGTAA |
| 2494 | Table 3A | Hs.811 | NM_003337 | 4507770 | ubiquitin-conjugating enzyme E2B (RAD6 homolog) (UBE2B), mRNA /cds=(421,879) | 1 | TCCGCACTATATAATTGCGACACATT AATTAGGGTTTATGTACCATACAA |
| 2495 | literature | Hs.75355 | NM_003348 | 4507792 | ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13) (UBE2N), mRNA /cds=(63,521) | 1 | GCTTGTGACCATTTTGTATGGCTTGT CTGGAACCTCTGTAAATCTTATG |
| 2496 | Table 3A | Hs.283667 | NM_003349 | 12025659 | arginyl aminopeptidase (aminopeptidase B) (RNPEP), mRNA /cds=(9,1982) | 1 | TGCTGATTATGCAAAGGGCTGGCAT TCTGATGCTTTTCAGGTTTAATCC |
| 2497 | literature | Hs.79300 | NM_003350 | 12025664 | ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA /cds=(21,458) | 1 | TGCATTCTGGCAGTCTTTTAGGATT ATAGGTTGCCAAATATCCAAATAT |
| 2498 | Table 3A | Hs.80658 | NM_003355 | 13259540 | uncoupling protein 2 (mitochondrial, proton carrier) (UCP2), nuclear gene encoding mitochondrial protein, mRNA /cds=(380,1309) | 1 | CCGACAGCCCAGCCTAGCCCACTTG TCATCCATAAAGCAAGCTCAACCTT |
| 2499 | literature | Hs.78853 | NM_003362 | 6224978 | uracil-DNA glycosylase (UNG), mRNA /cds=(106,1020) | 1 | TTTGCTGTTAGTCGGGTTAGAGTTGG CTCTACGCGAGGTTTGTAAATAAA |
| 2500 | Table 3A | Hs.77500 | NM_003363 | 4507852 | ubiquitin specific protease 4 (proto-oncogene) (USP4), mRNA /cds=(3,2894) | 1 | CAGACTGCTAGTGTCTGTCTAAAAA CCAGACAAGGAAATACCTTCTTT |
| 2501 | literature | Hs.173554 | NM_003366 | 4507842 | ubiquinol-cytochrome c reductase core protein II (UQCRC2), mRNA /cds=(53,1414) | 1 | TTTTCCAGTGAGGTAATAAAGGCAT AAATGCAGGTAATTATCCCAGCT |
| 2502 | Table 3A | Hs.93649 | NM_003367 | 4507846 | upstream transcription factor 2, c-fos interacting (USF2), mRNA /cds=(0,1040) | 1 | CCGGCACTTCTAGTGGTCTCACCTGG AGGCAAGAGGGAGGGTACAGAGCC |
| 2503 | Table 3A | Hs.284192 | NM_003374 | 4507878 | clone HQ0072 /cds=UNKNOWN | 1 | TTTAGAGTCTTCCATTTTGTGGAATT AGATCTCCCTTCAAATGCTGT |
| 2504 | Table 3A | Hs.155191 | NM_003379 | 9257254 | villin 2 (ezrin) (VIL2), mRNA /cds=(117,1877) | 1 | TTCTCCTTCACAGCTAAGATGCCATG TGCAGGTGGATTCCATGCCGAGA |
| 2505 | Table 3A | Hs.297753 | NM_003380 | 4507894 | vimentin (VIM), mRNA /cds=(122,1522) | 1 | TTTCCAGCAAGTATCCAACCACTTG GTTCTGCTTCAATAAATCTTTGGA |
| 2506 | Table 3A | Hs.24143 | NM_003387 | 8400739 | Wiskott-Aldrich syndrome protein interacting protein (WASPIP), mRNA /cds=(108,1619) | 1 | ATGACTTGCATCCAGCTTTCCACCA ACCAAATCAAACATCACTGCTT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|---|
| 2507 | literature | Hs.150930 | NM_003401 | 12408643 | X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), transcript variant 3, mRNA /cds=(175,1179) | 1 | TGTATGAGACTTTTTGTTGCAAAGGA CACATTTATCATATTCATTACACAC |
| 2508 | Table 3A | Hs.279920 | NM_003404 | 4507948 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide (YWHAB), mRNA /cds=(372,1112) | 1 | TGATCTGTCCAGTGTCACTCTGTACC CTCAACATATATCCCTTGTGCGAT |
| 2509 | Table 3A | Hs.75544 | NM_003405 | 4507950 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide (YWHAH), mRNA /cds=(200,940) | 1 | AATTCACCCCTCCACCTCTTTCTTC AATTAATGAAAAGCGTTAAGGGA |
| 2510 | Table 3A | Hs.75103 | NM_003406 | 4507952 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YVHAZ), mRNA /cds=(84,821) | 1 | CTCAGTACTTTGCGAAAAACACCAAA CAAAAATGCCATTTTAAAAAAGGT |
| 2511 | Table 3A | Hs.55481 | NM_003447 | 4508000 | zinc finger protein 165 (ZNF165), mRNA /cds=(567,2024) | 1 | AGCCTTCAGTCAGAGCTCAAACCTTA GTCAACACCAGAGAATTCACATGA |
| 2512 | Table 3A | Hs.88219 | NM_003454 | 4508012 | zinc finger protein 200 (ZNF200), mRNA /cds=(239,1423) | 1 | AACCCCTCTAGAATACCTGTTTAAGT CTTGAGTGTGAAAGGAATGTTT |
| 2513 | Table 3A | Hs.62112 | NM_003457 | 4508016 | zinc finger protein 207 (ZNF207), mRNA /cds=(202,1638) | 1 | CCACTGCCTGAAAGGTTTGTACAGAT GCATGCCACATGATGATGCCACAT |
| 2514 | Table 3A | Hs.89414 | NM_003467 | 4503174 | chemokine (C-X-C motif), receptor 4 (fusin) (CXCR4), mRNA /cds=(88,1146) | 1 | TCAGGAGTGGGTGATTTCAGCACCT ACAGTGACAGTCTTGATTAAGT |
| 2515 | Table 3A | Hs.78683 | NM_003470 | 4507856 | ubiquitin specific protease 7 (herpes virus-associated) (USP7), mRNA /cds=(199,3507) | 1 | CCTTCAGTTATACTTTCAATGACCTTT TGTGCATCTGTTAAGGCAAAACA |
| 2516 | Table 3A | Hs.110713 | NM_003472 | 4503248 | DEK oncogene (DNA binding) (DEK), mRNA /cds=(33,1160) | 1 | AAGTGAACAAAATAAGCAACTAAATG AGACCTAATAATTGGCCTTCGATT |
| 2517 | Table 3A | Hs.155017 | NM_003489 | 4505454 | nuclear receptor interacting protein 1 (NRIP1), mRNA /cds=(287,3763) | 1 | CACAACCAAAATTTGATGCGATCTGCT CAGTAATATAATTTGCCATTTTAA |
| 2518 | Table 3A | Hs.28777 | NM_003512 | 4504244 | H2A histone family, member L (H2AFL), mRNA /cds=(97,489) | 1 | ACATTGTGAATAGAAACAGATTTCCCA AATTCAGCCTGGCATGAGGTAAT |
| 2519 | literature | Hs.2178 | NM_003528 | 4504276 | H2B histone family, member Q (H2BFQ), mRNA /cds=(42,422) | 1 | CAGACTGAATAGATCTTAACTGTCTC CTACATGTGTGTTTTCAAATGTGT |
| 2520 | Table 3A | Hs.278571 | NM_003563 | 4507182 | sortilin-related receptor, L (DLR class) A repeats-containing (SORL1), mRNA /cds=(197,6841) | 1 | GATATCCCAGCGGTGGTACTTCGGA GACACCTGTCTGCATCTGACTGAGC |
| 2521 | Table 3A | Hs.2864 | NM_003566 | 4503468 | early endosome antigen 1, 162kD (EEA1), mRNA /cds=(136,4368) | 1 | ACACTTTCCTCTGCCTTTTTCTCTTAT ATGTGGGTTCATGGTTCAGTTTCG |
| 2522 | Table 3A | Hs.9006 | NM_003574 | 4507866 | VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA), mRNA /cds=(0,728) | 1 | AGATAATGTCACCAGTCCTCTTCTCT CACTTCTTGTGTGAATTGCAGCCA |
| 2523 | literature | Hs.66718 | NM_003579 | 4506396 | RAD54 (S.cerevisiae)-like (RAD54L), mRNA /cds=(100,2343) | 1 | CCGGCACACAGGGACTAGGTCTAGT GAGAACATCAGGAGCAGCCAGGGAT |
| 2524 | Table 3A | Hs.78687 | NM_003580 | 4505464 | neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA /cds=(12,2765) | 1 | CATCGGGTTTTGGGTGTGTGTTTTCA TAGCGTGTTACTTTCTATAATGC |
| 2525 | Table 3A | Hs.14611 | NM_003584 | 4503414 | dual specificity phosphatase 11 (RNA/RNP complex 1-interacting) (DUSP11), mRNA /cds=(124,1116) | 1 | ATGTAATTTCTTTCTGACTAGACTTGTG ATATGCGTGTGTTATGTACAGA |
| 2526 | Table 3A | Hs.155976 | NM_003588 | 13270466 | cullin 4B (CUL4B), mRNA /cds=(78,2231) | 1 | GTTCTGTATCAGTTGAATTTTTGTGCT CTTTCCCTGTGTACGTGGTGGT |
| 2527 | Table 3A | Hs.183874 | NM_003589 | 11140810 | cullin 4A (CUL4A), mRNA /cds=(160,2139) | 1 | CATTATGAGTTCATGATATGTGGT CTAAGAAAGACCAACAGATTTCT |
| 2528 | Table 3A | Hs.82919 | NM_003591 | 4503162 | cullin 2 (CUL2), mRNA /cds=(146,2383) | 1 | AAATCGGTTGGGTACCATGCTTTTTTC TCCCTTCACGTTTGCAGTTGATG |
| 2529 | Table 3A | Hs.14541 | NM_003592 | 4503160 | cullin 1 (CUL1), mRNA /cds=(124,2382) | 1 | GTTTCATGTTGGAAAGAATGAAACAA CTTCAAGTTCATAGGCAGCCAGCC |
| 2530 | Table 3A | Hs.9456 | NM_003601 | 4507074 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 (SMARCA5), mRNA /cds=(202,3360) | 1 | TGTCATTTAAAGACATCAGGTTTCATCT GTTTACTGAGCTAGAAACATAGT |
| 2531 | Table 3A | Hs.100293 | NM_003605 | 6006036 | O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) (OGT), mRNA /cds=(2039,4801) | 1 | ATCTGGTGCCAAATGAAGATTTTTAG GAGTGATTACTAATTATCAAGGGC |
| 2532 | Table 3A | Hs.131924 | NM_003608 | 4507420 | G protein-coupled receptor 65 (GPR65), mRNA /cds=(0,1013) | 1 | TTCTGCACTGGGAGGTGTAATACATC ACAAAGACAAAGAAAACGCATACT |
| 2533 | Table 3A | Hs.104925 | NM_003633 | 4505460 | ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA /cds=(399,2168) | 1 | AGTTGAAGGAAAATGTTTCATGTTTCAT ATGTACTTGTGTTGCTATGACTACA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|---|
| 2534 | db mining | Hs.323879 | NM_003639 | 4504630 | cDNA FLJ20586 fis, clone KAT09466, highly similar to AF091453 NEMO protein /cds=UNKNOWN | 1 | CACTGGGGAAGTCAAGAATGGGGCC TGGGGCTCTCAGGGAGAACTGCTTC |
| 2535 | Table 3A | Hs.146360 | NM_003641 | 4504580 | interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA /cds=(110,487) | 1 | CCCTAGATACAGCAGTTTATACCCAC ACACCTGTCTACAGTGTCATTCAA |
| 2536 | Table 3A | Hs.167218 | NM_003658 | 6633797 | BarH-like homeobox 2 (BARX2), mRNA /cds=(96,935) | 1 | GAAAGTGCTTAGCTCTCTCCCTCCTG ACCTCTGGGCAGCCAGTCATCAAA |
| 2537 | Table 3A | Hs.155172 | NM_003664 | 4501974 | adaptor-related protein complex 3, beta 1 subunit (AP3B1), mRNA /cds=(53,3334) | 1 | ATCATGTATGCAACTTTCCCCCTTT TTGCTTTGCTAACCAAGAGCAT |
| 2538 | Table 3A | Hs.239307 | NM_003680 | 4507946 | tyrosyl-tRNA synthetase (YARS), mRNA /cds=(0,1586) | 1 | CTGCTGTCTCTTCAGTCTGCTCCATC CATCACCCATTACCATCTCTCA |
| 2539 | Table 3A | Hs.82548 | NM_003682 | 4505070 | MAP-kinase activating death domain (MADD), mRNA /cds=(325,5091) | 1 | TATAGAAAATGTACAGTTGTGTGAAT GTGAAATAAATGTCCTCAACTCCC |
| 2540 | literature | Hs.47504 | NM_003686 | 4504368 | exonuclease 1 (EXO1), mRNA /cds=(218,2629) | 1 | GGCCGTGTTCAAAGAGCAATATTCCA GTAAATGCAGACTGCTGCAAGCT |
| 2541 | Table 3A | Hs.18571 | NM_003690 | 4505580 | protein kinase, interferon-inducible double stranded RNA dependent activator (PRKRA), mRNA /cds=(96,1037) | 1 | AGCTGCTGACTTGACTGTCATCCTGT TCTTGTTAGCCATTGTGAATAAGA |
| 2542 | db mining | Hs.296776 | NM_003721 | 4506498 | regulatory factor X-associated ankyrin-containing protein (RFXANK), mRNA /cds=(417,1199) | 1 | GAACTGACTTCAAAGGCAGCTTCTGG ACAGGTGGTGGGAGGGGACCCCTTC |
| 2543 | Table 3A | Hs.118633 | NM_003733 | 11321576 | 2'-5'oligoadenylate synthetase-like (OASL), mRNA /cds=(6,1550) | 1 | GGAGAGGCTCTGTTTCCAGCCAGTTA GTTTTCTCTGGGAGACTTCTCTGT |
| 2544 | Table 3A | Hs.5120 | NM_003746 | 4505812 | dynein, cytoplasmic, light polypeptide (PIN), mRNA /cds=(93,362) | 1 | TTTCTATTCCATACTTCTGCCACGTT GTTTTCTCTCAAATCCATTCTCT |
| 2545 | Table 3A | Hs.57783 | NM_003751 | 4503526 | eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD) (EIF3S9), mRNA /cds=(53,2674) | 1 | CCTGTACACAGCCGAGCAGCATTTCC GTTGAAGGACTTGCATCCCCATTG |
| 2546 | Table 3A | Hs.57973 | NM_003753 | 4503522 | caspase recruitment domain protein 10 mRNA, complete cds /cds=(40,3138) | 1 | TTGATGCTTAGTGGAATGTGTGTCTA ACTTGCTCTCTGACATTAGCAGA |
| 2547 | Table 3A | Hs.58189 | NM_003756 | 4503514 | eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD) (EIF3S3), mRNA /cds=(5,1063) | 1 | AAGAAGTTAACATGAACTCTTGAAGT CACACCAGGGCAACTCTTGAAGA |
| 2548 | Table 3A | Hs.192023 | NM_003757 | 4503512 | eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD) (EIF3S2), mRNA /cds=(17,994) | 1 | GGTGGATCTCCAACCAGGCCAGAGA AGATTCTCAGAGAAGGTTTTGAACT |
| 2549 | Table 3A | Hs.172684 | NM_003761 | 14043025 | vesicle-associated membrane protein 8 (endobrevin) (VAMP8), mRNA /cds=(53,355) | 1 | GGCTGGGAAACTGTTGGTGGCCAGT GGGTAATAAAGACCTTTCAGTATCC |
| 2550 | Table 3A | Hs.77608 | NM_003769 | 4506902 | splicing factor, arginine/serine-rich 9 (SFRS9), mRNA /cds=(52,717) | 1 | GGTTCGCTCTACTATGGAGATCAACA GTTACTGTGACTGAGTCGGCCCAT |
| 2551 | db mining | Hs.89862 | NM_003789 | 13378136 | TNFRSF1A-associated via death domain (TRADD), mRNA /cds=(66,1004) | 1 | GCTCACACTCAGCGTGGGACCCCGA ATGTTAAGCAATGATAATAAAGTAT |
| 2552 | db mining | Hs.251216 | NM_003790 | 4507568 | hypothetical protein DKFZp434A196 (DKFZP434A196), mRNA /cds=(168,2732) | 1 | CTGCTCGCCCTATCGCTCCAGCCAA GGCGAAGAAGCAGCAACGAATGTC |
| 2553 | Table 3A | Hs.75890 | NM_003791 | 4506774 | membrane-bound transcription factor protease, site 1 (MBTPS1), mRNA /cds=(496,3654) | 1 | ACCTGCCACCATGTTTTGTAATTTGA GGTCTTGATTTACCAATTGTCGGT |
| 2554 | Table 3A | Hs.7943 | NM_003796 | 4506542 | RPB5-mediating protein (RMP), mRNA /cds=(465,1991) | 1 | AACGAAAGGAAGTTCTGTTGGAAGCA TCTGAAGAACTGGAAGAGGGTT |
| 2555 | db mining | Hs.155566 | NM_003805 | 4503030 | CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), mRNA /cds=(37,636) | 1 | ACATTACCTGAATGTTGTCTGAGGA CTGAAGTGTGGACTTTACTATTCA |
| 2556 | Table 3A | Hs.87247 | NM_003806 | 4504492 | harakiri, BCL2-interacting protein (contains only BH3 domain) (HRK), mRNA /cds=(120,395) | 1 | AAATCCAGCTGCAGAAACAGACACCC CAATGCTATTTACATACAGCTCTA |
| 2557 | literature | Hs.54673 | NM_003808 | 4507598 | tumor necrosis factor (ligand) superfamily, member 13 (TNFSF13), mRNA /cds=(281,1033) | 1 | CCCCGTTCTCACTTTTCCCTTTTCAT TCCCACCCCTAGACTTTGATTT |
| 2558 | literature | Hs.26401 | NM_003809 | 4507596 | tumor necrosis factor (ligand) superfamily, member 12 (TNFSF12), mRNA /cds=(17,766) | 1 | TTCAGGCACTAAGAGGGGCTGGACC TGGCGGCAGGAAGCCAAAGAGACTG |
| 2559 | literature | Hs.83429 | NM_003810 | 4507592 | tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10), mRNA /cds=(87,932) | 1 | CGCAACAATCCATCTCTCAAGTAGTG TATCACAGTAGTGCCTCCAGGTT |
| 2560 | literature | Hs.1524 | NM_003811 | 4507608 | tumor necrosis factor (ligand) superfamily, member 9 (TNFSF9), mRNA /cds=(3,767) | 1 | CCCAGGCTAGGGGGCTATAGAAACA TCTAGAAATAGACTGAAAGAAAATC |
| 2561 | Table 3A | Hs.2442 | NM_003816 | 4501914 | a disintegrin and metalloproteinase domain 9 (meltrin gamma) (ADAM9), mRNA /cds=(78,2537) | 1 | ACCTACAAAAAGTTACTGTGGTATC TATGAGTTATCATCTTAGCTGTGT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|--|
| 2562 | literature | Hs.279899 | NM_003820 | 4507570 | tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator) (TNFRSF14), mRNA /cds=(293,1144) | 1 | TGGTGTTTAGTGGATACCACATCGGA AGTGATTTTCTAAATTGGATTGTA |
| 2563 | db mining | Hs.86131 | NM_003824 | 4505228 | Fas (TNFRSF6)-associated via death domain (FADD), mRNA /cds=(129,755) | 1 | TCACTATCTTTCTGATAACAGAATTGC CAAGGCAGCGGGATCTCGTATCT |
| 2564 | literature | Hs.114676 | NM_003839 | 4507564 | tumor necrosis factor receptor superfamily, member 11a, activator of NFkB (TNFRSF11A), mRNA /cds=(38,1888) | 1 | GAAAAAGATGGAGAAAATGAACAGGAC ATGGGGCTCCTGGAAAGAAAGGGC |
| 2565 | literature | Hs.129844 | NM_003840 | 4507562 | tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain (TNFRSF10D), mRNA /cds=(82,1242) | 1 | GTGGTTTTAGGATGTCATTCTTTGCA GTTCTTCATCATGAGACAAGTCTT |
| 2566 | literature | Hs.119684 | NM_003841 | 10835042 | tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain (TNFRSF10C), mRNA /cds=(29,928) | 1 | AAGGGTGAGGATGAGAAGTGGTCAC GGGATTTATTACGCTTGGTCAGAG |
| 2567 | literature | Hs.249190 | NM_003844 | 4507558 | tumor necrosis factor receptor superfamily, member 10a (TNFRSF10A), mRNA /cds=(0,1406) | 1 | GAGAAGATTCAGGACCTCTTGGTGGA CTCTGGAAAGTTCATCTACTTAGA |
| 2568 | Table 3A | Hs.7043 | NM_003849 | 11321580 | succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA /cds=(31,1032) | 1 | AGTACAACGTGAAGCCAAAACAAGGT GGAAGATGTCCTGAATTAAGACGT |
| 2569 | Table 3A | Hs.5085 | NM_003859 | 4503362 | dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit (DPM1), mRNA /cds=(0,782) | 1 | GTTGCTGGCCTAATGAGCAATGTTCT CAATTTTCGTTTTTCATTTTGCTGT |
| 2570 | Table 3A | Hs.153687 | NM_003866 | 4504706 | inositol polyphosphate-4-phosphatase, type II, 105kD (INPP4B), mRNA /cds=(121,2895) | 1 | ACAGACCTCCAGAGGGGACTTATGG AAAAGCTGACACCTAAGTTTACCAA |
| 2571 | Table 3A | Hs.1742 | NM_003870 | 4506786 | IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA /cds=(467,5440) | 1 | TGAATTTACTTCCTCCCAAGAGTTTG GACTGCCCGTCAGATTGTTTCTGC |
| 2572 | Table 3A | Hs.279789 | NM_003883 | 13128861 | histone deacetylase 3 (HDAC3), mRNA /cds=(55,1341) | 1 | TGGCTTTATGTCCATTTTACCAGTGT TTTATCCAATAAACTAAGTCGGT |
| 2573 | Table 3A | Hs.76095 | NM_003897 | 4503328 | immediate early response 3 (IER3), mRNA /cds=(11,481) | 1 | GCTGTCACGGAGCGACTGTCGAGAT CGCCTAGTATGTTCTGTGAACACAA |
| 2574 | Table 3A | Hs.7165 | NM_003904 | 4508020 | zinc finger protein 259 (ZNF259), mRNA /cds=(28,1407) | 1 | CCTTTAAGGTTGGAACCTTGAAGTTG GAGAAGGTGGAATAAAGTTACACC |
| 2575 | Table 3A | Hs.61828 | NM_003905 | 4502168 | amyloid beta precursor protein-binding protein 1, 59kD (APBP1), mRNA /cds=(73,1677) | 1 | TGCCTTCGGGTTGTGCTTTAGTCTGT AAAATTCTAAAGGAGAGCTGCTAA |
| 2576 | Table 3A | Hs.8991 | NM_003917 | 4503842 | adaptor-related protein complex 1, gamma 2 subunit (AP1G2), mRNA /cds=(45,2402) | 1 | GCAAAAACCTGGGACCAGCCCCCTT CTCCACAAAATAAGCCCAATAAAG |
| 2577 | Table 3A | Hs.58589 | NM_003918 | 5453673 | glycogenin 2 (GYG2), mRNA /cds=(283,1788) | 1 | GTCATCGGCTTTTCAGAGGGAGACCA CGGGAATGTTTCAGGGAACCAATGTC |
| 2578 | Table 3A | Hs.306359 | NM_003922 | 4557025 | clone 25038 mRNA sequence /cds=UNKNOWN | 1 | TGAATTGCCTGTTTCAGGGTTCTTAT GCAGAGAAATAAAGCAGATTTCAGG |
| 2579 | literature | Hs.35947 | NM_003925 | 4505120 | methyl-CpG binding domain protein 4 (MBD4), mRNA /cds=(176,1918) | 1 | ACCAACCACCTTTCCAGCCATAGAGA TTTTAATTAGCCCAACTAGAACGCC |
| 2580 | literature | Hs.194685 | NM_003935 | 4507634 | topoisomerase (DNA) III beta (TOP3B), mRNA /cds=(113,2701) | 1 | CTACTTTGTATGATGACCCTGTCCTC CCTCACCAGGCTGCAATGCCATG |
| 2581 | Table 3A | Hs.169139 | NM_003937 | 4504936 | kynureninase (L-kynurenine hydrolase) (KYNU), mRNA /cds=(106,1503) | 1 | AAAGAGGAGTGGTTGTGACAAGCG GAATCCAAATGGCATTGAGTGGCT |
| 2582 | Table 3A | Hs.24322 | NM_003945 | 4502318 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) 9kD (ATP6H), mRNA /cds=(62,307) | 1 | GAAGAGCCATCTCAACAGAATCGCAC CAAACATACCTTCAGGATGAATT |
| 2583 | Table 3A | Hs.47007 | NM_003954 | 4505396 | mitogen-activated protein kinase kinase kinase 14 (MAP3K14), mRNA /cds=(232,3075) | 1 | TCTGGGTTGTAGAGAACTCTTTGTAA GCAATAAAGTTTGGGGTGATGACA |
| 2584 | literature | Hs.24439 | NM_003958 | 4504866 | ring finger protein (C3HC4 type) 8 (RNF8), mRNA /cds=(112,1569) | 1 | CTGCTGTCCACTTTCTTCAGGCTCT GTGAATACTTCAACCTGCTGTGAT |
| 2585 | Table 3A | Hs.108371 | NM_003973 | 4506600 | E2F transcription factor 4, p107/p130-binding (E2F4), mRNA /cds=(62,1303) | 1 | GCACCTGCTCCAAAGGCATCTGGCA AGAAAGCATAAGTGGCAATCATAAA |
| 2586 | Table 3A | Hs.10315 | NM_003983 | 4507052 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 (SLC7A6), mRNA /cds=(261,1808) | 1 | CTCCTTTTAACTGTATTGACAAACC TCCCCAAAAGAATATGCAATTGT |
| 2587 | Table 3A | Hs.339840 | NM_003992 | 4502884 | Homo sapiens, clone MGC:16360 IMAGE:3927645, mRNA, complete cds /cds=(561,731) | 1 | AGCTGCCAGAAAGCACAGATTTGACC CAAGCTATTTATATGTTATAAAGT |
| 2588 | Table 3A | Hs.83428 | NM_003998 | 10835176 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) (NFKB1), mRNA /cds=(397,3303) | 1 | AGCTGCTGCTGGATCACAGCTGCTTT CTGTTGTCATTGCTGTTGTCCCTC |
| 2589 | literature | Hs.278443 | NM_004001 | 4557021 | Fc fragment of IgG, low affinity IIb, receptor for (CD32) (FCGR2B), mRNA /cds=(0,875) | 1 | GATGAGGCTGACAAAGTTGGGGCTG AGAACACAATCACCTATTCACTTCT |

Table 8

| | | | | | | | |
|------|-----------------------|-----------|-----------|----------|--|---|--|
| 2590 | Table 3A | Hs.12068 | NM_004003 | 4755131 | carbamate acetyltransferase (CRAT), nuclear gene encoding mitochondrial protein, transcript variant peroxisomal, mRNA /cds=(296,2113) | 1 | TCCTGCCCGCCCTGCTGTATGATA TTAATGTGGAAGGTCATCAATAAA |
| 2591 | Table 3A | Hs.169470 | NM_004010 | 5032314 | dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427p2, mRNA /cds=(702,11390) | 1 | AAACTGTAAATCATAATGTAAGTAA GCATAAACATCACATGGCATGTTT |
| 2592 | Table 3A | Hs.460 | NM_004024 | 4755127 | activating transcription factor 3 (ATF3), mRNA /cds=(164,520) | 1 | ACAAGGACGCTGGCTACTGTCTATTA AAATTCTGATGTTTCTGTGAAATT |
| 2593 | Table 3A | Hs.166120 | NM_004031 | 4809287 | interferon regulatory factor 7 (IRF7), transcript variant d, mRNA /cds=(335,1885) | 1 | CTTCCTTATGGAGCTGGAGCAGCCC GCCTAGAACCAGTCTAATGAGAAC |
| 2594 | Table 3A | Hs.78637 | NM_004034 | 4809278 | annexin A7 (ANXA7), transcript variant 2, mRNA /cds=(60,1526) | 1 | TGCATCTCATTTTGCCTAAATTGGTTC TGTATTTCATAAACACTTTCCACA |
| 2595 | Table 3A | Hs.217493 | NM_004039 | 4757755 | annexin A2 (ANXA2), mRNA /cds=(49,1068) | 1 | AGTGAAGTCTATGATGTGAACACTT TGCCTCCTGTGTACTGTGTCTATAA |
| 2596 | Table 3A | Hs.227817 | NM_004049 | 14574570 | BCL2-related protein A1 (BCL2A1), mRNA /cds=(183,710) | 1 | TTGATGATGTAACCTTGACCTCCAGA GTTATGGAAATTTTGTCCCATGT |
| 2597 | Table 3A | Hs.155935 | NM_004054 | 4757887 | complement component 3a receptor 1 (C3AR1), mRNA /cds=(0,1448) | 1 | AGCTCACACGTTCCACCACTGTCCC TCAAACAATGTCAATTCAGAAAGA |
| 2598 | Table 3A | Hs.153640 | NM_004073 | 4758015 | cytokine-inducible kinase (CNK), mRNA /cds=(36,1859) | 1 | GGACCACTTTTATTTATTTGTGAGACA CTTATTTATTTGGGATGTGAGCCCC |
| 2599 | Table 3A | Hs.108080 | NM_004078 | 4758085 | cysteine and glycine-rich protein 1 (CSR1), mRNA /cds=(54,635) | 1 | GGGCTGTACCCAAGCTGATTTCTCAT CTGGTCAATAAAGCTGTTTGAAGC |
| 2600 | literature | Hs.76394 | NM_004092 | 12707569 | enoyl Coenzyme A hydratase, short chain, 1, mitochondrial (ECHS1), nuclear gene encoding mitochondrial protein, mRNA /cds=(71,943) | 1 | GCTCTGAGGGAAACGCTGTCTGCTG CCTTCATACAGATGCTGATTAAAGT |
| 2601 | literature | Hs.4756 | NM_004111 | 6325465 | chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene /cds=(2644,3786) | 1 | TTTTAGCTCAGGAAAATATGTCAGGC TCAAACCACTTCTCAGGCAGTTTA |
| 2602 | Table 3A | Hs.171862 | NM_004120 | 6996011 | guanylate binding protein 2, interferon-inducible (GBP2), mRNA /cds=(156,1931) | 1 | TTGTTGAACCATAAAGTTTGCAAGT AAAGGTTAAGTATGAGGTCAATGT |
| 2603 | Table 3A | Hs.284265 | NM_004124 | 4758441 | pRGR1 mRNA, partial cds /cds=(0,538) | 1 | TGTGGTTTCAGTCTCTGCTAGTTCAT ATTGCATGTTTATTTTGGACAGTC |
| 2604 | Table 3A | Hs.3069 | NM_004134 | 4758569 | heat shock 70kD protein 9B (mortalin-2) (HSPA9B), mRNA /cds=(29,2068) | 1 | AGCAGAAATTTTGAAGCCAGAAAGGAC AACATATGAAGCTTAGGAGTGAAG |
| 2605 | Table 3A | Hs.80350 | NM_004156 | 4758951 | protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform (PPP2CB), mRNA /cds=(21,950) | 1 | ACTGCTTCATCTCCTTTTGCCTTATT TGAAATTTTATGTTATAGTGT |
| 2606 | Table 3A | Hs.180062 | NM_004159 | 4758969 | proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7) (PSMB8), mRNA /cds=(220,1038) | 1 | GAGAGAGTACGGGCTCAGCAGCCAG AGGAGGCCGGTGAAGTGCATCTTCT |
| 2607 | Table 3A | Hs.272493 | NM_004166 | 14589962 | small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15), transcript variant 2, mRNA /cds=(474,815) | 1 | CCGAGTCACCCCTCTGGAGCTTCCCT GCTTTGAATTAAGACCACTCATG |
| 2608 | Table 3A | Hs.272493 | NM_004167 | 14602450 | small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15), transcript variant 2, mRNA /cds=(474,815) | 1 | CCGAGTCACCCCTCTGGAGCTTCCCT GCTTTGAATTAAGACCACTCATG |
| 2609 | Table 3A | Hs.469 | NM_004168 | 4759079 | succinate dehydrogenase complex, subunit A, flavoprotein (Fp) (SDHA), nuclear gene encoding mitochondrial protein, mRNA /cds=(24,2018) | 1 | GGAGCGTGGCACTTACCTTTGTCCCT TGCTTCATCTTGTGAGATGATAA |
| 2610 | Table 3A | Hs.75379 | NM_004172 | 4759125 | solute carrier family 1 (glial high affinity glutamate transporter), member 3 (SLC1A3), nuclear gene encoding mitochondrial protein, mRNA /cds=(178,1806) | 1 | GCATACACATGCACTCAGTGTGGACT GGGAAGCATTACTTTGTAGATGTA |
| 2611 | Table 3A | Hs.172791 | NM_004182 | 4759297 | ubiquitously-expressed transcript (UXT), mRNA /cds=(56,529) | 1 | AAGCCTCACCACTTGACTTCTTCCCCC CATCCTCAGACATTAAGAGCCTG |
| 2612 | literature | Hs.212680 | NM_004195 | 4759245 | tumor necrosis factor receptor superfamily, member 18 (TNFRSF18), mRNA /cds=(0,725) | 1 | CTGACCTCGGCCAGCTTGGAGTGC ACATCTGGCAGCTGAGGAGTCACTG |
| 2613 | Table 3A | Hs.18720 | NM_004208 | 4757731 | programmed cell death 8 (apoptosis-inducing factor) (PDCD8), mRNA /cds=(42,1883) | 1 | GGAAGATCATTAAAGACGGTGAGCA GCATGAAGATCTCAATGAAGTAGCC |
| 2614 | Table 3A | Hs.79197 | NM_004233 | 4757945 | CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA /cds=(41,658) | 1 | TTACCTCTGTCTTGGCTTTCATGTTAT TAAACGTATGCATGTGAAGAAGG |
| 2615 | RG housekeeping genes | Hs.6566 | NM_004237 | 11321606 | thyroid hormone receptor interactor 13 (TRIP13), mRNA /cds=(45,1343) | 1 | AGTTACTGGTCTCTTCTGCCGAATG TTATGTTTTGCTTTTATCTCACAG |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|--|
| 2616 | Table 3A | Hs.85092 | NM_004239 | 10863904 | thyroid hormone receptor interactor 11 (TRIP11), mRNA /cds=(356,6295) | 1 | CACAAAGTGGCCTTTGGGGAGAAAGTCATGATTTGTTTCGCAATTATGCT |
| 2617 | Table 3A | Hs.151787 | NM_004247 | 4759279 | U5 snRNP-specific protein, 116 kD (U5-116KD), mRNA /cds=(60,2978) | 1 | ATTTACTCCAAGTCTCTCCCCAGCTACCACCAGTCCCTTACTCTGTTCT |
| 2618 | Table 3A | Hs.184276 | NM_004252 | 4759139 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1 (SLC9A3R1), mRNA /cds=(212,1288) | 1 | GCCCCATCCCTGAGCCAGGTACCACCATTGTAAGGAAACACTTTTCAGAAAT |
| 2619 | literature | Hs.31442 | NM_004260 | 4759029 | RecQ protein-like 4 (RECQL4), mRNA /cds=(0,3626) | 1 | AGGACCCGACGCTTCTGGAGAAAATACCTGCACCTGAGCTTCGATGCCCTG |
| 2620 | Table 3A | Hs.90606 | NM_004261 | 4759095 | 15 kDa selenoprotein (SEP15), mRNA /cds=(4,492) | 1 | TTACACAAAGATTTGCGTTAATGAAGACTACACAGAAAACCTTTCTAGGGA |
| 2621 | Table 3A | Hs.15259 | NM_004281 | 14043023 | BCL2-associated athanogene 3 (BAG3), mRNA /cds=(306,2033) | 1 | ATACCTGACTTTAGAGAGAGTAAAAATGTGCCAGGAGCCATAGGAATATCT |
| 2622 | Table 3A | Hs.341182 | NM_004288 | 8670550 | 602417256F1 cDNA, 5' end /clone=IMAGE:4536829 /clone_end=5' | 1 | ATGGAAGATGTGGTCTGAGATGGGTGCTGCAAAGATCATAATAAAGTCA |
| 2623 | Table 3A | Hs.75393 | NM_004300 | 4757713 | acid phosphatase 1, soluble (ACP1), transcript variant a, mRNA /cds=(775,1251) | 1 | ACATCCAGAAAGAAGGACACTTGTATGCTAGTCTATGGTCAGTTGAGGAA |
| 2624 | Table 3A | Hs.274350 | NM_004301 | 4757717 | BAF53 (BAF53A), mRNA /cds=(136,1425) | 1 | TTGACTAGTAAAAGTTACTGCCTAGTCTTTTTACCTTAGGCTTACAGAAT |
| 2625 | Table 3A | Hs.109918 | NM_004310 | 4757769 | ras homolog gene family, member H (ARHH), mRNA /cds=(579,1154) | 1 | TTGCCAGGCCAGTTAGAAAATCCCTTGGGGAAGTGTGATGAATATTCCA |
| 2626 | Table 3A | Hs.75811 | NM_004315 | 4757785 | N-acylsphingosine amidohydrolase (acid ceramidase) (ASAH), mRNA /cds=(17,1204) | 1 | ATAATCAGACTTGTGTTCTGCAGACTCAATAACAGTCACTGGAAGAGT |
| 2627 | literature | Hs.234799 | NM_004327 | 11038638 | breakpoint cluster region (BCR), transcript variant 1, mRNA /cds=(488,4303) | 1 | TGACCGGATTCCCTCACTGTTGTATCTTGAAATAACGCTGCTGCTCATC |
| 2628 | db mining | Hs.2534 | NM_004329 | 4757853 | bone morphogenetic protein receptor, type IA (BMPRI1A), mRNA /cds=(309,1907) | 1 | CCAAAGTTGGAGCTTCTATTGCCATGAACCATGCTTACAAAGAAAGCACT |
| 2629 | literature | Hs.82794 | NM_004344 | 4757901 | centrin, EF-hand protein, 2 (CETN2), mRNA /cds=(47,565) | 1 | GTGAACCTCTGCAGTGGCATTGGATGTGTGTTAATGCTATTGTTTGT |
| 2630 | Table 3A | Hs.170019 | NM_004350 | 4757917 | runt-related transcription factor 3 (RUNX3), mRNA /cds=(9,1256) | 1 | GCTGGGTGGAACTGCTTGCAGTATCGTTTGCTTGGTGTGTTGTTTAA |
| 2631 | Table 3A | Hs.84298 | NM_004355 | 10835070 | CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) (CD74), mRNA /cds=(7,705) | 1 | GCTTGTATCAGCTTTCAGGGCCATGTTCACATTAGAATAAAAGGTAGT |
| 2632 | Table 3A | Hs.75564 | NM_004357 | 4757941 | CD151 antigen (CD151), mRNA /cds=(84,845) | 1 | CTTTGCCTTGCAGCCACATGGCCCCATCCCAGTTGGGGAAGCCAGGTGAG |
| 2633 | Table 3A | Hs.75887 | NM_004371 | 6996002 | coatamer protein complex, subunit alpha (COPA), mRNA /cds=(466,4140) | 1 | TGCGGGTATTGATTGTCTTTTACAACTATTGTTCTCATATTCTCACA |
| 2634 | Table 3A | Hs.79194 | NM_004379 | 4758053 | cAMP responsive element binding protein 1 (CREB1), mRNA /cds=(116,1099) | 1 | AGTTATTAGTTCTGCTTTAGCTTTCCAATATGCTGTATAGCCTTTGTCAT |
| 2635 | Table 3A | Hs.23598 | NM_004380 | 4758055 | CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP), mRNA /cds=(198,7526) | 1 | GCTGTTTTCAACATTGTATTGGACTATGCATGTGTTTTTCCCCATTGT |
| 2636 | Table 3A | Hs.76053 | NM_004396 | 13514826 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD) (DDX5), mRNA /cds=(170,2014) | 1 | AAGTAAATGTACAGTGATTGAAATACAATAATGAAGGCAATGCATGGCC |
| 2637 | Table 3A | Hs.155595 | NM_004404 | 4758157 | neural precursor cell expressed, developmentally down-regulated 5 (NEDD5), mRNA /cds=(258,1343) | 1 | CCCACACTGCTACACTTCTGATCCCCTTTGGTTTTACTACCCAAATCTAA |
| 2638 | Table 3A | Hs.171695 | NM_004417 | 7108342 | dual specificity phosphatase 1 (DUSP1), mRNA /cds=(248,1351) | 1 | TCTTAAGCAGGTTTGTGTTTCAGCACTGATGGAAATACCAGTGTGGGT |
| 2639 | Table 3A | Hs.1183 | NM_004418 | 12707563 | dual specificity phosphatase 2 (DUSP2), mRNA /cds=(85,1029) | 1 | GGGGTTGAAACTTAGCACTTTATATTTATACAGAACATTCAGGATTTGT |
| 2640 | Table 3A | Hs.2128 | NM_004419 | 12707565 | dual specificity phosphatase 5 (DUSP5), mRNA /cds=(210,1364) | 1 | ACCCGTGTGAATGTGAAGAAAAGCAGTATGTTACTGGTGTGTTGTTGT |
| 2641 | Table 3A | Hs.74088 | NM_004430 | 4758251 | early growth response 3 (EGR3), mRNA /cds=(357,1520) | 1 | TTGCACTGTGAGCAAATGCTAATACAGTAAATATATTGTGTTTGTGCTGACA |
| 2642 | Table 3A | Hs.55921 | NM_004446 | 4758293 | glutamyl-prolyl-tRNA synthetase (EPRS), mRNA /cds=(58,4380) | 1 | AAATGAAGTACACAGGACAATTATTCTTATGCCTAAGTTAACAGTGGAT |
| 2643 | Table 3A | Hs.48876 | NM_004462 | 4758349 | farnesyl-diphosphate farnesyltransferase 1 (FDFT1), mRNA /cds=(44,1297) | 1 | GTCCGTGCATATGTGACTGTGATGAGATCCCTACTAGTATGATCCTGGCT |
| 2644 | Table 3A | Hs.76362 | NM_004492 | 4758485 | general transcription factor IIA, 2 (12kD subunit) (GTF2A2), mRNA /cds=(141,470) | 1 | AAGGACAAAAGTTGTTGCCCTTCCTAAGAACCCTCTTTAATAAACTCATTT |
| 2645 | Table 3A | Hs.103804 | NM_004501 | 14141160 | heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRPU), transcript variant 1, mRNA /cds=(217,2691) | 1 | CTGCATTTTGATTCTGAAAAGAAAGCTGGCTTGGCCATTTCTTATTAAA |
| 2646 | db mining | Hs.171545 | NM_004504 | 7262381 | HIV-1 Rev binding protein (HRB), mRNA /cds=(243,1931) | 1 | ACCTGTCTGCATAATAAAGCTGATCATGTTTTGCTACAGTTGCAGGTGA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|--|
| 2647 | literature | Hs.152983 | NM_004507 | 4758575 | HUS1 (S. pombe) checkpoint homolog (HUS1), mRNA /cds=(60,902) | 1 | TACTGGTAGATGTGCTCATTCTCCCT GAAACATACCCATCATATTGTCCT |
| 2648 | Table 3A | Hs.38125 | NM_004510 | 4758587 | interferon-induced protein 75, 52kD (IFI75), mRNA /cds=(170,1396) | 1 | AGGAAGCAATGTGGTTGGACCTGGTT AAGGGAAAGGCTGATTACGGAAAT |
| 2649 | Table 3A | Hs.75117 | NM_004515 | 4758601 | interleukin enhancer binding factor 2, 45kD (ILF2), mRNA /cds=(39,1259) | 1 | AACTAATACTTTGCTGTTGAAATGTTG TGAATGTGTAAGTGTCTGGAAAT |
| 2650 | Table 3A | Hs.6196 | NM_004517 | 4758605 | integrin-linked kinase (ILK), mRNA /cds=(156,1514) | 1 | GAGCTTTGTCACCTGCCACATGGTGT CTTCCAACATGGGAGGGATCAGCC |
| 2651 | db mining | Hs.111301 | NM_004530 | 11342665 | matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase) (MMP2), mRNA /cds=(289,2271) | 1 | CCCTGTTCACTACTTAGCATGTCC CTACCGAGTCTCTTCCACTGGA |
| 2652 | Table 3A | Hs.198271 | NM_004544 | 4758767 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10 (42kD) (NDUFA10), mRNA /cds=(21,1088) | 1 | TGCACATTGTTTTCTTCTGACTTCCA GAAATAAAGTGTTCATGGGA |
| 2653 | Table 3A | Hs.173611 | NM_004550 | 4758785 | NADH dehydrogenase (ubiquinone) Fe-S protein 2 (49kD) (NADH-coenzyme Q reductase) (NDUFS2), mRNA /cds=(6,1397) | 1 | ACTAAAAAGGAGAAATTATAATAAAT TAGCCGTCTTGCGCCCTAGGCC |
| 2654 | Table 3A | Hs.80595 | NM_004552 | 4758789 | NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) (NDUFS5), mRNA /cds=(71,391) | 1 | ACGACAAACCTCCTTGTCAAAGTGTG TAAAAATAAAGGATTGCTCCATCC |
| 2655 | Table 3A | Hs.91640 | NM_004556 | 4758805 | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon (NFKBIE), mRNA /cds=(33,1535) | 1 | CCACTGGGGAAGGGAAGTTTCAGTA ACATGACACTAAATGGCAGAGACG |
| 2656 | Table 3A | Hs.74497 | NM_004559 | 4758829 | nuclease sensitive element binding protein 1 (NSEP1), mRNA /cds=(234,1202) | 1 | AAAGATTGGAGCTGAAGACCTAAAGT GCTTGCTTTTTGCCCGTTGACCAG |
| 2657 | Table 3A | Hs.158225 | NM_004571 | 4758929 | PBX/knotted 1 homeobox 1 (PKNOX1), mRNA /cds=(85,1392) | 1 | GAAGTCAGTGGGAAACACACAGAAAT TTATTTTAAATCTTTCAGGAGCT |
| 2658 | Table 3A | Hs.7688 | NM_004576 | 4758953 | protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform (PPP2R2B), mRNA /cds=(525,1856) | 1 | AGATGTATTAGAAAGTCTGACTTTCA AGTGTAATTTGCTTTGGAGGAGGA |
| 2659 | literature | Hs.240457 | NM_004584 | 4759021 | RAD9 (S. pombe) homolog (RAD9), mRNA /cds=(76,1251) | 1 | CTGTGCAGAAGAGCTGCCAGGCAGT GTCTTAGATGTGAGACGGAGGCCAT |
| 2660 | Table 3A | Hs.75498 | NM_004591 | 4759075 | small inducible cytokine subfamily A (Cys-Cys), member 20 (SCYA20), mRNA /cds=(58,348) | 1 | ACATCATGGAGGGTTAGTGCTTATC TAATTTGTGCCTCACTGGACTTGT |
| 2661 | Table 3A | Hs.30035 | NM_004593 | 4759097 | splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10 (SFRS10), mRNA /cds=(121,987) | 1 | TTGCTTACCAAAGGAGGCCCAATTTT ACTCAAATGTTTTGAGAACTGTGT |
| 2662 | Table 3A | Hs.53125 | NM_004597 | 7242206 | small nuclear ribonucleoprotein D2 polypeptide (16.5kD) (SNRPD2), mRNA /cds=(30,386) | 1 | TCACTCCTCTGTCTATGAAGACCGC TGCCATTGGTGTGAGAATAATAA |
| 2663 | literature | Hs.91175 | NM_004618 | 10835217 | topoisomerase (DNA) III alpha (TOP3A), mRNA /cds=(177,3182) | 1 | GTTAAGCCAGGACATCCAGAATTCAT TGCTTTAATAAAGAACCCAGGCCG |
| 2664 | Table 3A | Hs.75066 | NM_004622 | 4759269 | translin (TSN), mRNA /cds=(81,767) | 1 | TCAGTTTAAACAAATGCTATTAAAGTG GAGAAGCACACTCTGGTCTTGGGA |
| 2665 | db mining | Hs.320 | NM_004628 | 4759331 | xeroderma pigmentosum, complementation group C (XPC), mRNA /cds=(191,2662) | 1 | CTCACTGCCTCTTTTGCACTAGGGGAG AGAGCAGAGAAGTACAGGTCATCT |
| 2666 | literature | Hs.8047 | NM_004629 | 4759335 | Fanconi anemia, complementation group G (FANCG), mRNA /cds=(492,2360) | 1 | TTGACTTTGCTCGAGGCACCTTTTTT CCTGTTTCTCCTTTTCTGTTGTCTG |
| 2667 | Table 3A | Hs.159627 | NM_004632 | 4758117 | death associated protein 3 (DAP3), mRNA /cds=(73,1269) | 1 | AAATGGGTTTCACTGTGAATGCGTGGA CAATAAGATATTCCCTTGTTCCCTA |
| 2668 | Table 3A | Hs.237955 | NM_004637 | 13794266 | mRNA for RAB7 protein /cds=(602,1225) | 1 | AACGAATTTCTGAACCTATCAAACCT GGACAAGAATGACCGGGCCAAAGGC |
| 2669 | Table 3A | Hs.25911 | NM_004638 | 4758107 | HLA-B associated transcript 2 (BAT2), mRNA /cds=(101,6529) | 1 | CTTCCCCTGGTCCCCTGTCCCTGGG GCTGTTTGTAAAAAAGAGTAATAA |
| 2670 | Table 3A | Hs.966 | NM_004645 | 4758023 | coilin (COIL), mRNA /cds=(22,1752) | 1 | ACCGTGAAAATTGGTTTCATTTAACAA AAGATCAGATCCCTCCTTCAGCT |
| 2671 | Table 3A | Hs.77578 | NM_004652 | 11641424 | ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), transcript variant 1, mRNA /cds=(59,7750) | 1 | TTCTGTTTACACCCACTGCACCTCTG CAACCAGTGTGCTGCTCATGG |
| 2672 | Table 3A | Hs.80358 | NM_004653 | 4759149 | SMC (mouse) homolog, Y chromosome (SMCY), mRNA /cds=(275,4894) | 1 | GGGAAAAACAAGAAATTCATGACTCT ACCTGTGGTCTATCTTTAATTTCA |
| 2673 | Table 3A | Hs.121102 | NM_004665 | 4759313 | vanin 2 (VNN2), mRNA /cds=(11,1573) | 1 | GCTGTGCCCTTGAGAGAAATAGTAAT GATGGGAATTTAGAGGTTTATGAC |
| 2674 | Table 3A | Hs.6856 | NM_004674 | 4757789 | ash2 (absent, small, or homeotic, Drosophila, homolog)-like (ASH2L), mRNA /cds=(4,1890) | 1 | TCCAAGGAAATGGTAACCTGTTTCTG AGAACACCTGAAATCAATGGCTAT |
| 2675 | Table 3A | Hs.155103 | NM_004681 | 4758253 | eukaryotic translation initiation factor 1A, Y chromosome (EIF1AY), mRNA /cds=(132,566) | 1 | TTCAATTGTAATCCACTGTTTGGCTTT CATGAACAAGTAAATACAGTGT |

Table 8

| | | | | | | | |
|------|-----------|-----------|-----------|---------|---|---|------------------------------|
| 2676 | Table 3A | Hs.54483 | NM_004688 | 4758813 | N-myc (and STAT) interactor (NMI), mRNA /cds=(280,1203) | 1 | ACTTATTTCCATGTTTCTGAATCTTCT |
| 2677 | Table 3A | Hs.5097 | NM_004710 | 4759201 | synaptogyrin 2 (SYNGR2), mRNA /cds=(29,703) | 1 | TTGTTTCAAATGGTGCTGCATGT |
| 2678 | Table 3A | Hs.40323 | NM_004725 | 4757879 | BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog (BUB3), mRNA /cds=(70,1056) | 1 | ATGCCCGGCCTGGGATGCTGTTTGG |
| 2679 | Table 3A | Hs.77324 | NM_004730 | 4759033 | eukaryotic translation termination factor 1 (ETF1), mRNA /cds=(135,1448) | 1 | AGACGGAATAAATGTTTTCTCATTC |
| 2680 | Table 3A | Hs.326159 | NM_004735 | 4758689 | leucine rich repeat (in FLII) interacting protein 1 (LRRFIP1), mRNA /cds=(178,2532) | 1 | TACTCTAAACCTGTTATTTCTGTGCTA |
| 2681 | Table 3A | Hs.333513 | NM_004757 | 4758265 | small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating) (SCYE1), mRNA /cds=(49,987) | 1 | ATAAACGAGATGCAGAACCCCTTG |
| 2682 | Table 3A | Hs.9075 | NM_004760 | 4758191 | serine/threonine kinase 17a (apoptosis-inducing) (STK17A), mRNA /cds=(117,1361) | 1 | TGCAGAGAGATACTAAGCAGCAAAAT |
| 2683 | Table 3A | Hs.170160 | NM_004761 | 4758531 | RAB2, member RAS oncogene family-like (RAB2L), mRNA /cds=(0,2333) | 1 | CTTGGTGTGTGATGTACAGAAAT |
| 2684 | Table 3A | Hs.1050 | NM_004762 | 4758963 | pleckstrin homology, Sec7 and coiled/coiled domains 1(cytohesin 1) (PSCD1), transcript variant 1, mRNA /cds=(69,1265) | 1 | AGTCTTTGATCTTGAACCGATACCTTT |
| 2685 | Table 3A | Hs.11482 | NM_004768 | 4759099 | splicing factor, arginine/serine-rich 11 (SFRS11), mRNA /cds=(83,1537) | 1 | GGATCTCATTTGTTGATATACCTG |
| 2686 | Table 3A | Hs.15589 | NM_004774 | 4759265 | PPAR binding protein (PPARBP), mRNA /cds=(235,4935) | 1 | TGGAATCAAATAAAATGCTTCCACTA |
| 2687 | Table 3A | Hs.26703 | NM_004779 | 4758945 | CCR4-NOT transcription complex, subunit 8 (CNOT8), mRNA /cds=(244,1122) | 1 | CCAAAAGACATTAGAGAAAACCTT |
| 2688 | Table 3A | Hs.23965 | NM_004790 | 4759041 | solute carrier family 22 (organic anion transporter), member 6 (SLC22A6), mRNA /cds=(0,1652) | 1 | TGCCGAATACCTTAAAGTAACTAATTA |
| 2689 | Table 3A | Hs.77965 | NM_004792 | 4758105 | peptidyl-prolyl isomerase G (cyclophilin G) (PPIG), mRNA /cds=(157,2421) | 1 | TCCTTACACACAAAAGGCTCAGT |
| 2690 | Table 3A | Hs.28757 | NM_004800 | 4758873 | transmembrane 9 superfamily member 2 (TM9SF2), mRNA /cds=(133,2124) | 1 | CTTTCCCAGGATCAAGGCCACAGGG |
| 2691 | Table 3A | Hs.49587 | NM_004811 | 4758669 | leupaxin (LPXN), mRNA /cds=(93,1253) | 1 | AGGAAGATTGCACGGGCACTGTTCT |
| 2692 | Table 3A | Hs.168103 | NM_004818 | 4759277 | prp28, U5 snRNP 100 kd protein (U5-100K), mRNA /cds=(39,2501) | 1 | CTTGTAACCTAGCGCCAAGGAACCTGC |
| 2693 | Table 3A | Hs.3628 | NM_004834 | 4758523 | mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA /cds=(79,3576) | 1 | CTTGTAACCTAGCGCCAAGGAACCTGC |
| 2694 | Table 3A | Hs.102506 | NM_004836 | 4758891 | eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), mRNA /cds=(72,3419) | 1 | GCAGGAAAGGGAAACAGACGCGACA |
| 2695 | Table 3A | Hs.227806 | NM_004841 | 4758807 | RAS protein activator like 2 (RASAL2), mRNA /cds=(125,3544) | 1 | GCAACAAGAGCACCAGAAGTATATG |
| 2696 | db mining | Hs.76364 | NM_004847 | 6680470 | allograft inflammatory factor 1 (AIF1), transcript variant 2, mRNA /cds=(453,851) | 1 | TCCATTCTGTTTCGGATTTTAAAGTTTG |
| 2697 | Table 3A | Hs.10649 | NM_004848 | 4758579 | basement membrane-induced gene (ICB-1), mRNA /cds=(128,982) | 1 | AGAGACTTGCTAATGAATCTCCT |
| 2698 | Table 3A | Hs.274472 | NM_004850 | 6633807 | high-mobility group (nonhistone chromosomal) protein 1 (HMG1), mRNA /cds=(52,699) | 1 | CCTTCAGAAACACCGTAATCTAAAT |
| 2699 | Table 3A | Hs.178710 | NM_004859 | 4758011 | clathrin, heavy polypeptide (Hc) (CLTC), mRNA /cds=(172,5199) | 1 | AAACCTCTTCCCATACACCTTTCC |
| 2700 | Table 3A | Hs.76507 | NM_004862 | 4758913 | LPS-induced TNF-alpha factor (PIG7), mRNA /cds=(233,919) | 1 | CTGGACAACCTTTGAGTACTGACATCA |
| 2701 | Table 3A | Hs.59403 | NM_004863 | 4758667 | serine palmitoyltransferase, long chain base subunit 2 (SPTLC2), mRNA /cds=(188,1876) | 1 | TTGATAAATAAAGTGGCTTGTGGT |
| 2702 | Table 3A | Hs.5409 | NM_004875 | 4759045 | RNA polymerase I subunit (RPA40), mRNA /cds=(22,1050) | 1 | CCCAGGGGATTTTTTAAAGTAGATGGG |
| 2703 | Table 3A | Hs.86371 | NM_004876 | 4758513 | zinc finger protein 254 (ZNF254), mRNA /cds=(134,1195) | 1 | GGGACACGGTGAACCTGGCTGTGTC |
| 2704 | Table 3A | Hs.75258 | NM_004893 | 4758495 | H2A histone family, member Y (H2AFY), mRNA /cds=(173,1288) | 1 | ACTCCAAAATAAATCAAGGCTGCAAT |
| 2705 | Table 3A | Hs.80426 | NM_004899 | 4757871 | brain and reproductive organ-expressed (TNFRSF1A modulator) (BRE), mRNA /cds=(146,1297) | 1 | GCAGCTGGTGCTGTTTCAAGTTCCA |
| 2706 | Table 3A | Hs.145696 | NM_004902 | 4757925 | splicing factor (CC1.3) (CC1.3), mRNA /cds=(149,1723) | 1 | TGAAATCTTAAGTGCTTATATGTAAT |
| | | | | | | 1 | CCTGTAGGTTGGTACTTCCCCCA |
| | | | | | | 1 | TGGGAGTCTTCTCTTTTAGACAGGGG |
| | | | | | | 1 | CTTTTTGTTTTTAACCCCAATTGT |
| | | | | | | 1 | TGACCCAGATATGGAACAGAAAGACA |
| | | | | | | 1 | AAATTGTAAGCCAGAGTCAACAAA |
| | | | | | | 1 | AGGTTTCATCAGGTGGTTAAAGTCGT |
| | | | | | | 1 | CAAAGTTGTAAGTGACTAACCAG |
| | | | | | | 1 | ATGCTGTCAAAGTTACAGTTACGCA |
| | | | | | | 1 | GGACATTCTTGCCGTATTCTCATG |
| | | | | | | 1 | TGTGTGTTTACTAACCCCTTCCTGAG |
| | | | | | | 1 | GCTTGTGTATGTTGGATATTGTGG |
| | | | | | | 1 | TCTGTAATCAAATGATTGGTGTCATTT |
| | | | | | | 1 | TCCCATTTGCCAATGTAGTCTCA |
| | | | | | | 1 | TGCCACGACGCCATCTTAATACATTA |
| | | | | | | 1 | AACCAGTTTAAAAAATACCTTCCA |
| | | | | | | 1 | GCCAGAGTTGCCAACCCCGGCTGG |
| | | | | | | 1 | ATACCTTCAGCAGAGAAATCTCCG |
| | | | | | | 1 | AATCCATTAAACACCTGCTCACATCTTA |
| | | | | | | 1 | CTCAAAATTTAGAGAGTTTCATAGT |
| | | | | | | 1 | ATTTGCAATTTGGAATTTGTGTGAGTT |
| | | | | | | 1 | GATTTAGTAAAAATGTTAAACCGC |
| | | | | | | 1 | AAGTAAAGCCTCAGGAATGCCACG |
| | | | | | | 1 | CCTTTCTTCCAAAGCCTTTGTCTCT |
| | | | | | | 1 | TCAAACAAATGACTTTTCATATTGCAAC |
| | | | | | | 1 | AATCTTTGTAAGAACCACTCAAA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|--|
| 2707 | Table 3A | Hs.119 | NM_004906 | 4758635 | Wilms' tumour 1-associating protein (KIAA0105), mRNA /cds=(124,579) | 1 | GGGGAATGTGTTCTTCATTGTATTT GGGCCCTTTTGTATTGCACTCTTGA |
| 2708 | Table 3A | Hs.737 | NM_004907 | 4758313 | Homo sapiens, Similar to kinesin family member 5B, clone MGC:15265 IMAGE:4297793, mRNA, complete cds /cds=(424,1566) | 1 | TTGTTTACCTTTCTGTCGGTGGATTCT TTTTTAACTCCGCTCTACCTGGCGT |
| 2709 | Table 3A | Hs.288156 | NM_004911 | 4758303 | cDNA: FLJ21819 fis, clone HEP01185 /cds=UNKNOWN | 1 | GGGGTTTGTGCTATACACTGGGATGT CTAATTGCAGCAATAAGCCTTTTC |
| 2710 | Table 3A | Hs.81964 | NM_004922 | 4758633 | SEC24 (S. cerevisiae) related gene family, member C (SEC24C), mRNA /cds=(114,3491) | 1 | ACCTGGGATGCCCTGCTCTGGACC TCTCATTTCTCTTCATTGGTTATT |
| 2711 | Table 3A | Hs.333417 | NM_004930 | 4826658 | capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA /cds=(0,818) | 1 | AGCCTGCTTCTGCCACACCTCGCTCT CAGTCTCTCCACATTTCCATAGAG |
| 2712 | Table 3A | Hs.2299 | NM_004931 | 4826666 | CD8 antigen, beta polypeptide 1 (p37) (CD8B1), mRNA /cds=(50,682) | 1 | AAGTTTCTCAGCTCCCATTTCTACTCT CCCATTGGCTTCATGCTTCTTTCA |
| 2713 | Table 3A | Hs.171872 | NM_004941 | 4826689 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA helicase) (DDX8), mRNA /cds=(73,3735) | 1 | GAGCTACTGTGCTCATCTAAAGTGTT TGCCCCACTTCCCACCCGCTCTCC |
| 2714 | Table 3A | Hs.251064 | NM_004965 | 4826757 | high-mobility group (nonhistone chromosomal) protein 14 (HMG14), mRNA /cds=(150,452) | 1 | ATGTTAAGATTTGTGTACAAATTGAAA TGCTGTACTGATCCTCAACCAA |
| 2715 | Table 3A | Hs.808 | NM_004966 | 14141150 | heterogeneous nuclear ribonucleoprotein F (HNRPF), mRNA /cds=(323,1570) | 1 | TCTGTTGATAGCTGGAGAACTTTAGT TTCAAGTACTACATTGTGAAAGCA |
| 2716 | literature | Hs.115541 | NM_004972 | 13325062 | Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA /cds=(494,3892) | 1 | TGAGGGGTTTCAGAAATTTGCATTGC AGTCATAGAAGAGATTTATTTCT |
| 2717 | Table 3A | Hs.40154 | NM_004973 | 11863151 | jumonji (mouse) homolog (JMJ), mRNA /cds=(244,3984) | 1 | CCTTGGGAGGGAGACTTCATGTGGTT TATTGCGAGTTTTTTGTTTACTTT |
| 2718 | Table 3A | Hs.184050 | NM_004985 | 4826811 | v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog (KRAS2), mRNA /cds=(192,758) | 1 | GTATGTTAATGCCAGTCACCAGCAGG CTATTTCAAGGTCAGAAGTAATGA |
| 2719 | Table 3A | Hs.279946 | NM_004990 | 14043021 | methionine-tRNA synthetase (MARS), mRNA /cds=(23,2725) | 1 | GCCCCATAAGGCAAGAAGAAAAAGTA AAAGACCTTGGCTCATAGAAAGTC |
| 2720 | Table 3A | Hs.75103 | NM_005005 | 6274549 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ), mRNA /cds=(84,821) | 1 | AGTGAAATATGTTACAGAACATGCAC TTGCCCTAATAAAAAATCAGTGAA |
| 2721 | Table 3A | Hs.8248 | NM_005006 | 4826855 | NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1), mRNA /cds=(46,2229) | 1 | TGCAGATGCTCTTAAAGCATTGATA ACCTTTGTGACGAACATAAAGAGA |
| 2722 | Table 3A | Hs.182255 | NM_005008 | 4826859 | non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA /cds=(94,480) | 1 | GCTAGTTCATGTGTTCTCCATTCTTGT GAGCATCCTAATAAATCTGTTCC |
| 2723 | Table 3A | Hs.151134 | NM_005015 | 4826879 | oxidase (cytochrome c) assembly 1-like (OXA1L), mRNA /cds=(0,1487) | 1 | AACCCTCCCAATATCCCTAGCAGCAG CAGCAAACCAAGTCAAAGTATCC |
| 2724 | Table 3A | Hs.75721 | NM_005022 | 4826897 | profilin 1 (PFN1), mRNA /cds=(127,549) | 1 | CACCTCCCCCTACCCATATCCCTCCC GTGTGTGGTTGGAAACTTTTGT |
| 2725 | db mining | Hs.100724 | NM_005037 | 4826929 | peroxisome proliferative activated receptor, gamma (PPARG), mRNA /cds=(172,1608) | 1 | GAGTCCTGAGCCACTGCCAACATTTTC CCTTCTCCAGTTGCACTATTCTG |
| 2726 | literature | Hs.180455 | NM_005053 | 4826963 | RAD23 (S. cerevisiae) homolog A (RAD23A), mRNA /cds=(36,1127) | 1 | CCCCACCCGAGAAGCAACCGTGTC TCTGATAAGGTTTTGAAGTGAATA |
| 2727 | Table 3A | Hs.180610 | NM_005066 | 4826997 | splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-associated) (SFPQ), mRNA /cds=(85,2208) | 1 | CCCATTCTTGTTTTTAAAGACCAAC AAATCTCAAGCCCTATAAATGGC |
| 2728 | Table 3A | Hs.149923 | NM_005080 | 14110394 | X-box binding protein 1 (XBP1), mRNA /cds=(48,833) | 1 | AGTGTAAGCTTCTGAAAGGTGCTTTCT CCATTTATTTAAACTACCCATGCG |
| 2729 | Table 3A | Hs.1579 | NM_005082 | 4827064 | zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147), mRNA /cds=(39,1931) | 1 | GAGTGCCCGATTCTCTTAGAGAAAA TCCATAGCCTTCAGATCTTGGTGT |
| 2730 | Table 3A | Hs.82712 | NM_005087 | 4826735 | fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA /cds=(12,1877) | 1 | ACTTTGACACCTACTGTGTTATAAAAT ATATCATCAGATGCGCTTGAGA |
| 2731 | Table 3A | Hs.21595 | NM_005088 | 10835221 | DNA segment on chromosome X and Y (unique) 155 expressed sequence (DXYS155E), mRNA /cds=(166,1323) | 1 | AGCTGTAACGTTTCGCGTTAGGAAAGA TGGTGTATTCCAGTTTGCAATT |
| 2732 | literature | Hs.248197 | NM_005092 | 4827033 | tumor necrosis factor (ligand) superfamily, member 18 (TNFSF18), mRNA /cds=(0,533) | 1 | TGATATTCAACTCTGAGCATCAGGTT CTAAAAAATAATACATACTGGGGT |
| 2733 | Table 3A | Hs.75243 | NM_005104 | 12408641 | bromodomain-containing 2 (BRD2), mRNA /cds=(1701,4106) | 1 | GTCATCTCCCCATTTGGTCCCCTGGA CTGCTTTTGTGATTCTAACTTGT |
| 2734 | Table 3A | Hs.95220 | NM_005109 | 4826877 | oxidative-stress responsive 1 (OSR1), mRNA /cds=(342,1925) | 1 | GAGAATAATGATGTACCAATAAGTGG AGATTCTCCTCTTATGATGTATGCT |
| 2735 | literature | Hs.241382 | NM_005118 | 4827031 | tumor necrosis factor (ligand) superfamily, member 15 (TNFSF15), mRNA /cds=(1123,1647) | 1 | ACAAGACAGACTCCACTCAAATTTA TATGAACACCACTAGATACTTCCT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|--|
| 2736 | Table 3A | Hs.11861 | NM_005121 | 4827043 | thyroid hormone receptor-associated protein, 240 kDa subunit (TRAP240), mRNA /cds=(77,6601) | 1 | TCCATACCATTGTGTGTGGAGGATTT ACAGCTAAGCTGTAGTTGCAGAGT |
| 2737 | Table 3A | Hs.3382 | NM_005134 | 4826933 | protein phosphatase 4, regulatory subunit 1 (PPP4R1), mRNA /cds=(93,2894) | 1 | ACACTTTTGATTGTTTTCTAGATGTCT ACCAATAAATGCAATTTGTGACC |
| 2738 | Table 3A | Hs.75981 | NM_005151 | 4827049 | ubiquitin specific protease 14 (IRNA-guanine transglycosylase) (USP14), mRNA /cds=(91,1575) | 1 | ACTGTACAAATTTCTGAAGATGGTTATT AACACTGTGCTGTTAAGCATCCA |
| 2739 | Table 3A | Hs.152818 | NM_005154 | 4827053 | ubiquitin specific protease 8 (USP8), mRNA /cds=(317,3673) | 1 | TCAGTCCTTTCTTAGGGAATGACAG GGCAAAGCAATTTTCTGTTGGCT |
| 2740 | Table 3A | Hs.89399 | NM_005176 | 6671590 | ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 (ATP5G2), mRNA /cds=(59,484) | 1 | AGTACAAGGCCCGAAGGGTAGTGAT GGTGCTAAACTCAACATGGATTGG |
| 2741 | Table 3A | Hs.431 | NM_005180 | 4885094 | murine leukemia viral (bmi-1) oncogene homolog (BIM1), mRNA /cds=(479,1459) | 1 | CCCCAGTCTGCAAAAGAAGCACAATT CTATTGCTTTGTCTTGCTTATAGT |
| 2742 | Table 3A | Hs.838 | NM_005191 | 4885122 | CD80 antigen (CD28 antigen ligand 1, B7-1 antigen) (CD80), mRNA /cds=(375,1241) | 1 | CTTCTTTTGCCATGTTTCCATTCTGCC ATCTTGAATTGTCTTGTCAGCCA |
| 2743 | Table 3A | Hs.247824 | NM_005214 | 4885166 | cytotoxic T-lymphocyte-associated protein 4 (CTLA4), mRNA /cds=(0,671) | 1 | GGGTCTATGTGAAAATGCCCCCAACA GAGCCAGAAATGTGAAAAGCAATTT |
| 2744 | literature | Hs.211567 | NM_005215 | 4885174 | deleted in colorectal carcinoma (DCC), mRNA /cds=(0,4343) | 1 | CCTTCTTTCACAGGCATCAGGAATTG TCAAATGATGATTATGAGTTCCT |
| 2745 | literature | Hs.34789 | NM_005216 | 4885176 | dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST), mRNA /cds=(0,1370) | 1 | CATCTTCAGCATCGTCTTCTTGACA TGAAGGAGAAGGAGAAGTCCGACT |
| 2746 | literature | Hs.89296 | NM_005236 | 4885216 | excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA /cds=(0,2750) | 1 | GGGAATGCTGCAAAATGCCAAACAGCT TTATGATTTCAATTCACACCTCTTT |
| 2747 | Table 3A | Hs.129953 | NM_005243 | 4885224 | Ewing sarcoma breakpoint region 1 (EWSR1), transcript variant EWS, mRNA /cds=(43,2013) | 1 | TTAAAAATGGTTGTTTAAGACTTTAAC AATGGGAACCCCTTGAGCATG |
| 2748 | Table 3A | Hs.1422 | NM_005248 | 4885234 | Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR), mRNA /cds=(147,1736) | 1 | GGGAGAAGTTTGACAGAGCACTTCCC ACCTCTCTGAATAGTGTGTATGTGT |
| 2749 | Table 3A | Hs.79022 | NM_005261 | 4885262 | GTP-binding protein overexpressed in skeletal muscle (GEM), mRNA /cds=(213,1103) | 1 | TGGTTGACCCTTGATGTACAGAGCTC TGCTCTATTATTATTATTTGCA |
| 2750 | Table 3A | Hs.73172 | NM_005263 | 4885266 | growth factor independent 1 (GFI1), mRNA /cds=(267,1535) | 1 | TGGGAAGGAAGGCTCTGTCTTCAACT CTTTGACCCTCCATGTGTACCATA |
| 2751 | Table 3A | Hs.237519 | NM_005271 | 4885280 | yz35c09.s1 cDNA, 3' end /clone=IMAGE:285040 /clone_end=3' | 1 | GCATGGCTTAACCTGGTGATAAAAGC AGTTATTAAAAGTCTACGTTTTTCC |
| 2752 | Table 3A | Hs.239891 | NM_005301 | 4885320 | G protein-coupled receptor 35 (GPR35), mRNA /cds=(0,929) | 1 | CTCCCCGTGCTAAGGCCACAAAAAGC CCAGGACTCTCTGTGCGTGACCCTC |
| 2753 | Table 3A | Hs.289101 | NM_005313 | 4885358 | glucose regulated protein, 58kD (GRP58), mRNA /cds=(0,1517) | 1 | AATTCAAGAAGAAAACCCAGAAGA AGAAGAAGGCACAGGAGGATCTCT |
| 2754 | literature | Hs.89578 | NM_005316 | 4885364 | Homo sapiens, general transcription factor IIH, polypeptide 1 (62kD subunit), clone MGC:8323 IMAGE:2819217, mRNA, complete cds /cds=(169,1815) | 1 | TCCCAGAGCTGATGCTATTGTACTTG CACATTGGAGACTGAAAGGAAAGA |
| 2755 | literature | Hs.136857 | NM_005320 | 4885376 | H1 histone family, member 3 (H1F3), mRNA /cds=(0,665) | 1 | GGGGAAGCCGAAGGTTACAAAGGCA AAGAAGGCAGCTCCGAAGAAAAAGT |
| 2756 | Table 3A | Hs.14601 | NM_005335 | 4885404 | hematopoietic cell-specific Lyn substrate 1 (HCLS1), mRNA /cds=(42,1502) | 1 | TCCCTGAAGAAATATCTGTGAACCTT CTTTCTGTTCAAGTCTAAATTCG |
| 2757 | Table 3A | Hs.132834 | NM_005337 | 4885410 | hematopoietic protein 1 (HEM1), mRNA /cds=(1582,3423) | 1 | CCTCTCCGACCTTCATCAGTATTCTTA GGATAATGCTGGCGGGCAGAGAT |
| 2758 | Table 3A | Hs.193989 | NM_005345 | 5579469 | TAR DNA binding protein (TARDBP), mRNA /cds=(88,1332) | 1 | ACTGCCATCTTACGACTATTCTTCTT TTTAATACACTTAACTCAGGCCA |
| 2759 | Table 3A | Hs.274402 | NM_005346 | 5579470 | heat shock 70kD protein 1B (HSPA1B), mRNA /cds=(152,2077) | 1 | AGGGTGTTTCGTTCCCTTTAAATGAA TCAACACTGCCACCTCTGTACGA |
| 2760 | Table 3A | Hs.289088 | NM_005348 | 13129149 | heat shock 90kD protein 1, alpha (HSPCA), mRNA /cds=(60,2258) | 1 | GACCCTACTGCTGATGATACCAAGTGC TGCTGTAAGTGAAGAAATGCCACC |
| 2761 | Table 3A | Hs.1765 | NM_005356 | 4885448 | lymphocyte-specific protein tyrosine kinase (LCK), mRNA /cds=(51,1580) | 1 | CATTTCTGAGACCACCAGAGAGAG GGGAGAAGCCTGGGATTGACAGAAG |
| 2762 | Table 3A | Hs.1765 | NM_005356 | 4885448 | lymphocyte-specific protein tyrosine kinase (LCK), mRNA /cds=(51,1580) | 1 | CATTTCTGAGACCACCAGAGAGAG GGGAGAAGCCTGGGATTGACAGAAG |
| 2763 | db mining | Hs.75862 | NM_005359 | 4885456 | MAD (mothers against decapentaplegic, Drosophila) homolog 4 (MADH4), mRNA /cds=(128,1786) | 1 | GCTAAGAAGCCTATAAGAGGAATTTT TTTCTCTTCAATTCATAGGGAAAGG |
| 2764 | Table 3A | Hs.297939 | NM_005385 | 6631099 | cathepsin B (CTSB), mRNA /cds=(177,1196) | 1 | ACTGACAGAGTGAAGTACAGAAATAG CTTTTCTTCTAAAGGGGATTGTT |
| 2765 | literature | Hs.301862 | NM_005395 | 4885552 | postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA /cds=(0,794) | 1 | CAGACAATGGATGTGGGGTAGAGA AGAAAACCTTTGAAGGCTTAATCTCT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|--|
| 2766 | Table 3A | Hs.288757 | NM_005402 | 4885568 | v-ral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA /cds=(0,629) | 1 | AAAAGAAGAGGAAAAGTTTAGCCAAG AGAATCAGAGAAAGATGCTGCATT |
| 2767 | literature | Hs.103982 | NM_005409 | 14790145 | small inducible cytokine subfamily B (Cys-X-Cys), member 11 (SCYB11), mRNA /cds=(93,377) | 1 | AGTGCACATATTTTCATAACCAAAATTAG CAGCACC GGCTCTTAATTTGATGT |
| 2768 | Table 3A | Hs.72988 | NM_005419 | 4885614 | signal transducer and activator of transcription 2, 113kD (STAT2), mRNA /cds=(57,2612) | 1 | TAGACCTCTTTTTCTTACCAGTCTCCT CCCCTACTCTGCCCCCTAAGCTG |
| 2769 | literature | Hs.129727 | NM_005431 | 4885656 | X-ray repair complementing defective repair in Chinese hamster cells 2 (XRCC2), mRNA /cds=(86,928) | 1 | AGCACAGTAAAAAGTAAAGACTATTCT GTTTCTAGGCTGTTGAATCAAAGT |
| 2770 | literature | Hs.99742 | NM_005432 | 12408644 | X-ray repair complementing defective repair in Chinese hamster cells 3 (XRCC3), mRNA /cds=(353,1393) | 1 | CATGGGCACAGTGGTGACCCCTTG ATTCCACCGTACAAACCCCTCCAC |
| 2771 | literature | Hs.75238 | NM_005441 | 4885104 | chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA /cds=(62,1741) | 1 | CGTTATCCAGTGTGAAAATCAGTGAG TCCTCCCTGGCATCCTCGTGAAAG |
| 2772 | Table 3A | Hs.301704 | NM_005442 | 11321608 | eomesodermin (Xenopus laevis) homolog (EOMES), mRNA /cds=(0,2060) | 1 | GCTGAAGAGTATAGTAAAGACACCTC AAAAGGCATGGGAGGGTATTATGC |
| 2773 | Table 3A | Hs.169487 | NM_005461 | 4885446 | Kreisler (mouse) maf-related leucine zipper homolog (KRML), mRNA /cds=(73,1044) | 1 | TTCAGACTGGTTTCTGTTTTTGGTTA TTAAATGGTTTCTATTTTGTCT |
| 2774 | Table 3A | Hs.170311 | NM_005463 | 14110410 | heterogeneous nuclear ribonucleoprotein D-like (HNRPD), transcript variant 1, mRNA /cds=(580,1842) | 1 | TTTATGATTAGGTGACGAGTTGACAT TGAGATTGCTCTTCCCTGATC |
| 2775 | literature | Hs.24284 | NM_005484 | 11496991 | ADP-ribosyltransferase (NAD+; poly(ADP-ribose) polymerase)-like 2 (ADPRTL2), mRNA /cds=(149,1753) | 1 | CCCCAACCGGTCCGTATGCGGTAC CTTTTAAAGGTTCAAGTTAATTTCC |
| 2776 | literature | Hs.271742 | NM_005485 | 11496992 | ADP-ribosyltransferase (NAD+; poly(ADP-ribose) polymerase)-like 3 (ADPRTL3), mRNA /cds=(246,1847) | 1 | TCCTGCAAGGCTGGACTGTGATCTTC AATCATCTGCCCATCTCTGGTAC |
| 2777 | Table 3A | Hs.180370 | NM_005507 | 5031634 | cofilin 1 (non-muscle) (CFL1), mRNA /cds=(51,551) | 1 | GGTCACGGCTACTCATGGAAGCAGG ACCAGTAAGGACCTTCGATTAATAA CCTTCTAACCTGAACGTATGGGTTTC |
| 2778 | literature | Hs.184926 | NM_005508 | 5031626 | chemokine (C-C motif) receptor 4 (CCR4), mRNA /cds=(182,1264) | 1 | TCCAGAGGGAATTGCAGAGTACTG ATGTGTAGGAGGAAGAGTTCAAGTG GAAAAGGAGGAGCTACTCTCAGGC |
| 2779 | Table 3A | Hs.77961 | NM_005514 | 5031742 | major histocompatibility complex, class I, B (HLA-B), mRNA /cds=(0,1088) | 1 | AACGATTGTCTGCCCATGTCTGCCT GAAATACCATGATTGTTTATGGAA TTCTTTTAGGTATATTGCGCTAAGT GAACTTGTCAAATAAATCCTCCT |
| 2780 | Table 3A | Hs.334767 | NM_005517 | 5031748 | hypothetical protein MGC5629 (MGC5629), mRNA /cds=(285,539) | 1 | GTCTTGACTTTGGCAAATGAGCCGGA GCCCCCTGGGACGGTCACACAACC |
| 2781 | Table 3A | Hs.245710 | NM_005520 | 5031752 | heterogeneous nuclear ribonucleoprotein H1 (H) (HNRPH1), mRNA /cds=(72,1421) | 1 | GATACAGAGTTGTCCTTGAGGATGG AGACAGGTGCAAGGCCAAGATGTG |
| 2782 | Table 3A | Hs.177559 | NM_005534 | 5031782 | interferon gamma receptor 2 (interferon gamma transducer 1) (IFNGR2), mRNA /cds=(648,1661) | 1 | TCCCATGATGGAAGTCTGCGTAACCA ATAAATTGTCCTTTCTCACTCAA |
| 2783 | literature | Hs.121544 | NM_005535 | 5031784 | interleukin 12 receptor, beta 1 (IL12RB1), mRNA /cds=(64,2052) | 1 | TCTACATGTCTTGGGGCGGGCTCA AATTCTTCGAAAGTGTTGGATTAA ACCTGTTATCCTTTGTAGAGCACACA GAGTTAAAAGTTGAATATAGCAAT TGAGCTTCTCCAGCAGTGCGGGTCC TGGGCTCCTGAAGGCTTATCCATC GCATGTCCTCATCCTTCTGCCATA AAAGCTATGACACGAGAATCAGAA ACCCCTCCCATGAACACAAGGGTTT TATCTTTCTTTAAAAACAGTGT |
| 2784 | Table 3A | Hs.155939 | NM_005541 | 5031798 | inositol polyphosphate-5-phosphatase, 145kD (INPP5D), mRNA /cds=(140,3706) | 1 | TGCAACCAACTATCCAAGTGTATAC CAACTAAAACCCCAATAAACCTT ATGCCAGACAAAAAGCTAATACCAG TCACTCGATAATAAAGTATTGCGA TGGCACTGAGAAACATGCAAGATACA GGAAAAATGAAAATGTTACAAGCT |
| 2785 | Table 3A | Hs.56205 | NM_005542 | 5031800 | insulin induced gene 1 (INSIG1), mRNA /cds=(414,1247) | 1 | TCTCAAAGGAGTAACTGCAGCTTGGT TTGAAATTTGACTGTTTCTATCA |
| 2786 | Table 3A | Hs.211576 | NM_005546 | 5031810 | IL2-inducible T-cell kinase (ITK), mRNA /cds=(2021,3883) | 1 | TGCAACCAACTATCCAAGTGTATAC CAACTAAAACCCCAATAAACCTT ATGCCAGACAAAAAGCTAATACCAG TCACTCGATAATAAAGTATTGCGA TGGCACTGAGAAACATGCAAGATACA GGAAAAATGAAAATGTTACAAGCT |
| 2787 | Table 3A | Hs.23881 | NM_005556 | 5031842 | keratin 7 (KRT7), mRNA /cds=(56,1465) | 1 | TCTCAAAGGAGTAACTGCAGCTTGGT TTGAAATTTGACTGTTTCTATCA |
| 2788 | Table 3A | Hs.81915 | NM_005563 | 13518023 | stathmin 1/oncoprotein 18 (STMN1), mRNA /cds=(91,540) | 1 | GTCAACCTTTGTGAGAAGCCGTATCC ACTTCACAGGATAAAATGTCCAT |
| 2789 | Table 3A | Hs.2488 | NM_005565 | 7382491 | lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD) (LCP2), mRNA /cds=(207,1808) | 1 | TGCAACCAACTATCCAAGTGTATAC CAACTAAAACCCCAATAAACCTT ATGCCAGACAAAAAGCTAATACCAG TCACTCGATAATAAAGTATTGCGA TGGCACTGAGAAACATGCAAGATACA GGAAAAATGAAAATGTTACAAGCT |
| 2790 | Table 3A | Hs.314760 | NM_005566 | 5031856 | HOA7-1-F8 cDNA | 1 | TGCAACCAACTATCCAAGTGTATAC CAACTAAAACCCCAATAAACCTT ATGCCAGACAAAAAGCTAATACCAG TCACTCGATAATAAAGTATTGCGA TGGCACTGAGAAACATGCAAGATACA GGAAAAATGAAAATGTTACAAGCT |
| 2791 | db mining | Hs.153863 | NM_005585 | 5031898 | Smad6 mRNA, complete cds /cds=(936,2426) | 1 | TGCAACCAACTATCCAAGTGTATAC CAACTAAAACCCCAATAAACCTT ATGCCAGACAAAAAGCTAATACCAG TCACTCGATAATAAAGTATTGCGA TGGCACTGAGAAACATGCAAGATACA GGAAAAATGAAAATGTTACAAGCT |
| 2792 | literature | Hs.20555 | NM_005590 | 5031920 | meiotic recombination (S. cerevisiae) 11 homolog A (MRE11A), mRNA /cds=(170,2296) | 1 | TGCAACCAACTATCCAAGTGTATAC CAACTAAAACCCCAATAAACCTT ATGCCAGACAAAAAGCTAATACCAG TCACTCGATAATAAAGTATTGCGA TGGCACTGAGAAACATGCAAGATACA GGAAAAATGAAAATGTTACAAGCT |
| 2793 | Table 3A | Hs.158164 | NM_005594 | 5031930 | transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) (TAP1), mRNA /cds=(30,2456) | 1 | GTCAACCTTTGTGAGAAGCCGTATCC ACTTCACAGGATAAAATGTCCAT |
| 2794 | Table 3A | Hs.18069 | NM_005606 | 5031990 | Homo sapiens, protease, cysteine, 1 (legumain), clone MGC:15832 IMAGE:3507728, mRNA, complete cds /cds=(1124,2425) | 1 | GTCAACCTTTGTGAGAAGCCGTATCC ACTTCACAGGATAAAATGTCCAT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|---|
| 2795 | Table 3A | Hs.256290 | NM_005620 | 5032056 | S100 calcium-binding protein A11 (calgizzarin) (S100A11), mRNA /cds=(120,437) | 1 | ATCTCCACAGCCCACCCATCCCCTGA GCACACTAACCCACCTCATGCAGGC |
| 2796 | Table 3A | Hs.8180 | NM_005625 | 5032082 | syndecan binding protein (syntenin) (SDCBP), mRNA /cds=(148,1044) | 1 | TTTCCTGACTCCTCCTTGCAAAACAAA ATGATAGTTGACACTTTATCCTGA |
| 2797 | Table 3A | Hs.76122 | NM_005626 | 5032088 | splicing factor, arginine/serine-rich 4 (SFRS4), mRNA /cds=(47,1531) | 1 | CCTGCAGTAACCCATAGACAAATAAAC TGTAGAGTTCATATTTCTGCGGCC |
| 2798 | Table 3A | Hs.296323 | NM_005627 | 5032090 | serum/glucocorticoid regulated kinase (SGK), mRNA /cds=(42,1337) | 1 | TAGAAAGGGTTTTATGGACCAATGC CCCAGTTGTGAGTCAGAGCCGTTG |
| 2799 | Table 3A | Hs.155188 | NM_005642 | 14717406 | TATA box binding protein (TBP)-associated factor, RNA polymerase II, F, 55kD (TAF2F), mRNA /cds=(740,1789) | 1 | TGTGATGACGTGAGATCAATAAGAAAG AACCTAGTCTAGAGACAATGATGC |
| 2800 | literature | Hs.100030 | NM_005652 | 5032168 | telomeric repeat binding factor 2 (TERF2), mRNA /cds=(124,1626) | 1 | GTGCTTGCTGTCTCTCCCGGACACCC TTAAAGACTGTCTTTTAGCAAAA |
| 2801 | Table 3A | Hs.82173 | NM_005655 | 5032176 | TGFB inducible early growth response (TIEG), mRNA /cds=(123,1565) | 1 | AACATTGTTTTGTATATTGGGTGTAG ATTTCTGACATCAAAACCTTGGAC |
| 2802 | literature | Hs.170263 | NM_005657 | 5032188 | tumor protein p53-binding protein, 1 (TP53BP1), mRNA /cds=(173,6091) | 1 | TGTGTAACCTGGATTCTTGCATGGAT CTTGTATATAGTTTTATTGCTGA |
| 2803 | Table 3A | Hs.2134 | NM_005658 | 5032192 | TNF receptor-associated factor 1 (TRAF1), mRNA /cds=(75,1325) | 1 | CAGGACCTCCAAGCCACTGAGCAAT GTATAACCCCAAGGGAATTCAAAA |
| 2804 | Table 3A | Hs.7381 | NM_005662 | 5032220 | voltage-dependent anion channel 3 (VDAC3), mRNA /cds=(99,950) | 1 | GATCTGACCCACCAAGTTGTACATCA CGTCTGCATGTGCCACACCATTT |
| 2805 | Table 3A | Hs.155968 | NM_005667 | 5031824 | zinc finger protein homologous to Zfp103 in mouse (ZFP103), mRNA /cds=(922,2979) | 1 | ACAATCTCTGTCCAGCACCTCTTGGT TAAATAATGTATGCTGTGAGACAT |
| 2806 | Table 3A | Hs.172813 | NM_005678 | 13027652 | PAK-interacting exchange factor beta (P85SPR), mRNA /cds=(473,2413) | 1 | TGCGTCTGTGAAATGTGTAGAGTG TTTGTGAGCTTTTGTCCCTCAT |
| 2807 | Table 3A | Hs.30570 | NM_005710 | 5031956 | polyglutamine binding protein 1 (PQBP1), mRNA /cds=(257,1054) | 1 | CTTCGGCCTCCCTGGCCCTGGGTTA AAATAAAGACTTCTGTTGATCCTG |
| 2808 | Table 3A | Hs.82425 | NM_005717 | 5031592 | actin related protein 2/3 complex, subunit 5 (16 kD) (ARPC5), mRNA /cds=(24,479) | 1 | TGAGCTTGCTTAGTATTTACATTG GATGCCAGTTTTGTAATCACTGAC |
| 2809 | Table 3A | Hs.6895 | NM_005719 | 5031596 | actin related protein 2/3 complex, subunit 3 (21 kD) (ARPC3), mRNA /cds=(25,561) | 1 | ATTTGAAATTTTCTGCAGCATTAAAGC TGGCGCTTAATAAGAATAAGTAA |
| 2810 | Table 3A | Hs.10927 | NM_005721 | 7262289 | HSZ78330 cDNA /clone=2.49-(CEPH) | 1 | TGCGATTCTGTTTCTTGCTTTAAAGA AGAGTAAAGACAAGAGTGTGGA |
| 2811 | Table 3A | Hs.42915 | NM_005722 | 5031570 | ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA /cds=(74,1258) | 1 | CCTGCCAGTGTGAGAAATCCTATTT ATGAATCCTGTCCGTATTCCTTGG |
| 2812 | Table 3A | Hs.173125 | NM_005729 | 5031986 | peptidylprolyl isomerase F (cyclophilin F) (PPIF), mRNA /cds=(83,706) | 1 | CTGTGAGCCAAGGTGCCTGAAACGAT ACGTGTGCCACTCCACTGTCACA |
| 2813 | Table 3A | Hs.83583 | NM_005731 | 5031598 | actin related protein 2/3 complex, subunit 2 (34 kD) (ARPC2), mRNA /cds=(84,986) | 1 | GAAGCGGCTGGCAACTGAAGGCTGG AACACTTGCTACTGGATAATCGTAG |
| 2814 | literature | Hs.41587 | NM_005732 | 5032016 | Rad50 (Rad50) mRNA, complete cds /cds=(388,4326) | 1 | TCGATCAGTGCTCAGAGATTGTGAAA TGCAGTGTAGTCCCTGGGATTTC |
| 2815 | Table 3A | Hs.182591 | NM_005739 | 6382080 | RAS guanyl releasing protein 1 (calcium and DAG-regulated) (RASGRP1), mRNA /cds=(103,2496) | 1 | AGGACAAATCTTGTTGATTAACAGC AGGGTCACCTCTCATTTCTTTGC |
| 2816 | Table 3A | Hs.182429 | NM_005742 | 5031972 | protein disulfide isomerase-related protein (P5), mRNA /cds=(94,1416) | 1 | AGTTCGTATTCTGTACATAATATTTTG AAGAAAACCTGGCTGTGCAAAACA |
| 2817 | Table 3A | Hs.291904 | NM_005745 | 10047078 | accessory proteins BAP31/BAP29 (DXS1357E), mRNA /cds=(136,876) | 1 | AGGAGGTTCTCTTGAGGGCAATAAA TGGAGTTTCTCTTGAGGGCAATAAA |
| 2818 | Table 3A | Hs.291904 | NM_005745 | 10047078 | accessory proteins BAP31/BAP29 (DXS1357E), mRNA /cds=(136,876) | 1 | AGGAGGTTCTCTTGAGGGCAATAAA TGGAGTTTCTCTTGAGGGCAATAAA |
| 2819 | Table 3A | Hs.239138 | NM_005746 | 5031976 | pre-B-cell colony-enhancing factor (PBEF), mRNA /cds=(27,1502) | 1 | TGCACCTCAAGATTTTAAGGAGATAA TGTTTTAGAGAGAATTTCTGCTT |
| 2820 | Table 3A | Hs.179608 | NM_005771 | 5032034 | retinol dehydrogenase homolog (RDHL), mRNA /cds=(7,978) | 1 | GCTTATGGTCCCCAGCATTACAGTA ACTTGTGAATGTGTTAAGTATCATCT |
| 2821 | Table 3A | Hs.173993 | NM_005777 | 5032032 | RNA binding motif protein 6 (RBM6), mRNA /cds=(133,3504) | 1 | CTTGTTTTGTTGTCTCTCTTTTCTT TTGTTACTGTTCTTGCTGCTAGA |
| 2822 | Table 3A | Hs.201675 | NM_005778 | 5032030 | RNA binding motif protein 5 (RBM5), mRNA /cds=(148,2595) | 1 | TTTTGGAAGATTTTCAGTCTAGTTGC CAAATCTGGCTCCTTTACAAAAGA |
| 2823 | Table 3A | Hs.152720 | NM_005792 | 5031918 | M-phase phosphoprotein 6 (MPHOSPH6), mRNA /cds=(32,514) | 1 | TCAAGAATAAAAATGCCTCTCCAGCC TTAAGTATTTACATGCTCCAGGT |
| 2824 | Table 3A | Hs.179982 | NM_005802 | 5032190 | tumor protein p53-binding protein (TP53BPL), mRNA /cds=(540,2987) | 1 | TCTGGAAGTGTGTTAAGTACAGGAG AATCCCTTTGGACAGCTTTTATTT |
| 2825 | Table 3A | Hs.143460 | NM_005813 | 6563384 | protein kinase C, nu (PRKCN), mRNA /cds=(555,3227) | 1 | ATTTCTATCACCATACTTTCCATGT GAAAACCTGAGCCTATTCTAGT |
| 2826 | Table 3A | Hs.142023 | NM_005816 | 5032140 | T cell activation, increased late expression (TACTILE), mRNA /cds=(928,2637) | 1 | TGGCTGTTGCTTTGCTTCATGTGTAT GGCTATTTGATTTAACAAGACTT |
| 2827 | Table 3A | Hs.157144 | NM_005819 | 5032130 | syntaxin 6 (STX6), mRNA /cds=(0,767) | 1 | ATAGCCATCCTCTTTGCACTCCTGTT GGTTGTGCTCATCCTCTTCTAGT |
| 2828 | Table 3A | Hs.99491 | NM_005825 | 5031622 | RAS guanyl releasing protein 2 (calcium and DAG-regulated) (RASGRP2), mRNA /cds=(253,2082) | 1 | AGGGCCAGGGCTGGTGCCTTAAGG TTGTACAGACTCTTGTAATATTTG |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|---|
| 2829 | Table 3A | Hs.15265 | NM_005826 | 14141188 | heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA /cds=(90,1991) | 1 | GCCGTGACAATTTGTTCTTTGATGTG ATTGTATTCCAAATTTCTTGTTC |
| 2830 | Table 3A | Hs.18192 | NM_005839 | 5032118 | Ser/Arg-related nuclear matrix protein (plenty of prolines 101-like) (SRM160), mRNA /cds=(5,2467) | 1 | TGGTATATACAACCTTCAGAGCCTCT TGTATTTGGAAGGCTGGAAGGGCC |
| 2831 | Table 3A | Hs.29117 | NM_005859 | 5032006 | purine-rich element binding protein A (PURA), mRNA /cds=(59,1027) | 1 | GCTACTGCAGGGTGAGGAAGAAGGG GAAGAAGATTGATCAAACAGAATGA |
| 2832 | Table 3A | Hs.23964 | NM_005870 | 12056471 | sin3-associated polypeptide, 18kD (SAP18), mRNA /cds=(573,1034) | 1 | TGTTTCAAGCCCTCTGTAAAATATGA AGAAAAGTCTCTTAGCATTCTGT |
| 2833 | Table 3A | Hs.22960 | NM_005872 | 5031652 | breast carcinoma amplified sequence 2 (BCAS2), mRNA /cds=(48,725) | 1 | TTCTAAACACATTCTTGATCACCAAAC AATTCAGAAAGACAGTGACTGT |
| 2834 | Table 3A | Hs.21756 | NM_005875 | 5031710 | translation factor sui1 homolog (GC20), mRNA /cds=(241,582) | 1 | ATCTTTGTGAGCAATTATGCTCCCAA ATCTAAGCAAGTAATAAAGAAGGG |
| 2835 | Table 3A | Hs.21189 | NM_005880 | 7549807 | DnaJ (Hsp40) homolog, subfamily A, member 2 (DNAJA2), mRNA /cds=(52,1290) | 1 | TGTAAGTTTGTACAATTTGTCTGAA GCTTTGTGTTGGCTGCACCTGC |
| 2836 | Table 3A | Hs.277721 | NM_005899 | 14110374 | membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen CA125) (M17S2), transcript variant 2, mRNA /cds=(459,3359) | 1 | ACAGTATAACTCCTGAATGCTACTTA AATAAACAGGATTCAAACTGCAA |
| 2837 | db mining | Hs.82483 | NM_005901 | 5174510 | MAD (mothers against decapentaplegic, Drosophila) homolog 2 (MADH2), mRNA /cds=(55,1458) | 1 | AGAAGCAGATTTTCTGTAGAAAAAC TAATTTTTCTGCCTTTTACCAAAA |
| 2838 | db mining | Hs.288261 | NM_005902 | 5174512 | cDNA: FLJ23037 fis, clone LNG02036, highly similar to HSU68019 mad protein homolog (hMAD-3) mRNA /cds=UNKNOWN | 1 | GAGCTTGCTCCAGATTCTGATGCATA CGGCTATATTGGTTTATGTAGTCA |
| 2839 | db mining | Hs.100602 | NM_005904 | 5174516 | MAD (mothers against decapentaplegic, Drosophila) homolog 7 (MADH7), mRNA /cds=(295,1575) | 1 | ATGGGTGTTATCACCTAGCTGAATGT TTTTCTAAAGGAGTTTATGTTCCA |
| 2840 | Table 3A | Hs.75375 | NM_005917 | 5174538 | malate dehydrogenase 1, NAD (soluble) (MDH1), mRNA /cds=(55,1059) | 1 | ACGTGCTTCTTGGTACAGGTTTGTGA ATGACAGTTTATCGTCATGCTGTT |
| 2841 | Table 3A | Hs.32353 | NM_005922 | 5803087 | mitogen-activated protein kinase kinase kinase 4 (MAP3K4), transcript variant 1, mRNA /cds=(142,4965) | 1 | TGTTGTTGTTGGCAAGCTGCAGGTTT GTAATGCAAAAGGCTGATTACTGA |
| 2842 | Table 3A | Hs.68583 | NM_005932 | 5174566 | mitochondrial intermediate peptidase (MIPEP), nuclear gene encoding mitochondrial protein, mRNA /cds=(74,2215) | 1 | TCATTGTTGCTTCTGTAATCTGAAA AATTTAAACTGGTAGAACTGG |
| 2843 | Table 3A | Hs.211581 | NM_005955 | 5174588 | metal-regulatory transcription factor 1 (MTF1), mRNA /cds=(83,2344) | 1 | CCAGTGCTGTTTGGTGGTCTGCCTTC TTTTTAATGGTATTTCTTCTCTCA |
| 2844 | Table 3A | Hs.78103 | NM_005969 | 5174612 | nucleosome assembly protein 1-like 4 (NAP1L4), mRNA /cds=(149,1276) | 1 | GCCCCACCAATTCATCCTGTCTGAAGG TCCTGGGTTTGGTGTGACCGCTTG |
| 2845 | Table 3A | Hs.48029 | NM_005985 | 5174686 | snail 1 (drosophila homolog), zinc finger protein (SNAIL), mRNA /cds=(61,855) | 1 | CCGACAGGTGGGCTGGGAGGAAAAA TGTTTACATTTTAAAGGCACACTG |
| 2846 | Table 3A | Hs.12570 | NM_005993 | 8400735 | tubulin-specific chaperone d. (TBCD), mRNA /cds=(109,3687) | 1 | GGGGTGGACGCCTCTGCCTTCACTT GAACACAAATGTGCTTCTATAAAA |
| 2847 | Table 3A | Hs.1708 | NM_005998 | 5174726 | chaperonin containing TCP1, subunit 3 (gamma) (CCT3), mRNA /cds=(0,1634) | 1 | GGCAGCCCCAGTCCCTTCTGTCTCC CAGCTCAGTTTCCAAAAGACACTG |
| 2848 | Table 3A | Hs.3712 | NM_006003 | 5174742 | ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRC1), nuclear gene encoding mitochondrial protein, mRNA /cds=(90,914) | 1 | CTGTTAAGCACTGTTATGCTCAGTCA TACACGCGAAAGGTACAATGTCTT |
| 2849 | Table 3A | Hs.73818 | NM_006004 | 5174744 | ubiquinol-cytochrome c reductase hinge protein (UQCRH), mRNA /cds=(36,311) | 1 | ATGGGTTTGGCTTGAGGCTGGTAGCT TCTATGTAATCGCAATGATTCCA |
| 2850 | Table 3A | Hs.3776 | NM_006007 | 5174754 | zinc finger protein 216 (ZNF216), mRNA /cds=(288,929) | 1 | TTCAGTTTGTCTTCAATTTTATGTAC CTTAGTCTGAGTTAGACCTGCA |
| 2851 | Table 3A | Hs.272897 | NM_006009 | 5174732 | Tubulin, alpha, brain-specific (TUBA3), mRNA /cds=(0,1355) | 1 | AAGGATTATGAGGAGGTTGGTGTGCA TTCTGTTGAAGGAGGAGGGTGAGGA |
| 2852 | Table 3A | Hs.75412 | NM_006010 | 5174392 | arginine-rich, mutated in early stage tumors (ARMET), mRNA /cds=(132,836) | 1 | TCCCTTCTTCTGTTGCTGGTGTACT CTAGGACTTCAAAGTGTGTCTGGG |
| 2853 | Table 3A | Hs.43910 | NM_006016 | 5174406 | CD164 antigen, sialomucin (CD164), mRNA /cds=(79,648) | 1 | AGTTCATTAATAAACTGCAAAACCAAT CTGTATCATGTACCAACTGACTT |
| 2854 | Table 3A | Hs.137555 | NM_006018 | 5174460 | putative chemokine receptor, GTP-binding protein (HM74), mRNA /cds=(60,1223) | 1 | TGCACGTTCTCCTGGTTCCTTCGCT TGTGTTCTGTACTTACCAAAAAAT |
| 2855 | Table 3A | Hs.46465 | NM_006019 | 5174620 | T-cell, immune regulator 1 (TCIRG1), mRNA /cds=(57,2546) | 1 | TGCCAGACCTCCTTCTGACCTCTGA GGCAGGAGAGGAATAAAGACGGTC |
| 2856 | literature | Hs.54418 | NM_006020 | 5174384 | alkylation repair, alkB homolog (ABH), mRNA /cds=(223,1122) | 1 | AGTCCCAAGGGTGTTTTGTACTGTT TTCTCCATGAATAAACTCACTTGA |
| 2857 | Table 3A | Hs.43628 | NM_006021 | 5174494 | deleted in lymphocytic leukemia, 2 (DLEU2), mRNA /cds=(240,494) | 1 | ATTAATGTCATTTCTGGAAGTGTGAA AATGTTAATGTTCAACAAGCAACA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|--|
| 2858 | Table 3A | Hs.82043 | NM_006023 | 5174422 | D123 gene product (D123), mRNA /cds=(280,1290) | 1 | GCGGGTGGGCGGAGCAGTGTGGACA TCAGCCACTTTTTATATTCATGTAC |
| 2859 | Table 3A | Hs.997 | NM_006025 | 5174622 | protease, serine, 22 (P11), mRNA /cds=(154,1263) | 1 | CCACTGAGAACTAAATGCTGTACCAC AGAGCCGGGTGTGAACATATGTTT |
| 2860 | Table 3A | Hs.109804 | NM_006026 | 5174448 | H1 histone family, member X (H1FX), mRNA /cds=(101,742) | 1 | AAACAATCGCTCCGGGCTCAGGGCT CGCGGGCTCTCCCTTCATCCATG |
| 2861 | Table 3A | Hs.24594 | NM_006048 | 5174482 | ubiquitination factor E4B (homologous to yeast UFD2) (UBE4B), mRNA /cds=(85,3993) | 1 | TGTCCTCTGTCAATTCCTAACGCAA ACTACAATAATGTTGACACACGT |
| 2862 | Table 3A | Hs.274243 | NM_006054 | 5174654 | receptor tyrosine kinase-like orphan receptor 1 (ROR1), mRNA /cds=(375,3188) | 1 | AGCACCTAAGGAGCTTGAATCTTGGT TCCTGTAAAAATTTCAAATGATGT |
| 2863 | Table 3A | Hs.54452 | NM_006060 | 5174500 | zinc finger protein, subfamily 1A, 1 (Ikaros) (ZNF1A1), mRNA /cds=(168,1727) | 1 | ACCAACACTGTCCCAAGGTGAAATGA AGCAACAGAGAGGAAATGTACAT |
| 2864 | Table 3A | Hs.318501 | NM_006074 | 5174698 | stimulated trans-acting factor (50 kDa) (STAF50), | 1 | TGTCAGCCATTTCAATGTCTTGGGAA ACAATTTTTGTITTTTGTCTGTT |
| 2865 | Table 3A | Hs.8024 | NM_006083 | 11038650 | IK cytokine, down-regulator of HLA II (IK), mRNA /cds=(111,1784) | 1 | AGAGCTTGATCGCCAGTGAAGAAG ATTAGTGCAATCATTGAGAAGAGGA |
| 2866 | Table 3A | Hs.1706 | NM_006084 | 5174474 | interferon-stimulated transcription factor 3, gamma (48kD) (ISGF3G), mRNA /cds=(34,1215) | 1 | TTTCCCTCTCCCTGACCTCCCAACT CTAAAGCCAAGCACTTTATATTTT |
| 2867 | Table 3A | Hs.5662 | NM_006098 | 5174446 | guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 (GNB2L1), mRNA /cds=(95,1048) | 1 | GGCAGGTGACCATTGGCACACGCTA GAAGTTTATGGCAGAGCTTTACAAA |
| 2868 | Table 3A | Hs.284142 | NM_006134 | 8659558 | chromosome 21 open reading frame 4 (C21orf4), mRNA /cds=(158,634) | 1 | CTGTTTGTAGATAGGTTTTTATCTCT CAGTACACATTTGCCAATGGAGT |
| 2869 | Table 3A | Hs.1987 | NM_006139 | 5453610 | CD28 antigen (Tp44) (CD28), mRNA /cds=(222,884) | 1 | GCTCACCTATTTGGTAAAGCATGCC AATTTAAAGAGACCAAGTGATGT |
| 2870 | Table 3A | Hs.82646 | NM_006145 | 5453689 | heat shock 40kD protein 1 (HSPF1), mRNA /cds=(40,1062) | 1 | TAGACTCATTGTAAGTTGCCACTGCC AACATGAGACCAAGGTGTGTGACT |
| 2871 | Table 3A | Hs.334851 | NM_006148 | 5453709 | LIM and SH3 protein 1 (LASP1), mRNA /cds=(75,860) | 1 | CAAACTTTCTGGCCTGTTATGATTC TGAACATTGACTTGAACCAACAG |
| 2872 | Table 3A | Hs.40202 | NM_006152 | 5453723 | lymphoid-restricted membrane protein (LRMP), mRNA /cds=(574,2241) | 1 | GGGAAAGTATAGCATGAAACCAGAG GTTCTCAGAATGACCGTAAGATAGC |
| 2873 | Table 3A | Hs.75512 | NM_006156 | 5453759 | neural precursor cell expressed, developmentally down-regulated 8 (NEDD8), mRNA /cds=(99,344) | 1 | AGTCCTGTGTGCTTCCCTCTCTTATG ACTGTGTCCTGGTTGTCAATAAA |
| 2874 | Table 3A | Hs.79389 | NM_006159 | 5453765 | nel (chicken)-like 2 (NELL2), mRNA /cds=(96,2546) | 1 | ATCTTCAGAATCAGTTAGGTTCTCTCA CTGCAAGAAATAAAATGTCAGGCA |
| 2875 | Table 3A | Hs.96149 | NM_006162 | 5453771 | transcription factor (NF-ATc/B) mRNA, complete cds /cds=(369,2846) | 1 | CTTCTGGCACCCCTGGGGTTCAATAC TGGAAGTGCCTATTTAACCAGAC |
| 2876 | Table 3A | Hs.75643 | NM_006163 | 5453773 | nuclear factor (erythroid-derived 2), 45kD (NFE2), mRNA /cds=(273,1394) | 1 | GGTCTTTAGCCTCCACCTTGCTAAG CTTTGGTCTATAAAGTGGCTACA |
| 2877 | Table 3A | Hs.155396 | NM_006164 | 5453775 | nuclear factor (erythroid-derived 2)-like 2 (NFE2L2), mRNA /cds=(39,1808) | 1 | TGATGATTATGACATCTGGCTAAAAAG AAATTATTGCAAACTAACCACGA |
| 2878 | Table 3A | Hs.95262 | NM_006165 | 5453777 | nuclear factor related to kappa B binding protein (NFRKB), mRNA /cds=(2220,5216) | 1 | TCCAAAGCAGTCTCCACTGTTGTTGT GACTACAGCTCCGTCTCCTAAACA |
| 2879 | Table 3A | Hs.15243 | NM_006170 | 5453791 | nucleolar protein 1 (120kD) (NOL1), mRNA /cds=(0,2567) | 1 | ATTGTCACCAGGTTGGAACCTTTGCC TCTGTGAGGATGCCTCTCTACTG |
| 2880 | Table 3A | Hs.82120 | NM_006186 | 5453821 | nuclear receptor subfamily 4, group A, member 2 (NR4A2), mRNA /cds=(317,2113) | 1 | TTTTCTTTGTATATTTCTAGTATGGCA CATGATATGAGTCACTGCCTTTT |
| 2881 | Table 3A | Hs.41694 | NM_006190 | 5453829 | origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L), mRNA /cds=(186,1919) | 1 | TGACCTTCATGATACCAGTGAGAAGC CAGGCTAGAGAAATAAAATCCTGA |
| 2882 | Table 3A | Hs.2853 | NM_006196 | 14141164 | poly(rC)-binding protein 1 (PCBP1), mRNA /cds=(177,1247) | 1 | ACGGATTGGTTAAAAATGCTTCATA TTTGAAAAAGCTGGGAATTGCTGT |
| 2883 | Table 3A | Hs.79709 | NM_006224 | 5453907 | phosphatidylinositol transfer protein (PITPN), mRNA /cds=(216,1028) | 1 | GTCTCTCTCCATTGTGTTCCGATCCA TTTCTGTGTGTTCCCCAACCTTT |
| 2884 | Table 3A | Hs.89040 | NM_006228 | 11079650 | prepronociceptin (PNOC), mRNA /cds=(211,741) | 1 | GCCACTGCCATAACTGTTTGTAAAA GAGCTGTTCTTTTGTACTGATTGT |
| 2885 | literature | Hs.166846 | NM_006231 | 5453925 | polymerase (DNA directed), epsilon (POLE), mRNA /cds=(44,6904) | 1 | GAACTATGCCAGCTACGGCACTGTG CGTACCTCTGGAGACCTGGAGT |
| 2886 | Table 3A | Hs.155079 | NM_006243 | 5453949 | protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A), mRNA /cds=(571,2031) | 1 | ATCTTCATTGGGGGATTGAGCAGCAT TTAATAAAGTCTATGTTTGTATTT |
| 2887 | Table 3A | Hs.9247 | NM_006251 | 5453963 | protein kinase, AMP-activated, alpha 1 catalytic subunit (PRKAA1), mRNA /cds=(23,1675) | 1 | TTATAACCGAGGGCTGGCGTTTGGAA ATCGAATTTCGACAGGGATTGGAA |
| 2888 | Table 3A | Hs.315366 | NM_006255 | 5453971 | protein kinase C, eta (PRKCH), mRNA /cds=(166,2214) | 1 | TTCCAGCATCAGCCTTAGAACAGA ACCTTACCTTCAAGGAGCAAGTGA |
| 2889 | Table 3A | Hs.75348 | NM_006263 | 5453989 | proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) (PSME1), mRNA /cds=(92,841) | 1 | CCAGATTTTCCCAACTTGCTTCTG TTGAGATTTTCCCTCACCTTGCC |
| 2890 | Table 3A | Hs.81848 | NM_006265 | 5453993 | RAD21 (S. pombe) homolog (RAD21), mRNA /cds=(184,2079) | 1 | AACCAAGGAGTTTTCCCGTTTGTAA AAAGACATTGTAGATAAATTGAATG |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|---|
| 2891 | Table 3A | Hs.199179 | NM_006267 | 6382078 | RAN binding protein 2 (RANBP2), mRNA /cds=(127,9801) | 1 | ACCATGTTCTTCGTTAAAGATTTGCT |
| 2892 | Table 3A | Hs.173159 | NM_006283 | 5454099 | transforming, acidic coiled-coil containing protein 1 (TACC1), mRNA /cds=(320,2737) | 1 | TTATACAAGATTGTTGCAGTACC CACATCTGCTCCACTGTGTTCCAC GGGTGCCATGAAGTGTGTGAGGAG |
| 2893 | Table 3A | Hs.89657 | NM_006284 | 5454105 | TATA box binding protein (TBP)-associated factor, RNA polymerase II, H, 30kD (TAF2H), mRNA /cds=(17,673) | 1 | CGCACTACTTCACCTGAGCCACCCAA CCTAAATGTACTTATCTGTCCCCA |
| 2894 | Table 3A | Hs.116481 | NM_001782 | 4502682 | CD72 antigen (CD72), mRNA /cds=(108,1187) | 1 | GGGCGGCCCGGAGCCAGCCAGGCA GTTTTATTGAAATCTTTTAAATAAT |
| 2895 | Table 3A | Hs.18420 | NM_006289 | 5454129 | tailin 1 (TLN1), mRNA /cds=(126,7751) | 1 | CTCTCCAAGAGTATTATTAACGCTGC TGTACCTCGATCTGAATCTGCCGG |
| 2896 | Table 3A | Hs.211600 | NM_006290 | 5454131 | tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), mRNA /cds=(66,2438) | 1 | TCCCTAATAGAAAGCCACCTATTCTTT GTTGGATTCTTCAAGTTTTTCT |
| 2897 | Table 3A | Hs.101382 | NM_006291 | 5454133 | tumor necrosis factor, alpha-induced protein 2 (TNFAIP2), mRNA /cds=(131,2095) | 1 | AGTACTGCTTTTGTATGTATGTTGAAC AGGATCCAGGTTTTTATAGCTTG |
| 2898 | Table 3A | Hs.118910 | NM_006292 | 5454139 | tumor susceptibility gene 101 (TSG101), mRNA /cds=(90,1262) | 1 | CACTTTCTATCCTCTGTAACTTTTTG TGCTGAATGTTGGGACTGCTAAA |
| 2899 | Table 3A | Hs.131255 | NM_006294 | 5454151 | ubiquinol-cytochrome c reductase binding protein (UQCRCB), mRNA /cds=(32,367) | 1 | GAAGAATGGGCAAGAAAGTAATCATG TAGTTGAAGTCTGTGGATGCAGCT |
| 2900 | Table 3A | Hs.279841 | NM_018062 | 8922359 | hypothetical protein FLJ10335 (FLJ10335), mRNA /cds=(33,1160) | 1 | CAAAGGTTCTTGAGACTCTTGATATTT CTGTCTTCTCCTTGCTCTTCTCT |
| 2901 | literature | Hs.98493 | NM_006297 | 5454171 | X-ray repair complementing defective repair in Chinese hamster cells 1 (XRCC1), mRNA /cds=(105,2006) | 1 | CCGATGGATCTACAGTTGCAATGAGA AGCAGAAGTTACTTCTCACCAGC |
| 2902 | Table 3A | Hs.293007 | NM_006310 | 5453987 | aminopeptidase puromycin sensitive (NPEPPS), mRNA /cds=(404,3031) | 1 | TTCCTGCATAACTCAATCTGAACCAA GGATTGTAGTTTAGTTTTCTCCT |
| 2903 | Table 3A | Hs.287994 | NM_006312 | 5454073 | nuclear receptor co-repressor 2 (NCOR2), mRNA /cds=(1,7554) | 1 | GCAGGGTGGTGGTATTCTGTCATTTA CACACGCTGTTCTAATTAAAGC |
| 2904 | Table 3A | Hs.10842 | NM_006325 | 6042206 | RAN, member RAS oncogene family (RAN), mRNA /cds=(114,764) | 1 | GCACTTTGTGTTGAATGTTAGATGCT TAGTGTGAAGTTGATACGCAAGC |
| 2905 | db mining | Hs.12540 | NM_006330 | 5453721 | lysophospholipase I (LYPLA1), mRNA /cds=(35,727) | 1 | GCAAGAAATATTCATTGAAATATTGT GCTGTAAATGGGAAAGTGTAAG |
| 2906 | literature | Hs.19400 | NM_006341 | 6006019 | MAD2 (mitotic arrest deficient, yeast, homolog)-like 2 (MAD2L2), mRNA /cds=(111,746) | 1 | GCCAACTGCTGTCTGCTCAAATACTG TGCTGTGAGTTGTTCAATAAAGG |
| 2907 | Table 3A | Hs.104019 | NM_006342 | 5454101 | transforming, acidic coiled-coil containing protein 3 (TACC3), mRNA /cds=(108,2624) | 1 | GACCTCATCTCCAAGATGGAGAAGAT CTGACCTCCACGGAGCCGCTGTCC |
| 2908 | Table 3A | Hs.43913 | NM_006346 | 5453889 | PIBF1 gene product (PIBF1), mRNA /cds=(0,2276) | 1 | CTTTACTAAAAAAGAACACCTGAGT GGTCTAAGAAACAAAGATGAAGA |
| 2909 | Table 3A | Hs.158196 | NM_006354 | 5454103 | Homo sapiens, Similar to transcriptional adaptor 3 (ADA3, yeast homolog)-like (PCAF histone acetylase complex), clone MGC:3508 IMAGE:3009860, mRNA, complete cds /cds=(557,1666) | 1 | GCCTGGAAGACTCTGAAGGAGCGTG AGAGCATCCTGAAGCTGCTGGATGG |
| 2910 | Table 3A | Hs.307099 | NM_006356 | 5453558 | clone 023e08 My032 protein mRNA, complete cds /cds=(46,459) | 1 | CAGGAGGAAGCTCTGGCCCTTGATT ACACATTCTGGACATTAAAAATAA |
| 2911 | Table 3A | Hs.69469 | NM_006360 | 5453653 | dendritic cell protein (GA17), mRNA /cds=(51,1175) | 1 | GCCTTTTGAGTCTTTCCGATACCTGA GTTTTATGCTTATAATTTTGT |
| 2912 | Table 3A | Hs.173497 | NM_006363 | 14591927 | Sec23 (S. cerevisiae) homolog B (SEC23B), transcript variant 3, mRNA /cds=(112,2415) | 1 | TTAAGCTGAGGATACAAACAGGAAAT GCAACGGTGTGAGATTGTGTTCAA |
| 2913 | Table 3A | Hs.104125 | NM_006367 | 10938021 | adenylyl cyclase-associated protein (CAP), mRNA /cds=(62,1489) | 1 | TCTACCCATTTCCTGAGGCCTGTGGA AATAAACCTTTATGTACTTAAAGT |
| 2914 | Table 3A | Hs.79089 | NM_006378 | 5454049 | sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (SEMA4D), mRNA /cds=(87,2675) | 1 | AGCAATAAACTCTGGATGTTTGTGCG CGTGTGTGGACAGTCTTATCTTCC |
| 2915 | Table 3A | Hs.279939 | NM_006389 | 13699861 | mitochondrial carrier homolog 1 (MTCH1), nuclear gene encoding mitochondrial protein, mRNA /cds=(0,1118) | 1 | AGCTGTTGATGCTGGTTGGACAGGTT TGAGTCAAATTGTACTTTGCTCCA |
| 2916 | Table 3A | Hs.296585 | NM_006392 | 5453793 | nucleolar protein (KKE/D repeat) (NOP56), mRNA /cds=(21,1829) | 1 | AGGTGACATTTCCACCTGTGCCCG TGTTCCCAATAAAAAACAATTCAC |
| 2917 | Table 3A | Hs.84153 | NM_006400 | 13259506 | dynactin 2 (p50) (DCTN2), mRNA /cds=(136,1356) | 1 | CTGTGGCTGACTGTAATACTGTACAA CTGTTTCTGACCATTTAAATGCTGT |
| 2918 | Table 3A | Hs.80261 | NM_006403 | 5453679 | enhancer of filamentation 1 (cas-like docking; Grk-associated substrate related) (HEF1), mRNA /cds=(163,2667) | 1 | ACATATGCACACTGACACTCAAGAG TGGCTAGCTACACAGAGTCCATCT |
| 2919 | Table 3A | Hs.92384 | NM_006407 | 7669496 | vitamin A responsive; cytoskeleton related (JWA), mRNA /cds=(89,655) | 1 | TGACTTCACAGACATGGTCTAGAATC TGTAACCTTACCCACATATGAAGA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|---|
| 2920 | Table 3A | Hs.139120 | NM_006413 | 5454023 | Homo sapiens, ribonuclease P (30kD), clone MGC:12256 IMAGE:3827681, mRNA, complete cds /cds=(294,1100) | 1 | CCCAGTCTCTGTCAGCACTCCCTTCT TCCCTTTTATAGTTCATCAGCCAC |
| 2921 | Table 3A | Hs.82921 | NM_006416 | 5453620 | solute carrier family 35 (CMP-sialic acid transporter), member 1 (SLC35A1), mRNA /cds=(27,1040) | 1 | TGACTGAGTACCCCTTTAGTGAGTAC CCCTTTAGTGCTATATTTGTGCCA |
| 2922 | Table 3A | Hs.82316 | NM_006417 | 5453743 | interferon-induced, hepatitis C-associated microtubular aggregate protein (44kD) (MTAP44), mRNA /cds=(0,1334) | 1 | TGCCTTTTGAGCAAAATAGGGAATCTA AGGGAGGAAATTATCAACTGTGCA |
| 2923 | db mining | Hs.100431 | NM_006419 | 5453576 | small inducible cytokine B subfamily (Cys-X-Cys motif), member 13 (B-cell chemoattractant) (SCYB13), mRNA /cds=(90,419) | 1 | GCGGGGCCGGGGGACTCTGGTATC TAATCTTTAATGATTCTATAAAAT |
| 2924 | Table 3A | Hs.94631 | NM_006421 | 6715588 | brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA /cds=(141,5690) | 1 | ACAACTTTCTGTACAATATTGATTCCC ATCTGGGATATTCTAATCAGGTT |
| 2925 | Table 3A | Hs.108809 | NM_006429 | 5453606 | chaperonin containing TCP1, subunit 7 (eta) (CCT7), mRNA /cds=(68,1699) | 1 | TTTTACAAGGAAGGGGTAGTAATTGG CCCACCTCTTCTTACTGGAGGCT |
| 2926 | Table 3A | Hs.119529 | NM_006432 | 5453677 | epididymal secretory protein (19.5kD) (HE1), mRNA /cds=(10,465) | 1 | AACAACATTAACTTGTGGCCTCTTTCT ACACCTGGAAATTTACTCTTTGAA |
| 2927 | Table 3A | Hs.174195 | NM_006435 | 10835237 | interferon induced transmembrane protein 2 (1-8D) (IFITM2), mRNA /cds=(279,677) | 1 | ACAGCCGAGTCCTGCATCAGCCCTTT ATCCTCACACGCTTTTCTACAAATG |
| 2928 | Table 3A | Hs.77225 | NM_006437 | 11496990 | ADP-ribosyltransferase (NAD ⁺ ; poly (ADP-ribose) polymerase)-like 1 (ADPRTL1), mRNA /cds=(106,5280) | 1 | GTCAAGGCTAAGTCAAATGAACTGA ATTTTAAACTTTTTGCATGCTCT |
| 2929 | Table 3A | Hs.118131 | NM_006441 | 5453745 | 5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase) (MTHFS), mRNA /cds=(13,624) | 1 | AAACGACATGAAGGTAGATGAAGTCC TTTACGAAGACTCGTCAACAGCTT |
| 2930 | Table 3A | Hs.340268 | NM_006461 | 5453631 | qy37e05.x1 cDNA, 3' end /clone=IMAGE:2014208 /clone_end=3' | 1 | CCCAATACCAAGACCAACTGGCATAG AGCCAACGTAGATAAATGCTATTT |
| 2931 | Table 3A | Hs.233936 | NM_006471 | 5453739 | myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB), mRNA /cds=(114,629) | 1 | GGGTCTATACAGAGTCAATATATTTTT TCAGAGAAAGTTAGTTCCGGCTCG |
| 2932 | Table 3A | Hs.179526 | NM_006472 | 5454161 | upregulated by 1,25-dihydroxyvitamin D-3 (VDUP1), mRNA /cds=(221,1396) | 1 | CCAGAAAGTGTGGGCTGAAGATGGT TGGTTTCATGTGGGGGTATTATGTA |
| 2933 | Table 3A | Hs.5509 | NM_006495 | 5729817 | ecotropic viral integration site 2B (EVI2B), mRNA /cds=(0,1346) | 1 | TCCAACCTTGAGATCCAGTGCAGGA GTTCTCTATTCTCCCAACTCTGA |
| 2934 | literature | Hs.155573 | NM_006502 | 5729981 | polymerase (DNA directed), eta (POLH), mRNA /cds=(237,2378) | 1 | TGGCACAGAAAAGGGACCAAGTTTAA AAAAGGGTTTTAAATGTAATGAGA |
| 2935 | db mining | Hs.858 | NM_006509 | 5730006 | v-rel avian reticuloendotheliosis viral oncogene homolog B (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3) (RELB), mRNA /cds=(144,1883) | 1 | GGGGTAGGTTGGTTGTTTCAGAGCTT CCCAATAAAGATGAGTTTTTGAGC |
| 2936 | Table 3A | Hs.4888 | NM_006513 | 5730028 | seryl-tRNA synthetase (SARS), mRNA /cds=(75,1619) | 1 | TGGGCATAGGGACCCATCATTGATGA CTGATGAAACCATGTAATAAAGCA |
| 2937 | Table 3A | Hs.155040 | NM_006526 | 5730123 | zinc finger protein 217 (ZNF217), mRNA /cds=(271,3417) | 1 | ATTTTCTACAGCCCTTTGTACTTCAA AATATGTTTTTGTGTCCATCAGT |
| 2938 | Table 3A | Hs.251636 | NM_006537 | 5730109 | ubiquitin specific protease 3 (USP3), mRNA /cds=(93,1658) | 1 | TCAGCACTAACTAAATAAATTTGTTGG TTCAGTTGACTTGTCTCGCAAA |
| 2939 | Table 3A | Hs.86088 | NM_006546 | 5729881 | IGF-II mRNA-binding protein 1 (IMP-1), mRNA /cds=(9,1742) | 1 | AGAGGGTGATGCACACCTCAGTGGG AAGAAAATAAAATTTCTTCAGGT |
| 2940 | Table 3A | Hs.119537 | NM_006559 | 5730026 | GAP-associated tyrosine phosphoprotein p62 (Sam68) (SAM68), mRNA /cds=(106,1437) | 1 | TGTGTAAGTCTGCCTAAATAGGTAGC TTAAACTTATGTCAAAATGTCTGC |
| 2941 | Table 3A | Hs.59106 | NM_006568 | 5729764 | cell growth regulatory with ring finger domain (CGR19), mRNA /cds=(27,1025) | 1 | TCCTTTCTGCTTAGTGAATGAATACT GGAATCCATCTGTGTGATACAAT |
| 2942 | db mining | Hs.270737 | NM_006573 | 5730096 | tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), mRNA /cds=(0,857) | 1 | GCAATACCAAGAGAAAATGCACAAAT ATCACTGGATGGAGATGTCACATT |
| 2943 | Table 3A | Hs.4069 | NM_006582 | 13435376 | glucocorticoid modulatory element binding protein 1 (GMEB1), transcript variant 1, mRNA /cds=(138,1859) | 1 | TGGGGATCTCAGGGCCAGGAGTTAT GTTTTGATTTGGAATTTTAATTATT |
| 2944 | Table 3A | Hs.12820 | NM_006590 | 5730024 | SnRNP assembly defective 1 homolog (SAD1), mRNA /cds=(492,1466) | 1 | CCAGTAACTTCGCTCTGTTAGAGGTG GAGGATTTTCTATGTTCCCCCA |
| 2945 | literature | Hs.241517 | NM_006596 | 5729983 | DNA polymerase theta (POLQ) mRNA, complete cds /cds=(0,8174) | 1 | TGCTGAAAAGATTGTACTTTGTGATC CCAATCAGAGGGATGGAGCTAATC |
| 2946 | Table 3A | Hs.180414 | NM_006597 | 5729876 | heat shock 70kD protein 8 (HSPA8), mRNA /cds=(83,2023) | 1 | TCAGACTGCTGAGAAGGAAGAAATTTG AACATCAACAGAAAGAGCTGGAGA |
| 2947 | Table 3A | Hs.154672 | NM_006636 | 13699869 | methylene tetrahydrofolate dehydrogenase (NAD ⁺ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,1110) | 1 | TGGGCAGCTTGGGTAAGTACGCAAC TTACTTTTCCACCAAGAAGTGTCA |

Table 8

| | | | | | | | |
|------|----------|-----------|-----------|----------|---|---|---|
| 2948 | Table 3A | Hs.36927 | NM_006644 | 5729878 | heat shock 105kD (HSP105B), mRNA /cds=(313,2757) | 1 | TGTGAAAGTGTGGAATGGAAGAAATG TCGATCCTGTTGTAACGTATTGTG |
| 2949 | Table 3A | Hs.1845 | NM_006674 | 5729965 | MHC class I region ORF (P5-1), mRNA /cds=(304,735) | 1 | CTAATTTTCAGTGCTTGTGCTTGGTTG TTCAGGGCCATTTTCAGGTTTGGGT |
| 2950 | Table 3A | Hs.76807 | NM_006696 | 5730052 | major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA /cds=(26,790) | 1 | AGCTAGCAGATCGTAGCTAGTTTGTG TGTGCTTGTCATTTGTACAGACTT |
| 2951 | Table 3A | Hs.5300 | NM_006698 | 5729737 | bladder cancer associated protein (BLCAP), mRNA /cds=(254,517) | 1 | ATGGGGCCAGGCAGAGAACAGAAGCTG GAGGCAGTCCATCTAGGGAATGGGA |
| 2952 | Table 3A | Hs.75207 | NM_006708 | 5729841 | glyoxalase I (GLO1), mRNA /cds=(87,641) | 1 | GTTTCCTTTTTGGGTGAAATGGATTTA TGTGAGTGCTTTAAACAAATAGC |
| 2953 | Table 3A | Hs.74861 | NM_006713 | 5729967 | activated RNA polymerase II transcription cofactor 4 (PC4), mRNA /cds=(0,383) | 1 | GAACAATGGAGCCAGCTGAAGGAAC AGATTTCTGACATAGATGACGCAGT |
| 2954 | Table 3A | Hs.195471 | NM_006732 | 5803016 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), mRNA /cds=(114,1676) | 1 | CGTCCCTCTCCCCTTGGTTCTGCAC TGTGCCAATAAAAAGCTCTTAA |
| 2955 | Table 3A | Hs.75367 | NM_006748 | 5803170 | Src-like-adaptor (SLA), mRNA /cds=(41,871) | 1 | GAGCACCAGAGGGATTTCAGTG GGAAGCATTACACTTTGCTAAATCA |
| 2956 | Table 3A | Hs.77837 | NM_006759 | 13027637 | UDP-glucose pyrophosphorylase 2 (UGP2), mRNA /cds=(84,1610) | 1 | AGCACAGATGGTGCAATACCTTTCCTT CTTTGAAGAGATCCCAAAGTTAGT |
| 2957 | Table 3A | Hs.75462 | NM_006763 | 5802987 | BTG family, member 2 (BTG2), mRNA /cds=(71,547) | 1 | TGGAAGAATGTACAGCTTATGGACAA ATGTACACCTTTTGTACTTTAA |
| 2958 | Table 3A | Hs.100555 | NM_006773 | 13787205 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 18 (Myc-regulated) (DDX18), mRNA /cds=(71,2083) | 1 | TTTTGGAGCAAAAACATGGGTTGTA ATTTGAATAAAGTGTCACTAAGCA |
| 2959 | Table 3A | Hs.143604 | NM_006777 | 10048402 | Kaiso (ZNF-kaiso), mRNA /cds=(0,2018) | 1 | TTCAGCAGGAAAATGATTCAATTTTAA AACAAAAATGTAACAGATGGCAGT |
| 2960 | Table 3A | Hs.33085 | NM_006784 | 5803220 | WD repeat domain 3 (WDR3), mRNA /cds=(47,2878) | 1 | AAGTAGCCAAAGCTAAGATGCCTGGCT GGGCTTCTGAGGAATTAATACACT |
| 2961 | Table 3A | Hs.4943 | NM_006787 | 10863906 | hepatocellular carcinoma associated protein; breast cancer associated gene 1 (JCL-1), mRNA /cds=(69,1889) | 1 | CTGACCGCCACTCTCACATTTGGGCT CTTGCTGGCCTTGGTGAGCTGG |
| 2962 | Table 3A | Hs.6353 | NM_006791 | 5803101 | MORF-related gene 15 (MRG15), mRNA /cds=(131,1102) | 1 | TGCATTGTGTAGCTAGTTTTCTGGAA AAGTCAATCTTTTAGGAATTGTTT |
| 2963 | Table 3A | Hs.88764 | NM_006800 | 5803103 | male-specific lethal-3 (Drosophila)-like 1 (MSL3L1), mRNA /cds=(105,1670) | 1 | ACAGCTATACTTTGTTGTGTAATGTTA TGGTTCCCTTTCTGTAATGTTT |
| 2964 | Table 3A | Hs.77897 | NM_006802 | 5803166 | splicing factor 3a, subunit 3, 60kD (SF3A3), mRNA /cds=(8,1513) | 1 | GACAGGATCCCCAGAGACCCCATTT GCCTCTCAACACTCAGACCTTCAA |
| 2965 | Table 3A | Hs.272168 | NM_006811 | 5803192 | DNA sequence from clone RP1-179M20 on chromosome 20 Contains a 3' end of a novel gene similar to cellular retinaldehyde-binding protein, the TDE1 gene (Tumour differentially expressed 1), the PKIG gene encoding protein kinase (cAMP-dependent, catalytic) inhibitor gamma, the 3' end of the ADA gene encoding adenosine deaminase, 2 CpG islands, ESTs, STSs and GSSs /cds=(69,1490) | 1 | TTTGGTTTAAAAATGTAAGATAGGAAAA TGTGGATATTTGAGGCCATGCT |
| 2966 | Table 3A | Hs.75969 | NM_006813 | 5802981 | proline-rich protein with nuclear targeting signal (B4-2), mRNA /cds=(113,1096) | 1 | AATCTACATTTTCTTACCAGGAGCAG CATTGAGGTTTTTGAGCATAGTAC |
| 2967 | Table 3A | Hs.75841 | NM_006817 | 13124889 | chromosome 12 open reading frame 8 (C12orf8), mRNA /cds=(11,796) | 1 | ACTAACCCACGATTCTGAGCCCTGAG TATGCCTGGACATTGATGCTAACA |
| 2968 | Table 3A | Hs.75612 | NM_006819 | 5803180 | stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA /cds=(62,1693) | 1 | TTATTCTGCGTCCCCTTCTCCAATAAA ACAAGCCAGTTGGCGGTGTTAT |
| 2969 | Table 3A | Hs.75470 | NM_006820 | 5803026 | hypothetical protein, expressed in osteoblast (GS3686), mRNA /cds=(241,1482) | 1 | TCCTTCCCCTCTCTCCAACATCACCA TTCACTTTAAATTTTCTGTATAT |
| 2970 | Table 3A | Hs.74405 | NM_006826 | 5803226 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide (YWHAQ), mRNA /cds=(100,837) | 1 | AGTCCCAAAAAGCCTTGTGAAAATG TTATGCCCTATGTAACAGCAGAGT |
| 2971 | Table 3A | Hs.15591 | NM_006833 | 5803095 | COP9 subunit 6 (MOV34 homolog, 34 kD) (MOV34-34KD), mRNA /cds=(43,936) | 1 | AGGGGAGGGCACTACACTTCCTTGA GAGAAACCGCTGTCAATAATAAAG |
| 2972 | Table 3A | Hs.79933 | NM_006835 | 5802991 | cyclin I (CCNI), mRNA /cds=(0,1133) | 1 | AGGCTGTAGAAGGAAATATACCTTAA CAGGCTGATTTGGAGTGACCCAGA |
| 2973 | Table 3A | Hs.278613 | NM_006837 | 5803045 | interferon, alpha-inducible protein 27 (IFI27), mRNA /cds=(54,422) | 1 | ACCAGTTACCCAAAATCTGATTAGAA GTATAAGGTGCTCTGAAGTGTCCCT |
| 2974 | Table 3A | Hs.78504 | NM_006839 | 5803114 | inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA /cds=(92,2368) | 1 | TGAGGCTTGTGAGGCCAATCAAAATA ATGTTTGTGATCTCTACTACTGTT |
| 2975 | Table 3A | Hs.75916 | NM_006842 | 5803154 | splicing factor 3b, subunit 2, 145kD (SF3B2), mRNA /cds=(48,2666) | 1 | CAGTTCCCAAGGACTTGTCAATTCAT GTTCTTATTTTAGACCTGTTTGT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|--|
| 2976 | db mining | Hs.105928 | NM_006847 | 5803063 | leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA /cds=(49,1944) | 1 | ACCACTAGAAGATTCCGGGAACGTTG GGAGTCACCTGATTCTGCAAAGAT |
| 2977 | Table 3A | Hs.315463 | NM_006850 | 5803085 | interleukin 24 (IL24), mRNA /cds=(274,894) | 1 | GTCAAGCTGACCTTGCTGATGGTGAC ATTGCACCTGGATGTACTATCCAA |
| 2978 | Table 3A | Hs.64639 | NM_006851 | 5803150 | glioma pathogenesis-related protein (RTVP1), mRNA /cds=(128,928) | 1 | ACAGCTCAAGTACCCTAATTTAGTTC TTTTGGACTAATACAATTCAGGAA |
| 2979 | db mining | Hs.113277 | NM_006865 | 5803061 | leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3 (LILRA3), mRNA /cds=(62,1381) | 1 | GATGACGCTGGGCACAGAGGGTCAG GTCCTGTCAAGAGGAGCTGGGTGTC |
| 2980 | Table 3A | Hs.82143 | NM_006874 | 6857815 | E74-like factor 2 (ets domain transcription factor) (ELF2), mRNA /cds=(121,1722) | 1 | AACATCTCTCTTCTCTTCCCAACTAC TGCATGAAGAAATTCATTCTCCA |
| 2981 | Table 3A | Hs.80205 | NM_006875 | 5803124 | pim-2 oncogene (PIM2), mRNA /cds=(185,1189) | 1 | TTCTGCTGCCTGGATTATTTAAAAAGCC ATGTGTGGAACCCACTATTTAAT |
| 2982 | Table 3A | Hs.177530 | NM_006886 | 5901895 | ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), mRNA /cds=(91,246) | 1 | TGCTACATTTCCAGGTGAAGATGTG TGGGCACATGTTATGGCAGATTGA |
| 2983 | Table 3A | Hs.177656 | NM_006888 | 5901911 | calmodulin 1 (phosphorylase kinase, delta) (CALM1), mRNA /cds=(199,648) | 1 | ACAACCATCAACATTGCTGTTCAAAG AAATTACAGTTTACGTCCATTCCA |
| 2984 | Table 3A | Hs.155410 | NM_006899 | 5901981 | isocitrate dehydrogenase 3 (NAD+) beta (IDH3B), mRNA /cds=(79,1236) | 1 | CCCACCCATAGGCCCTGTCCATACCC ATGTAAGGTGTTCAATAAAGAACA |
| 2985 | Table 3A | Hs.118684 | NM_006923 | 14141194 | stromal cell-derived factor 2 (SDF2), mRNA /cds=(39,674) | 1 | ACTCTTCAGGAGCTTGGCATCATGGA CTGTTAATGTATGTGATTTTCCCC |
| 2986 | Table 3A | Hs.166975 | NM_006925 | 5902077 | splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(218,541) | 1 | GGTCAAGGGTGTCCTCCACTCTTTAA CAGCTGCTGGACAGACACATTAGA |
| 2987 | Table 3A | Hs.7594 | NM_006931 | 5902089 | solute carrier family 2 (facilitated glucose transporter), member 3 (SLC2A3), mRNA /cds=(242,1732) | 1 | GCAACTTCATGTCAACTTTCTGGCTC CTCAACAGTAGGTTGGCAGTAAG |
| 2988 | Table 3A | Hs.180139 | NM_006937 | 5902097 | SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA /cds=(90,377) | 1 | CCAAGTGAGACGGGGATGGGGAAA AATACTGATTCTGTGAAATATCCC |
| 2989 | Table 3A | Hs.86948 | NM_006938 | 5902101 | small nuclear ribonucleoprotein D1 polypeptide (16kD) (SNRPD1), mRNA /cds=(150,509) | 1 | TGTGTAATGTACCTGTGAGTGCCTCC TTTATTAAGGGGTTCTTTGAGAAAT |
| 2990 | Table 3A | Hs.237825 | NM_006947 | 5902123 | signal recognition particle 72kD (SRP72), mRNA /cds=(0,2015) | 1 | GCAGGGGCTCCAGCAACAAAAAAGA AACAGCAACAGAAAAAGAAGAAAGG |
| 2991 | Table 3A | Hs.108642 | NM_006963 | 5902159 | Homo sapiens, zinc finger protein 22 (KOX 15), clone MGC:9735 IMAGE:3852749, mRNA, complete cds /cds=(133,807) | 1 | AGACTCACTTACCCTCTTGGAAGCT GGTACAGAAGGAAGTCTGTGGCTG |
| 2992 | Table 3A | Hs.167741 | NM_006994 | 6325463 | butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA /cds=(171,1925) | 1 | CCTGGTCATTGGTGGATGTTAAACCC ATATTCTTTCAACTGCTGCCTGC |
| 2993 | Table 3A | Hs.225951 | NM_006999 | 6631114 | topoisomerase-related function protein 4-1 (TRF4), mRNA /cds=(37,1665) | 1 | AATGAATTGGCTGGCTGACTGATGTG GTCGCGTGCTACAGGTTTGACAAA |
| 2994 | Table 3A | Hs.97932 | NM_007015 | 5901931 | chondromodulin I precursor (CHM-I), mRNA /cds=(0,1004) | 1 | TTGATTTGCCATAAGTCTTCCCTTGCT TGCACTCTCCAAAGCTATTTTGA |
| 2995 | Table 3A | Hs.93502 | NM_007020 | 5902143 | U1-snRNP binding protein homolog (70kD) (U1SNRNPBP), transcript variant 1, mRNA /cds=(213,953) | 1 | AGTGAAGTTACAGTGGAATGAGTGG AGGGGGATTGCTTTCAACGCAGC |
| 2996 | Table 3A | Hs.149443 | NM_007022 | 5901883 | putative tumor suppressor (101F6), mRNA /cds=(0,668) | 1 | GCTTGGTCATTATGAACCAGGTGAGC AATGCCTACCTATACCGCAAGAGG |
| 2997 | literature | Hs.41693 | NM_007034 | 6631084 | DnaJ-like heat shock protein 40 (HLJ1), mRNA /cds=(176,1189) | 1 | AAGGCACTGAAAATATAAAAGGACTG GTAGTTTACTGTAGTAGATGTGAA |
| 2998 | Table 3A | Hs.87497 | NM_007047 | 5901905 | butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA /cds=(188,1147) | 1 | GCAGAAAAGGGGAACCTATTAGCTC ACGAGTGGTCCGAGTGAAGATTGAA |
| 2999 | Table 3A | Hs.169963 | NM_007049 | 5921460 | butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA /cds=(210,1793) | 1 | TATCTTGAGACGCCCTACAAATGATG GAGGATCCAAAGAGATTTTGTGTT |
| 3000 | Table 3A | Hs.164170 | NM_007063 | 5902153 | vascular Rab-GAP/TBC-containing (VRP), mRNA /cds=(1117,3810) | 1 | AAAATGTTGTGTGTACATACCATGC TTTCAATGTTGGCTTCCAAGTTT |
| 3001 | Table 3A | Hs.21907 | NM_007067 | 5901961 | histone acetyltransferase (HBOA), mRNA /cds=(42,1877) | 1 | GGTAGAATGTGCTCTTCTATATCTAC TCCTCAATAAAGCATGTTCTCTGC |
| 3002 | literature | Hs.37181 | NM_007068 | 5901995 | DMC1 (dosage suppressor of mck1, yeast homolog) meiosis-specific homologous recombination (DMC1), mRNA /cds=(53,1075) | 1 | CCACAGAGGATTTAAGGGAGGAAT GTTTATAGGACACACACAAAAAGC |
| 3003 | Table 3A | Hs.109606 | NM_007074 | 5902133 | coronin, actin-binding protein, 1A (CORO1A), mRNA /cds=(100,1485) | 1 | CTCCAGCAGGGTCAGGCCATTACAC CCATCCACTCACCTCCATTCCAG |
| 3004 | Table 3A | Hs.252574 | NM_007104 | 6325471 | ribosomal protein L10a (RPL10A), mRNA /cds=(15,668) | 1 | AAACTGGCAGAAATGTCGGGGCCTTAT ATATCAAGAGCACCATTGGGCAAGC |
| 3005 | Table 3A | Hs.29352 | NM_007115 | 6005905 | tumor necrosis factor, alpha-induced protein 6 (TNFAIP6), mRNA /cds=(68,901) | 1 | AACACACAGTGTTTATGTTGGAATCT TTTGGAACCTCTTGTATCTCACTG |
| 3006 | Table 3A | Hs.301819 | NM_007145 | 6005965 | zinc finger protein 146 (ZNF146), mRNA /cds=(856,1734) | 1 | TGGGAGTGAGGATGGGAATGCTGTA TCTGTGGAAGTCATGTTACTGGA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|--|
| 3007 | Table 3A | Hs.260523 | NM_007158 | 6005738 | neuroblastoma RAS viral (v-ras) oncogene homolog (NRAS), mRNA /cds=(253,822) | 1 | TGCTTAGATCACTGCAGCTTCTAGGA CCCCGTTTCTTTACTGATTAA |
| 3008 | Table 3A | Hs.301637 | NM_007167 | 6005977 | zinc finger protein 258 (ZNF258), mRNA /cds=(93,2264) | 1 | CTGAACACCAAATAGCTGTGGGCTT TCTGGAACCTGCTGGCTGGGTTGCT |
| 3009 | Table 3A | Hs.14963 | NM_007192 | 6005756 | chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA /cds=(291,3434) | 1 | GCTCTGTGACTTTAAGAGAAGGAAGG GGGAGGGGTCCCGGATTTTATGTT |
| 3010 | literature | Hs.146329 | NM_007194 | 6005849 | protein kinase Chk2 (RAD53), mRNA /cds=(0,1631) | 1 | AGAAATGTCCTTCTTTCACTCTGCAT CTTTCTTTTCTTTGAGTCGTTTTT |
| 3011 | literature | Hs.271699 | NM_007195 | 6005847 | polymerase (DNA directed) iota (POLI), mRNA /cds=(64,2211) | 1 | TCCAGATAAAGCAAGAATAGTTGCAA GAAGTAAATCTGGCACAAAGCGT |
| 3012 | literature | Hs.251398 | NM_007205 | 6005917 | three prime repair exonuclease 2 (TREX2), mRNA /cds=(0,710) | 1 | CCCACAATGGCTTTGATTATGATTTT CCCCTGCTGTGTGCCGAGCTGCGG |
| 3013 | literature | Hs.79086 | NM_007208 | 6005861 | mitochondrial ribosomal protein L3 (MRPL3), mRNA /cds=(76,1122) | 1 | AAATTACAGAAACATGTTAAAGGCCG GACAAAGGAAAGACAATAAATCA |
| 3014 | Table 3A | Hs.182825 | NM_007209 | 6005859 | ribosomal protein L35 (RPL35), mRNA /cds=(27,398) | 1 | GAAGTACGCGGTCAAGGCTGAGGG GCGCATTGTCAATAAAGCACAGCTG |
| 3015 | Table 3A | Hs.151678 | NM_007210 | 13124893 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 6 (GalNAc-T6) (GALNT6), mRNA /cds=(0,1868) | 1 | TCTACAGCCATGTCCTATTCTTGAT CATCCAAAGCACCTGCAGAGTCCA |
| 3016 | Table 3A | Hs.28866 | NM_007217 | 6005897 | programmed cell death 10 (PDCD10), mRNA /cds=(153,791) | 1 | AATGTAGCTTAATCATAATCTCACACT GAAGATTTTGCATCACTTTTGCT |
| 3017 | Table 3A | Hs.28285 | NM_007218 | 6005911 | patched related protein translocated in renal cancer (TRC8), mRNA /cds=(0,1994) | 1 | TGATGATGATGTTCAAAGAGAAAGAA ATGGAGTGATTACGACACACGGCG |
| 3018 | Table 3A | Hs.283646 | NM_007220 | 6005722 | carbonic anhydrase VB, mitochondrial (CA5B), nuclear gene encoding mitochondrial protein, mRNA /cds=(137,1090) | 1 | GCCACCAGCCAAAGCAACCCCTAAA ACATTCATATCTAGGCAGTATTTTG |
| 3019 | Table 3A | Hs.94446 | NM_007221 | 6005831 | polyamine-modulated factor 1 (PMF1), mRNA /cds=(111,608) | 1 | GCCTTTACCATGTTCTCTCCACATCC GTAAATAAACTTCCTTCACTACAA |
| 3020 | literature | Hs.334676 | NM_007248 | 6005752 | three prime repair exonuclease 1 (TREX1), mRNA /cds=(256,1170) | 1 | CCACACCTGGCGAGTAGGCCAAGAA GGAAAATCTGACGAATAAGAACCCC |
| 3021 | literature | Hs.78016 | NM_007254 | 6005835 | polynucleotide kinase 3'-phosphatase (PNKP), mRNA /cds=(0,1565) | 1 | GGGCTGAGCCCGCCAGCTCCCT CCACAATAAACGCTGTTTCTCCTTG |
| 3022 | Table 3A | Hs.10958 | NM_007262 | 6005748 | RNA-binding protein regulatory subunit (DJ-1), mRNA /cds=(20,589) | 1 | TTTCTCAGCCTACAAATTGTGTCTATA CATTTCTAAGCCTTGTGTCAGA |
| 3023 | db mining | Hs.10326 | NM_007263 | 6005734 | coatamer protein complex, subunit epsilon (COPE), mRNA /cds=(42,968) | 1 | GAGCCACCCCGACGCCCATCT GTTAATAAATATCTCAACTCCAAAA |
| 3024 | Table 3A | Hs.8813 | NM_007269 | 6005885 | syntaxin binding protein 3 (STXBP3), mRNA /cds=(51,1829) | 1 | TGGAGTGATTTACAGCTGTGTACTGT TTTGCCATACTTCTAAAGAACA |
| 3025 | Table 3A | Hs.8724 | NM_007271 | 6005813 | serine threonine protein kinase (NDR), mRNA /cds=(595,1992) | 1 | CCCTTTGGAATGGTGAAGGAACCCAG CCCAATAGAAGTACAGAGCCAGCT |
| 3026 | Table 3A | Hs.7771 | NM_007273 | 6005853 | B-cell associated protein (REA), mRNA /cds=(9,908) | 1 | CTCCCTCAAGGCTGGGAGGAGATAA ACACCAACCCAGGAATTCTCAATAA |
| 3027 | Table 3A | Hs.7719 | NM_007278 | 6005763 | GABA(A) receptor-associated protein (GABARAP), mRNA /cds=(104,457) | 1 | AGGGACTGAAATGTGGGGGGAAGG TAGGAGGCACATCAATAAAGAGGAA |
| 3028 | Table 3A | Hs.1298 | NM_007289 | 6042203 | membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 2b, mRNA /cds=(228,2480) | 1 | TGGGGCAAAACCTTGCTAATTTTCTC AAAAGCATTTATCATTCTTGTTGC |
| 3029 | literature | Hs.194143 | NM_007295 | 6552300 | breast cancer 1, early onset (BRCA1), transcript variant BRCA1b, mRNA /cds=(397,5988) | 1 | CCCCCAGTGTGAAGGGCAGTGAAG ACTTGATTGTACAAAATACGTTTTG |
| 3030 | Table 3A | Hs.21486 | NM_007315 | 6274551 | signal transducer and activator of transcription 1, 91kD (STAT1), mRNA /cds=(196,2448) | 1 | AGATGGCGAGAACCCTAAGTTTCAGTT GATTTTACAATTGAATGACTAAA |
| 3031 | Table 3A | Hs.3260 | NM_007318 | 7549812 | presenilin 1 (Alzheimer disease 3) (PSEN1), transcript variant 1-463, mRNA /cds=(553,1944) | 1 | TGTCAGACCTTCTCCACAGCAAATG AGATGTATGCCCAAAGCGGTAGAA |
| 3032 | Table 3A | Hs.279611 | NM_007329 | 6633800 | deleted in malignant brain tumors 1 (DMBT1), transcript variant 2, mRNA /cds=(106,7347) | 1 | GTTGCAGGGCGAGGTCAAGAGAGTT CTGACCTGGATGCCCATAGACCTG |
| 3033 | Table 3A | Hs.74335 | NM_007355 | 6680306 | heat shock 90kD protein 1, beta (HSPCB), mRNA /cds=(0,2174) | 1 | GACAGCAGGATTGGATGTTGTGTATT GTGGTTTATTTTATTTCTTCATT |
| 3034 | Table 3A | Hs.74085 | NM_007360 | 6679051 | DNA segment on chromosome 12 (unique) 2489 expressed sequence (D12S2489E), mRNA /cds=(338,988) | 1 | AGTGCCTTCCCTGCCTGTGGGGGTC ATGCTGCCACTTTTAAATGGGTCTC |
| 3035 | Table 3A | Hs.172207 | NM_007363 | 7657382 | non-POU-domain-containing, octamer-binding (NONO), mRNA /cds=(136,1551) | 1 | TTTGGAGTTTTCTGAAAAATGGAGC AGTAATGCAGCATCAACCTATTAA |
| 3036 | Table 3A | Hs.158135 | NM_011086 | 6755061 | mRNA for KIAA0981 protein, partial cds /cds=(0,1737) | 1 | CAATGGACAAGTATTTCTAATGGTA CCAGACCACTGGACAGGCTTGGGT |
| 3037 | Table 3A | Hs.9754 | NM_012068 | 12597624 | activating transcription factor 5 (ATF5), mRNA /cds=(319,1167) | 1 | GTGTTGGAGAGGGGCTGTGTCTGGG TGAGGGATGGCGGGGTACTGATTTT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|---|
| 3038 | Table 3A | Hs.97199 | NM_012072 | 11496985 | complement component C1q receptor (C1QR), mRNA /cds=(148,2106) | 1 | GTGCTTTGAGGGTCAGCCTTTAGGAA GGTGCAGCTTTGTTGTCTTTGAG |
| 3039 | Table 3A | Hs.173334 | NM_012081 | 6912353 | ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA /cds=(0,1922) | 1 | GGCTCACATCAAAAGGCTAATAGGTG AATTTGACCAACAGCAAGCAGAGT |
| 3040 | Table 3A | Hs.1710 | NM_012089 | 9961243 | ATP-binding cassette, sub-family B (MDR/TAP), member 10 (ABCB10), nuclear gene encoding mitochondrial protein, mRNA /cds=(43,2259) | 1 | CAGAAAGCAAACAACACAATTACAAG GTTGAATCTGAGGAAAATAATCCT |
| 3041 | Table 3A | Hs.342849 | NM_012097 | 6912243 | xv24a05.x1 cDNA, 3' end /clone=IMAGE:2814032 /clone_end=3' | 1 | TCTCTCTGTGTTCTCTGTATTGTACTA ACCAACCTCCCAATCGCTGAGC |
| 3042 | Table 3A | Hs.33979 | NM_012123 | 6912299 | CGI-02 protein (CGI-02), mRNA /cds=(268,2124) | 1 | CCTGGAATAAACTCAACATGCAGAT TTGCCTACTCATAGGGACTTTGCC |
| 3043 | Table 3A | Hs.22857 | NM_012124 | 6912303 | chord domain-containing protein 1 (CHP1), mRNA /cds=(84,1082) | 1 | TGCCCTCCCTGATGGAACCTATATAA AATTGTAGACTTAAAGGTTTGTG |
| 3044 | Table 3A | Hs.36794 | NM_012142 | 6912335 | cyclin D-type binding-protein 1 (CCNDBP1), mRNA /cds=(87,1172) | 1 | TTCATTGTAAAGATGTTGATGGTCTC AATAAAATGCTAACTTCCAGTGA |
| 3045 | Table 3A | Hs.83363 | NM_012151 | 12056462 | coagulation factor VIII-associated (intronic transcript) (F8A), mRNA /cds=(57,1172) | 1 | CGTCCGCACGGTACGCTTTCAGTGGG AGTCATTTTATTCCTTACAGCTTCC |
| 3046 | Table 3A | Hs.24178 | NM_012155 | 6912355 | microtubule-associated protein like echinoderm EMAP (EMAP-2), | 1 | TGGTGTGTTGGTTTGGGGTGTTTTTTA AGTTTTTCTTTTATATCATCCAG |
| 3047 | Table 3A | Hs.5912 | NM_012179 | 7106310 | F-box only protein 7 (FBXO7), mRNA /cds=(205,1773) | 1 | CTCCCTGCTCTTGGTTCTCCTCTAGA TTGAAGTTTGTCTTCTGATGCTGT |
| 3048 | Table 3A | Hs.79381 | NM_012198 | 6912387 | grancalcin, EF-hand calcium-binding protein (GCA), mRNA /cds=(119,772) | 1 | TGAAGACATAGTTCACCTAAAAATGGC ATCCTGCTCTGAATCTAGACTTTT |
| 3049 | Table 3A | Hs.14520 | NM_012199 | 6912351 | eukaryotic translation initiation factor 2C, 1 (EIF2C1), mRNA /cds=(213,2786) | 1 | CCCTTTGAGATTTGTGTTTGTGTCT GCTTTGAGCTGTACCTTGTCCAGT |
| 3050 | Table 3A | Hs.5734 | NM_012215 | 11024697 | meningioma expressed antigen 5 (hyaluronidase) (MGEA5), mRNA /cds=(395,3145) | 1 | TCCTGTAGAAAACGAACTGTAAAGA CCATGCAAGAGGCAAAATAAAACT |
| 3051 | literature | Hs.271353 | NM_012222 | 6912519 | mutY (E. coli) homolog (MUTYH), mRNA /cds=(134,1774) | 1 | CCAGTGACACCTCTGAAAGCCCCCAT TCCCTGAGAACTCCTGTTGTAGTA |
| 3052 | Table 3A | Hs.26719 | NM_012231 | 10092605 | PR domain containing 2, with ZNF domain (PRDM2), mRNA /cds=(855,6014) | 1 | CCTGGTCAGTGGTGGTCTTCAAGAC GACAGCTCTGTATCTGCCATGTGAA |
| 3053 | literature | Hs.44017 | NM_012237 | 13775599 | sirtuin (silent mating type information regulation 2, S.cerevisiae, homolog) 2 (SIRT2), transcript variant 1, mRNA /cds=(200,1369) | 1 | CCCACCTCCCATGCTGGATGGGCAG AAGACATTGCTTATTGGAGACAAAT |
| 3054 | Table 3A | Hs.31176 | NM_012238 | 13775598 | sirtuin (silent mating type information regulation 2, S. cerevisiae, homolog) 1 (SIRT1), mRNA /cds=(53,2296) | 1 | TTACTGGCATATGTTTTGTAGACTGTT TAATGACTGGATATCTTCCTTCA |
| 3055 | Table 3A | Hs.22891 | NM_012244 | 6912669 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA /cds=(730,2337) | 1 | AATGTAAGGTTGTTTTGGGGGATGGA GTTAGAACCTTAATGATAATTTCT |
| 3056 | Table 3A | Hs.79008 | NM_012245 | 6912675 | SKI-INTERACTING PROTEIN (SNW1), mRNA /cds=(27,1637) | 1 | TTTGGAGTGGGCAAAGTAACCTCTTG CTTGGTGCACTATTGTTTCAAA |
| 3057 | Table 3A | Hs.268555 | NM_012255 | 6912743 | 5'-3' exoribonuclease 2 (XRN2), mRNA /cds=(68,2920) | 1 | GCTTATAACACATTGTAGGTAATAGG AGGTCGGGTTTCCATAATGGGT |
| 3058 | Table 3A | Hs.10882 | NM_012257 | 6912409 | HMG-box containing protein 1 (HBP1), mRNA /cds=(23,1567) | 1 | TCTTATCATTCATACATTTTCTGGAT GCTTGAGCCATCAGATATCAGCT |
| 3059 | Table 3A | Hs.23170 | NM_012280 | 7110660 | homolog of yeast SPB1 (JM23), mRNA /cds=(300,1289) | 1 | TGCAGTGGGAATCTTGGAGTGGTC TTACCTCTTCTTAAACCTCTTCA |
| 3060 | Table 3A | Hs.173714 | NM_012286 | 6912447 | MORF-related gene X (KIAA0026), mRNA /cds=(305,1171) | 1 | TGCATTATTGTGTAGCCACGGTTTTTC TGGAAAAGTTGATATTTAGGAAT |
| 3061 | Table 3A | Hs.18895 | NM_012290 | 6912719 | tousled-like kinase 1 (TLK1), mRNA /cds=(212,2575) | 1 | ATTACATTGGAAGGAGCTTTCAAGA TGGTAGGATATTGACTAACTGAGC |
| 3062 | Table 3A | Hs.30687 | NM_012296 | 6912459 | GRB2-associated binding protein 2 (GAB2), mRNA /cds=(160,2076) | 1 | CATGGTACAGGCTTGGAGCTTGCAG GTCCCTTTCTACTGTGGTGTGGAG |
| 3063 | Table 3A | Hs.120165 | NM_012318 | 6912481 | leucine zipper-EF-hand containing transmembrane protein 1 (LETM1), mRNA /cds=(297,2516) | 1 | TGTGCAGGGACAGTTGGCTTCCAGA GGTTTCAGCTTTCAGTTATTTGAGA |
| 3064 | Table 3A | Hs.234279 | NM_012325 | 6912493 | microtubule-associated protein, RP/EB family, member 1 (MAPRE1), mRNA /cds=(64,870) | 1 | AATTCCATTTTATTGGGAACCCATTTT CCACCTGGTCTTCTTGACAGGG |
| 3065 | Table 3A | Hs.172740 | NM_012326 | 10800411 | microtubule-associated protein, RP/EB family, member 3 (MAPRE3), mRNA /cds=(153,998) | 1 | AAATAAACTGTGTGGTAAAAGTACA TGCCATGTGTCCCTCAACTGAAAA |
| 3066 | Table 3A | Hs.18625 | NM_012332 | 6912517 | Mitochondrial Acyl-CoA Thioesterase (MT-ACT48), mRNA /cds=(147,1367) | 1 | TTCAAGACAATTTAATTGTGAACCTA CCATGTTGCCCTCCACTCTCTGA |
| 3067 | Table 3A | Hs.215766 | NM_012341 | 6912531 | GTP-binding protein (NGB), mRNA /cds=(23,1924) | 1 | TTTGTAAGAGCTGGGAGCAAACACGT TTATGAGTGTGTCGGAATCCCGTG |
| 3068 | Table 3A | Hs.74420 | NM_012381 | 6912561 | origin recognition complex, subunit 3 (yeast homolog)-like (ORC3L), mRNA /cds=(26,2161) | 1 | CCCAACACGAGCATGTATCAAAACACC TGTGGAGTACTTTAGACTCCAACA |
| 3069 | Table 3A | Hs.241531 | NM_012392 | 6912581 | PEF protein with a long N-terminal hydrophobic domain (peflin) (PEF), mRNA /cds=(12,866) | 1 | TGGGGCCAAAAGTCCAGTGAAATTGT AAGCTTCAATAAAAGGATGAAACT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|---|
| 3070 | Table 3A | Hs.21807 | NM_012406 | 9055315 | PR domain containing 4 (PRDM4), mRNA /cds=(122,2527) | 1 | TGGGCTGGAGTAGAGGACTCTGGTG GGAAGGTTTTGCTGCTAATGTATTT |
| 3071 | Table 3A | Hs.79033 | NM_012413 | 9257235 | glutamyl-peptide cyclotransferase (glutamyl cyclase) (QPCT), mRNA /cds=(11,1096) | 1 | AGCTAAACAGTACTTAAATAGCGGTT GGAAGTAGGTAGCCTTTGCAATTT |
| 3072 | literature | Hs.128501 | NM_012415 | 6912621 | RAD54, <i>S. cerevisiae</i> , homolog of, B (RAD54B), mRNA /cds=(80,2812) | 1 | TGTCATTCATTTTTCAGAATATAACCA CTCAAGCTACTGGCAGATAGTGA |
| 3073 | Table 3A | Hs.333212 | NM_012417 | 6912623 | retinal degeneration B beta (RDGBB), mRNA /cds=(0,998) | 1 | TCTGATAGAGAAAAAGACTGCTTTGT CACTCAAACATGTTCTTCGACCT |
| 3074 | Table 3A | Hs.151242 | NM_012423 | 14591905 | serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1 (SERPING1), mRNA /cds=(60,1562) | 1 | GGCATCGCCCATGCTCCTCACCTGTA TTTTGTAATCAGAAATAAATTGCT |
| 3075 | Table 3A | Hs.334826 | NM_012433 | 6912653 | splicing factor 3b, subunit 1, 155kD (SF3B1), mRNA /cds=(0,3914) | 1 | TTTGATGTTAAACAGTAAATGCCAGT AGTGACCAAGAACACAGTGATTAT |
| 3076 | literature | Hs.159737 | NM_012444 | 6912679 | SPO11, meiotic protein covalently bound to DSB (<i>S. cerevisiae</i>)-like (SPO11), mRNA /cds=(108,1298) | 1 | CCTTTGCCCTTATACCTTAGGGGTCTT ACTCCATAATTCATTTGTTACA |
| 3077 | literature | Hs.244613 | NM_012448 | 6912687 | signal transducer and activator of transcription 5B (STAT5B), mRNA /cds=(146,2509) | 1 | TGCACGTTATGGTGTCTTCCCTCTC ACTGTCTGAGAGTTAGTTGTAGC |
| 3078 | Table 3A | Hs.109571 | NM_012456 | 6912707 | translocase of inner mitochondrial membrane 10 (yeast) homolog (TIMM10), mRNA /cds=(129,401) | 1 | CTGTAGAGAGTCTTCAAGATCCCGGA GTGGTAGCGCTGTCTCCTGGTGAA |
| 3079 | Table 3A | Hs.7797 | NM_012461 | 6912715 | TERF1 (TRF1)-interacting nuclear factor 2 (TINF2), mRNA /cds=(262,1326) | 1 | TAGTAGGAATGAAGTGGAAGTCCAG GCTTGGAATGCCCTAACTACACTGCT |
| 3080 | Table 3A | Hs.105806 | NM_012483 | 7108345 | granulysin (GNLY), transcript variant 519, mRNA /cds=(280,669) | 1 | GATCCAGAATCCACTCTCCAGTCTCC CTCCCTGACTCCCTCTGCTGTGCC |
| 3081 | Table 3A | Hs.199263 | NM_013233 | 7019542 | Ste-20 related kinase (SPAK), mRNA /cds=(173,1816) | 1 | ATTCCATTCTATTGTTACACAACGAT TACTCGAAGATGACTGCAAAAGGT |
| 3082 | Table 3A | Hs.283781 | NM_013234 | 10801344 | muscle specific gene (M9), mRNA /cds=(171,827) | 1 | AGCCAAGAAGAGAGCATTAAACCCAA GAACATTGTGGAGAAGATTGACTT |
| 3083 | Table 3A | Hs.13493 | NM_013236 | 7106298 | like mouse brain protein E46 (E46L), mRNA /cds=(198,1625) | 1 | TATATTGTACTTACTGTGACAGCAGA TAATAAACCACTCTCTTGGAGGGC |
| 3084 | Table 3A | Hs.279529 | NM_013237 | 7019508 | px19-like protein (PX19), mRNA /cds=(176,835) | 1 | CTTATTCTCCCATTTGGGAGCTGAGG ACCGAGGCACAGAGGTGCGGTGAC |
| 3085 | Table 3A | Hs.126355 | NM_013252 | 10281668 | C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5 (CLECSF5), mRNA /cds=(197,763) | 1 | TCACTGTATACCACTGGAGTTTCTG GTTATCTCTCGTATAGCAAAATCT |
| 3086 | Table 3A | Hs.169330 | NM_013259 | 10047091 | neuronal protein (NP25), mRNA /cds=(49,897) | 1 | GCTGCCACCTCTGTTCATTTAGAAC TATGCAAAGACTCCGCTTCCGTTT |
| 3087 | Table 3A | Hs.136748 | NM_013269 | 7019446 | lectin-like NK cell receptor (LLT1), mRNA /cds=(13,588) | 1 | ACAGCAAAGCCCCAACTAATCTTTAG AAGCATATTGGAACTGATAACTCC |
| 3088 | Table 3A | Hs.14805 | NM_013272 | 7706713 | solute carrier family 21 (organic anion transporter), member 11 (SLC21A11), mRNA /cds=(193,2325) | 1 | GCCAGCTTGGAGGATGGACATTTCTG GATACACATACACATACAAAACAG |
| 3089 | literature | Hs.129903 | NM_013274 | 7019490 | polymerase (DNA-directed), lambda (POLL), mRNA /cds=(371,2098) | 1 | GTCAACATCATCCGGCACCTCTGG GGTAGGAGAACAGCCATTCCACATG |
| 3090 | Table 3A | Hs.54642 | NM_013283 | 11034824 | methionine adenosyltransferase II, beta (MAT2B), mRNA /cds=(0,1004) | 1 | TCATATGTGTGGTTATACTCATAATAA TGGGCTTGTAAGCCTTTTTCACC |
| 3091 | literature | Hs.252646 | NM_013284 | 7019492 | wm25f06.x1 cDNA, 3' end /clone=IMAGE:2436995 /clone_end=3' | 1 | CTGCTTGACTCACCGGCTTCTATTT GATGCACCCAGGCCCTTGTGGC |
| 3092 | Table 3A | Hs.75528 | NM_013285 | 7019418 | nucleolar GTPase (HUMAUNTIG), mRNA /cds=(79,2274) | 1 | GGGACAGAAACACAAACGCAAAAAAT TCAGACAAAGCAGTAATGTTTAA |
| 3093 | Table 3A | Hs.106260 | NM_013322 | 7019536 | sorting nexin 10 (SNX10), mRNA /cds=(128,733) | 1 | GCGATCCTCATCCCTTCAGCAATATG TATTTGAGTTCACACTTATTTCTGT |
| 3094 | Table 3A | Hs.289080 | NM_013326 | 7019454 | colon cancer-associated protein Mic1 (MIC1), mRNA /cds=(76,1905) | 1 | TTTTGAACAGCGAAACAGCGTTTGC GAGGGAGCCCCAATTTACACCAG |
| 3095 | literature | Hs.283018 | NM_013347 | 9558730 | replication protein A complex 34 kd subunit homolog Rpa4 (HSU24186), mRNA /cds=(404,1189) | 1 | TTCCAAAAGAAAACTAGTTGCAGTC AGGGAGCCAGCGAAAGACAAAAA |
| 3096 | Table 3A | Hs.272409 | NM_013351 | 7019548 | T-box 21 (TBX21), mRNA /cds=(211,1818) | 1 | ACTGAGAGTGGTGTCTGGATATATTC CTTTTGTCTTCATCACTTTCTGAA |
| 3097 | Table 3A | Hs.58636 | NM_013352 | 7019520 | squamous cell carcinoma antigen recognized by T cell (SART-2), mRNA /cds=(149,3025) | 1 | GCATGCATTCATTGGTTGTTCAATAA GTGAGATGATTACAGATAATACTG |
| 3098 | literature | Hs.169138 | NM_013368 | 7019514 | RPA-binding trans-activator (RBT1), mRNA /cds=(291,881) | 1 | CTGATTTTCATAACCAGGCCGGACCAC GTGCAATAGGGTGGAACCAAACT |
| 3099 | Table 3A | Hs.136713 | NM_013378 | 7019566 | pre-B lymphocyte gene 3 (VPREB3), mRNA /cds=(42,413) | 1 | GAAGACGACGCGGATTACTACTGCTC TGTTGGCTACGGCTTTAGTCCCTA |
| 3100 | Table 3A | Hs.279784 | NM_013388 | 7019502 | prolactin regulatory element binding (PREB), mRNA /cds=(131,1384) | 1 | TGAACCTCAGCCCATTTAGGCAGGAAA AGTTGATATTTAATAACAAGGAA |
| 3101 | Table 3A | Hs.171825 | NM_013390 | 7019554 | basic helix-loop-helix domain containing, class B, 2 (BHLHB2), mRNA /cds=(196,1434) | 1 | CCAAGGCACCTGGTTTTCTGTTTTAT ATACTAATAATCAGGGCCCTAAGT |
| 3102 | Table 3A | Hs.272736 | NM_013392 | 7019332 | nuclear receptor binding protein (NRBP), mRNA /cds=(112,1719) | 1 | GGGGGCCATTGATTCCGCTCAGTT GCTGTGTAATAAAAGTCTACTTTT |
| 3103 | Table 3A | Hs.7838 | NM_013446 | 7305272 | makorin, ring finger protein, 1 (MKRN1), mRNA /cds=(122,1570) | 1 | ACTTTAAGAAAAACAAATAATTGTTG CAGAGGTCTCTGATTTTGCAGC |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|--|
| 3104 | Table 3A | Hs.8858 | NM_013448 | 7304918 | bromodomain adjacent to zinc finger domain, 1A (BAZ1A), mRNA /cds=(115,5139) | 1 | CTGTACCAGTGTCTGGCTGCAGGTATT AAGTCCAAGTTTATTAACAGATATA |
| 3105 | Table 3A | Hs.277401 | NM_013449 | 7304920 | bromodomain adjacent to zinc finger domain, 2A (BAZ2A), mRNA /cds=(739,6375) | 1 | GCCACCTCTGTGTTCTGTGCATAGCA AATATGGGACCATCACCAGCTTAC |
| 3106 | Table 3A | Hs.234680 | NM_013451 | 7305052 | fer-1 (C.elegans)-like 3 (myoferlin) (FER1L3), mRNA /cds=(96,6281) | 1 | TCCTGAGGTGATATACTTCATATTTGT AATCAACTGAAAGAGCTGTGCAT |
| 3107 | literature | Hs.100299 | NM_013975 | 7710125 | ligase III, DNA, ATP-dependent (LIG3), transcript variant alpha, mRNA /cds=(323,3091) | 1 | TGCTGGGTTTGCCATCTTTTGTTC TTTGAAGCAGCTTAGTTACCC |
| 3108 | Table 3A | Hs.8262 | NM_013995 | 7669502 | lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2B, mRNA /cds=(137,1369) | 1 | CCACTAGTTGATGTATGGTATCTTTA GATATTTGCCTGTCTGTTTGCTCA |
| 3109 | Table 3A | Hs.127649 | NM_014007 | 7662099 | KIAA0414 protein (KIAA0414), mRNA /cds=(1132,2535) | 1 | AATGGCCTACAACCAAGCTATTTGTC CCCTACTTTGAGTCTTAACGTGTGG |
| 3110 | Table 3A | Hs.301175 | NM_014029 | 7661739 | HSPC022 protein (HSPC022), mRNA /cds=(18,623) | 1 | ATCCTGAGCTGCACCTACCTGTGAGA GTCTTCAAACCTTTTAAACCTTGCC |
| 3111 | Table 3A | Hs.11125 | NM_014041 | 7661745 | HSPC033 protein (HSPC033), mRNA /cds=(168,443) | 1 | TGCTCTGAGATGGGGAACAGAACAC ACAAGTATGAAGTTTCTTTTCAGGTG |
| 3112 | Table 3A | Hs.182238 | NM_014052 | 7661715 | GW128 protein (GW128) | 1 | AAGCACCCCGTGGTTGTGAAAATAG TATAGCAAAAAGAAAAATCCCG |
| 3113 | Table 3A | Hs.76640 | NM_014059 | 7662650 | RGC32 protein (RGC32), mRNA /cds=(146,499) | 1 | TGTTTACCTGCTGCAGCATATTAGA ACAGACGATCCATGCTAATATTGT |
| 3114 | Table 3A | Hs.279040 | NM_014065 | 7661837 | HT001 protein (HT001), mRNA /cds=(241,1203) | 1 | AATCCTTACTTAAATCTTCCGTTAC CACCCTTGAACAATTAGCTTTT |
| 3115 | Table 3A | Hs.5327 | NM_014106 | 7662624 | PRO1914 protein (PRO1914), mRNA /cds=(1222,1425) | 1 | ATAACAGTTCTATTGGAATGATACC CACAACCTCTACAAGCATCTTATCC |
| 3116 | Table 3A | Hs.78961 | NM_014110 | 13699255 | protein phosphatase 1, regulatory (inhibitor) subunit 8 (PPP1R8), mRNA /cds=(935,1318) | 1 | ACAGATTTGTACATGTGTAAATAGG CCTTTTCATGCTTATGTGTAGCT |
| 3117 | Table 3A | Hs.26102 | NM_014112 | 7657658 | trichorhinophalangeal syndrome I gene (TRPS1), mRNA /cds=(638,4483) | 1 | TCTTGTTGTTATTTCTTATGCAAACAAT CTTCAGGCAGCAAAGATGTCTGT |
| 3118 | Table 3A | Hs.179898 | NM_014153 | 7661761 | HSPC055 protein (HSPC055), mRNA /cds=(1400,1903) | 1 | AACCTGTACTGTTGGTATTGTGTTAG TGTATGGACCAATACTGCCTGTAA |
| 3119 | Table 3A | Hs.279474 | NM_014160 | 8850222 | HSPC070 protein (HSPC070), mRNA /cds=(331,1581) | 1 | AATTGAGGGACCATCAGATAACTGTA TTTTGTGAGGTGCAATAAAAAACA |
| 3120 | Table 3A | Hs.5232 | NM_014165 | 7661785 | HSPC125 protein (HSPC125), mRNA /cds=(79,606) | 1 | CTATGTGTACTCCTCATCCTCCTCG TGTATATTTTCTCATTTTTTGGCT |
| 3121 | Table 3A | Hs.181112 | NM_014166 | 7661787 | HSPC126 protein (HSPC126), mRNA /cds=(25,837) | 1 | TTAAAGTAACAAAACTGCCATTGTA CAGTAAAGGCTCTTGGCTTCTGT |
| 3122 | Table 3A | Hs.279761 | NM_014169 | 7661793 | HSPC134 protein (HSPC134), mRNA /cds=(45,716) | 1 | GCTCCCTTCTCTTTGATAGCAATTAT AATGCCCTTGTCCCAATAAACT |
| 3123 | Table 3A | Hs.13645 | NM_014174 | 7661803 | HSPC144 protein (HSPC144), mRNA /cds=(446,1123) | 1 | CTGAGATACTGCTGCTGGAATGGGC GAGACATTGCTGCAAGAGATCAAG |
| 3124 | Table 3A | Hs.30026 | NM_014188 | 7661831 | cDNA FLJ13048 fis, clone NT2RP3001399, weakly similar to SSU72 PROTEIN /cds=(27,488) | 1 | CTGCGCGGTGTTAGGAATGACCTGG AATTGTCAATAAACAGATGCTGCTG |
| 3125 | Table 3A | Hs.121025 | NM_014205 | 7656935 | chromosome 11 open reading frame 5 (C11orf5), mRNA /cds=(45,1256) | 1 | AGCTCCCTAGCTGAACGGTTACCCCT GGTCATTAATAAAGCTGTGACTGG |
| 3126 | Table 3A | Hs.58685 | NM_014207 | 7656964 | CD5 antigen (p56-62) (CD5), mRNA /cds=(72,1559) | 1 | CTCATCTAAAGACACCTTCTTTCCA CTGGCTGTCAAGCAGGACAGGACC |
| 3127 | Table 3A | Hs.70499 | NM_014210 | 7657074 | ecotropic viral integration site 2A (EVI2A), mRNA /cds=(219,917) | 1 | GGCAGAATCCACACCAGCTTATCAAC CAACACAGCTAATTTTAGAATAGG |
| 3128 | Table 3A | Hs.173902 | NM_014225 | 7657474 | protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (PPP2R1A), mRNA /cds=(138,1907) | 1 | GACAGGACAGTGACCTTGGGAGGAA GGGCTACTCCGGCATCCTTAAAG |
| 3129 | Table 3A | Hs.273307 | NM_014230 | 7657616 | signal recognition particle 68kD (SRP68), mRNA /cds=(0,1859) | 1 | GGACAAGTTGGAACAGAAGACCAAG AGTGGCCTCACTGGATACATCAAGG |
| 3130 | Table 3A | Hs.332724 | NM_014232 | 7657674 | AV705126 cDNA, 5' end /clone=ADBCFB08 /clone_end=5' | 1 | CCCCAATTCTGTGGCGCATCCAGATT GTGAAAATGTACAATAAATGTGTA |
| 3131 | Table 3A | Hs.14084 | NM_014245 | 7657521 | ring finger protein 7 (RNF7), mRNA /cds=(53,394) | 1 | TTCAGAGAACTTTTGCATGCTTATG GTTGATCAGTAAAAAAGAATGTT |
| 3132 | Table 3A | Hs.279919 | NM_014248 | 7657507 | ring-box 1 (RBX1), mRNA /cds=(6,332) | 1 | TGCTGTTTCTGTAGCCATATTGTAATC TGTGTCAAATAAAGTCCAGTTGG |
| 3133 | Table 3A | Hs.74711 | NM_014280 | 7657610 | splicing factor similar to dnaJ (SPF31), mRNA /cds=(7,801) | 1 | ACGCCACCCAAACCTTTCACTTTCCA AAGAGCTAGCCGCTCCTCCACCCAG |
| 3134 | Table 3A | Hs.227823 | NM_014287 | 10947030 | pM5 protein (PM5), mRNA /cds=(0,3668) | 1 | GCATCTGAGATCCTGTTGGAAACCAC AGCAACCTGTATTATTATTAGGA |
| 3135 | Table 3A | Hs.54609 | NM_014291 | 7657117 | glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase) (GCAT), mRNA /cds=(3,1262) | 1 | GGACGTGACCTGTGCTGAGGGCTGT GAGAATGTGAACAACAGTGTGAAA |
| 3136 | Table 3A | Hs.10729 | NM_014306 | 7657014 | hypothetical protein (HSPC117), mRNA /cds=(75,1592) | 1 | GCCATCAGATTGATCTTCTTCACACC AAGCTCTGTTTACATTCCGAGAGG |
| 3137 | literature | Hs.5212 | NM_014311 | 7657596 | cDNA FLJ10927 fis, clone OVARC1000466 /cds=UNKNOWN | 1 | CCTTTCTCAGAGGACCAAGACAAA GCATGGGACATGAAATTAAGAGTG |
| 3138 | Table 3A | Hs.278994 | NM_014313 | 7657594 | Rhesus blood group, CcEe antigens (RHCE), mRNA /cds=(0,1253) | 1 | AAGCATGATTCACCAAGGACTAAGT ATCAGTGATTGTAAATTTCTCTGT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|---|
| 3139 | Table 3A | Hs.20597 | NM_014315 | 7657300 | host cell factor homolog (LCP), mRNA /cds=(316,1536) | 1 | ACCTGTTGGTTTTAATGTGCATGTGA ATGGCCTAGAGAACCTATTTTTGT |
| 3140 | Table 3A | Hs.7256 | NM_014319 | 7706606 | integral inner nuclear membrane protein (MAN1), mRNA /cds=(6,2741) | 1 | CCGACCAAGATCCCTCCCTGCAGA CAGATGGGAATGTGTATAATAACTA |
| 3141 | Table 3A | Hs.76556 | NM_014330 | 9790902 | protein phosphatase 1, regulatory (inhibitor) subunit 15A (PPP1R15A), mRNA /cds=(240,2264) | 1 | GGGAGGCCGTGGCTGAGACCAACTGG TTTGCCTATAATTTATTAACATTTT |
| 3142 | Table 3A | Hs.38738 | NM_014343 | 7656980 | claudin 15 (CLDN15), mRNA /cds=(254,940) | 1 | GGACGGTGTCCCGCACGTTTGTATT GTGTATAAATACATTCATTAATAA |
| 3143 | Table 3A | Hs.48433 | NM_014345 | 7657183 | endocrine regulator (HRIHFB2436), mRNA /cds=(621,6920) | 1 | ATCCTTTCCCTCAACCTCCTCCTTTCC CAATTAATTTCAACCATAGTACGA |
| 3144 | Table 3A | Hs.17839 | NM_014350 | 7657123 | TNF-induced protein (GG2-1), mRNA /cds=(197,769) | 1 | GCCAGCTATGTCTCTAGGAAATGAC AGACCCAAACCACAGCAATAAACA |
| 3145 | Table 3A | Hs.283737 | NM_014366 | 7657047 | AD-017 protein (LOC55830), mRNA /cds=(118,1233) | 1 | CTGTAAAAAGCAACTTCATCTCATGT GAGTGGAAAGTAGTTATCTGGAAT |
| 3146 | Table 3A | Hs.97101 | NM_014373 | 7657135 | putative G protein-coupled receptor (GPCR150), mRNA /cds=(321,1337) | 1 | GCATTTGAGAATGTGTCTTTTGAAGG GCTATTACAGTTATTAAGTAGTGT |
| 3147 | literature | Hs.279843 | NM_014381 | 7657336 | mutL (E. coli) homolog 3 (MLH3), mRNA /cds=(114,4403) | 1 | CCAGGGTTCTGCACTGGTCCCTCT TTTCCCTCAGTCTTCTCACTTC |
| 3148 | Table 3A | Hs.182470 | NM_014394 | 7657479 | PTD010 protein (PTD010), mRNA /cds=(129,1088) | 1 | ACACTGCTACACCATTACTTTCTTGA GACATTTGTAAAGTCCTTTGATACA |
| 3149 | Table 3A | Hs.128342 | NM_014406 | 7657252 | potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNMB3L), mRNA /cds=(243,1916) | 1 | TGAATAACTAGTGATACCCTCAATAA AACAGGGATTGCCAAGAAGGGAAC |
| 3150 | Table 3A | Hs.27258 | NM_014412 | 7656951 | calyculin binding protein (CACYBP), mRNA /cds=(117,803) | 1 | ACCTTTAACATGTAAAGATGCTCACC TTGTTGAGAAGAGATAAACCCAGT |
| 3151 | Table 3A | Hs.301956 | NM_014415 | 7657702 | zinc finger protein (ZNF-U69274), mRNA /cds=(161,3322) | 1 | TATGTCATAAACATGTAAATAAAGAT GTTGAATCTTGTTGAAAGCGCGG |
| 3152 | Table 3A | Hs.14125 | NM_014454 | 7657436 | p53 regulated PA26 nuclear protein (PA26), mRNA /cds=(11,1666) | 1 | TTGTATTCTGGAAGCGTGAATTGCTT TTGAAGTCTGTCAGTATTACTGGT |
| 3153 | Table 3A | Hs.326248 | NM_014456 | 7657448 | cDNA: FLJ22071 fis, clone HEP11691 /cds=UNKNOWN | 1 | TTTGTAAAGCAAGGAGATGGAGGTC GTCCTAAACCAGAGAGCTACTGAAT |
| 3154 | Table 3A | Hs.111632 | NM_014463 | 7657314 | Lsm3 protein (LSM3), mRNA /cds=(29,337) | 1 | ACTCACAACCTCTTAAGCTAAATGGT ATTTTCATTTTAAAGTCCTCAAGCTCC |
| 3155 | Table 3A | Hs.127011 | NM_014464 | 7657644 | tubulointerstitial nephritis antigen (TIN-AG), mRNA /cds=(1,1431) | 1 | AGTTTAGCAATATGACATCTTGGTG ACAGTGAATCTTTGTCTCTTCAC |
| 3156 | Table 3A | Hs.300684 | NM_014478 | 7656976 | calcitonin gene-related peptide-receptor component protein (CGRP-RCP), mRNA /cds=(61,507) | 1 | GCCACTGACCTTGGCTCACCTTAGAG GAATTTCTCGAGAACACACAGA |
| 3157 | literature | Hs.154149 | NM_014481 | 7656891 | Homo sapiens, apurinic/aprimidinic endonuclease(APEX nuclease)-like 2 protein, clone MGC:1418 IMAGE:3139156, mRNA, complete cds /cds=(38,1594) | 1 | ACTTCTGTCTTTGCTGGAAGTGTAT TTGTGCATAAATAAGTCTGTGTA |
| 3158 | Table 3A | Hs.120766 | NM_014487 | 13384595 | nucleolar cysteine-rich protein (HSA6591), mRNA /cds=(173,1135) | 1 | TTCTCTTTCTTCACAATGTATGCTCTC AGTGGTACCTATTATTGATGCCT |
| 3159 | Table 3A | Hs.296433 | NM_014499 | 10092632 | putative purinergic receptor (P2Y10), mRNA /cds=(0,1019) | 1 | CTGTGACCCGCTCCCGCTCATGAG CAAGGAGAGTGGTTCATCAATGATT |
| 3160 | Table 3A | Hs.187660 | NM_014504 | 7657495 | putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA /cds=(77,1552) | 1 | TGTAGGGTAAATGTGACTGGAATACA CCTTTGGAACGGAATCTTTATCA |
| 3161 | db mining | Hs.278457 | NM_014512 | 7657276 | killer cell immunoglobulin-like receptor, three domains, short cytoplasmic tail, 1 (KIR3DS1), mRNA /cds=(11,1174) | 1 | AGAACTTCCAAATGTGAGCCAGAT CCAAAGTTGTCTTCTGTCCACGAG |
| 3162 | Table 3A | Hs.239720 | NM_014515 | 7657384 | CCR4-NOT transcription complex, subunit 2 (CNOT2), mRNA /cds=(115,1737) | 1 | TGACAAATTAGAAGAACGGCCTCACC TGCCATCCACCTTCAACTACAACC |
| 3163 | Table 3A | Hs.17667 | NM_014521 | 7657561 | SH3-domain binding protein 4 (SH3BP4), | 1 | TGGATATTTTAACCTGTTAAGTGTGT GTGTGTTTTCTGTACCCAACCAGA |
| 3164 | Table 3A | Hs.275243 | NM_014624 | 9845517 | S100 calcium-binding protein A6 (calyculin) (S100A6), mRNA /cds=(102,374) | 1 | TAAATAGGGAAGATGGAGACACCTCT GGGGTCTCTCTGAGTCAAATCC |
| 3165 | Table 3A | Hs.173288 | NM_014633 | 7661949 | KIAA0155 gene product (KIAA0155), mRNA /cds=(86,3607) | 1 | TGTGTTAGGTTGAATAAGGTGTGGAA AATGCTTTTCTGTAGTAGAATGC |
| 3166 | Table 3A | Hs.170307 | NM_014636 | 7662069 | Ral guanine nucleotide exchange factor RalGPS1A (RalGPS1A), mRNA /cds=(267,1940) | 1 | GCAGTAACCACTGAACGTCAATCAGC CCTCCATGGGGTTCTTTGATTTT |
| 3167 | Table 3A | Hs.323580 | NM_014644 | 11036643 | cDNA FLJ10757 fis, clone NT2RP3004578, highly similar to mRNA for KIAA0477 protein /cds=UNKNOWN | 1 | GTTTGAAGTTGTGACTCTCCTGCTAC CAATTAATAAAGCTTACTTTGCC |
| 3168 | Table 3A | Hs.166318 | NM_014646 | 7662021 | lipin 2 (LPIN2), mRNA /cds=(239,2929) | 1 | TGCAAGATGAATGGCTAATATTTTGG TGCAAGTGTGATGTTCAAAACAA |
| 3169 | Table 3A | Hs.323712 | NM_014664 | 7662203 | KIAA0615 gene product (KIAA0615), mRNA /cds=(237,2927) | 1 | CTGCCTGTTGAGAAGTGTTAATAGC AGTTACTCTTGAGTGTATTTACCT |
| 3170 | Table 3A | Hs.132853 | NM_014666 | 7661967 | KIAA0171 gene product (KIAA0171), mRNA /cds=(101,1978) | 1 | ATTCTAGAGTTTGGAAATGCAAAATTA TTGTTTTACCCTCAAGCTGGGAA |
| 3171 | Table 3A | Hs.155291 | NM_014670 | 7661849 | KIAA0005 gene product (KIAA0005), mRNA /cds=(80,1339) | 1 | TGGGGTGAATTTGTTAAATGAGTAA CTTTGATAAAGTTTTTCATGCACA |

Table 8

| | | | | | | | |
|------|----------|-----------|-----------|----------|---|---|------------------------------|
| 3172 | Table 3A | Hs.154332 | NM_014674 | 7662001 | KIAA0212 gene product (KIAA0212), mRNA /cds=(58,2031) | 1 | AAAAGTATAGAGTTGGAAACTCTGGG |
| 3173 | Table 3A | Hs.151791 | NM_014679 | 7661899 | KIAA0092 gene product (KIAA0092), mRNA /cds=(53,1477) | 1 | AAACTTACGGAAATACACAAATG |
| 3174 | Table 3A | Hs.186840 | NM_014686 | 7662075 | KIAA0355 gene product (KIAA0355), mRNA /cds=(838,4050) | 1 | ATGTGTCAACCCACCATTTGAGCTATT |
| 3175 | Table 3A | Hs.111894 | NM_014713 | 13518239 | lysosomal-associated protein transmembrane 4 alpha (LAPTM4A), mRNA /cds=(148,849) | 1 | AAAACTCCTGTTATCTCCTTGTT |
| 3176 | Table 3A | Hs.181418 | NM_014730 | 7661947 | KIAA0152 gene product (KIAA0152), mRNA /cds=(128,1006) | 1 | TACATGCTTCCAAACTGGAACCTCTA |
| 3177 | Table 3A | Hs.81892 | NM_014736 | 7661905 | KIAA0101 gene product (KIAA0101), mRNA /cds=(61,396) | 1 | CATTTTGTATCTTTTAAAGCTCCT |
| 3178 | Table 3A | Hs.80905 | NM_014737 | 7661963 | Ras association (RalGDS/AF-6) domain family 2 (RASSF2), mRNA /cds=(196,1176) | 1 | GTGACTTGACTGTGTGGAAGATGATGGT |
| 3179 | Table 3A | Hs.108920 | NM_014739 | 7661957 | HT018 mRNA, complete cds /cds=(451,1179) | 1 | TGCATGTTTCTAGTTTGTATATGT |
| 3180 | Table 3A | Hs.79768 | NM_014740 | 7661919 | KIAA0111 gene product (KIAA0111), mRNA /cds=(214,1449) | 1 | CCTTCCATGTCCACCCCACTCCCAC |
| 3181 | Table 3A | Hs.77724 | NM_014749 | 7662189 | KIAA0586 gene product (KIAA0586), mRNA /cds=(274,4875) | 1 | CAAAAAGTACAAAATCAGGATGTT |
| 3182 | Table 3A | Hs.77665 | NM_014752 | 7661907 | KIAA0102 gene product (KIAA0102), mRNA /cds=(307,678) | 1 | TGGTGTTTGATTATTGGAATGGTGCC |
| 3183 | Table 3A | Hs.77329 | NM_014754 | 7662646 | phosphatidylserine synthase 1 (PTDSS1), mRNA /cds=(102,1523) | 1 | ATATTGTCACCTCTTCTACTTGCT |
| 3184 | Table 3A | Hs.76986 | NM_014757 | 13376996 | mastermind (drosophila)-like 1 (MAML1), mRNA /cds=(263,3313) | 1 | ACAGGGCCTCAGCAAGGGAGCCATA |
| 3185 | Table 3A | Hs.75824 | NM_014761 | 7661971 | KIAA0174 gene product (KIAA0174), mRNA /cds=(63,1157) | 1 | CATTTTGTAAACATTTTGATATGTT |
| 3186 | Table 3A | Hs.75574 | NM_014763 | 7661911 | mitochondrial ribosomal protein L19 (MRPL19), mRNA /cds=(34,876) | 1 | GGCTAAACGATTCTTACTCAGTGTGA |
| 3187 | Table 3A | Hs.75416 | NM_014764 | 7661885 | DAZ associated protein 2 (DAZAP2), mRNA /cds=(69,575) | 1 | TGTATAATGATGCAACAGGGACCC |
| 3188 | Table 3A | Hs.74583 | NM_014767 | 7662035 | KIAA0275 gene product (KIAA0275), mRNA /cds=(316,1590) | 1 | TAATGGGGTTTATATGGAATTTCTTCT |
| 3189 | Table 3A | Hs.52526 | NM_014779 | 7662235 | KIAA0669 gene product (KIAA0669), mRNA /cds=(1016,3358) | 1 | CATAAATGGCCTGCCGTCTCCCT |
| 3190 | Table 3A | Hs.28020 | NM_014805 | 7662293 | KIAA0766 gene product (KIAA0766), mRNA /cds=(116,1939) | 1 | ATACCTCTGAACGGGAAGAGACAGC |
| 3191 | Table 3A | Hs.23488 | NM_014814 | 7661913 | KIAA0107 gene product (KIAA0107), mRNA /cds=(25,1194) | 1 | CAGCACAGTGTTTATGCCACTGGT |
| 3192 | Table 3A | Hs.279849 | NM_014819 | 7662123 | KIAA0438 gene product (KIAA0438), mRNA /cds=(117,2243) | 1 | TTCCACTAGTATATCCCTGTTGATTG |
| 3193 | Table 3A | Hs.17969 | NM_014827 | 7662231 | KIAA0663 gene product (KIAA0663), mRNA /cds=(213,2645) | 1 | TTTGTGCTTTTATTAAGTCCCA |
| 3194 | Table 3A | Hs.194035 | NM_014828 | 7662273 | KIAA0737 gene product (KIAA0737), mRNA /cds=(32,1897) | 1 | TCATCTGTGCCATCTTCTGAACCTT |
| 3195 | Table 3A | Hs.173802 | NM_014832 | 7662197 | KIAA0603 gene product (KIAA0603), mRNA /cds=(347,4246) | 1 | GACCTTGATAGTTACCACGCTCTG |
| 3196 | Table 3A | Hs.15087 | NM_014837 | 7662023 | KIAA0250 gene product (KIAA0250), mRNA /cds=(184,1803) | 1 | ACTGCCCTTAACCTCTGGTATACACCA |
| 3197 | Table 3A | Hs.7764 | NM_014851 | 7662139 | KIAA0469 gene product (KIAA0469), mRNA /cds=(184,1803) | 1 | AAAAGAAATCTTACTTTCTCTGT |
| 3198 | Table 3A | Hs.6684 | NM_014856 | 7662151 | KIAA0476 gene product (KIAA0476), mRNA /cds=(568,4728) | 1 | AGGCAGCCTTCTTTAATGTTTTCAGT |
| 3199 | Table 3A | Hs.6336 | NM_014859 | 7662241 | KIAA0672 gene product (KIAA0672), mRNA /cds=(300,2756) | 1 | TGGTTTGTATTTTGTAGCTCAGT |
| 3200 | Table 3A | Hs.5737 | NM_014864 | 7662149 | KIAA0475 gene product (KIAA0475), mRNA /cds=(336,1565) | 1 | CCAGAATGGTCTTTAATGAGCATGGA |
| 3201 | Table 3A | Hs.5094 | NM_014868 | 7662652 | ring finger protein 10 (RNF10), mRNA /cds=(698,2983) | 1 | ACCTGAGCAAAAGGGAATAGGTGGG |
| 3202 | Table 3A | Hs.273397 | NM_014871 | 7662257 | KIAA0710 gene product (KIAA0710), mRNA /cds=(203,3550) | 1 | TCTCTCTCTACACTGTGGTGCACCTA |
| 3203 | Table 3A | Hs.3085 | NM_014877 | 7661883 | helicase KIAA0054 (KIAA0054), mRNA /cds=(145,5973) | 1 | ACTTGTGGAATTTTATACTAAAA |
| 3204 | Table 3A | Hs.1528 | NM_014882 | 7661881 | KIAA0053 gene product (KIAA0053), mRNA /cds=(193,2109) | 1 | ACTCAGCCTTAAGCAAACTACACT |
| 3205 | Table 3A | Hs.8170 | NM_014886 | 7662676 | hypothetical protein (YR-29), mRNA /cds=(82,864) | 1 | CCACACATGCATAAAGGAAATCAA |
| 3206 | Table 3A | Hs.23518 | NM_014887 | 7656970 | hypothetical protein from BCRA2 region (CG005), mRNA /cds=(165,1916) | 1 | TGTCAAAATAAAGAGAACGACAGGT |
| 3207 | Table 3A | Hs.239189 | NM_014905 | 7662327 | glutaminase (GLS), mRNA /cds=(19,2028) | 1 | TGTCAAATAAAAGAGAACGACAGGT |
| 3208 | Table 3A | Hs.131915 | NM_014913 | 7662345 | KIAA0863 protein (KIAA0863), mRNA /cds=(185,3580) | 1 | AGTTTGGTGGAGCTGAGCTAGTGT |
| 3209 | Table 3A | Hs.110488 | NM_014918 | 7662433 | KIAA0990 protein (KIAA0990), mRNA /cds=(494,2902) | 1 | TTTGATCATGTGATCAATGAGAGA |
| | | | | | | 1 | TATCATCCTCTTCTCAACCCATCTC |
| | | | | | | 1 | CCTAACCCACATGCTTGCCAGTT |
| | | | | | | 1 | TTCTGAAATTGGGAAACATTTATTTTA |
| | | | | | | 1 | AATGCAATCAGGTAGTGTGCTT |
| | | | | | | 1 | GACTGAATTTGACATCTGGTATGCTG |
| | | | | | | 1 | GATGATGCTCATACATCAAGAGT |
| | | | | | | 1 | TTGACTTTTCAGAACCATTTTGTCTC |
| | | | | | | 1 | ATTATTCTGTTTATGCTGAAGA |

Table 8

| | | | | | | | |
|------|----------|-----------|-----------|----------|--|---|---|
| 3210 | Table 3A | Hs.104305 | NM_014922 | 14719827 | death effector filament-forming Ced-4-like apoptosis protein (DEFCAP), transcript variant B, mRNA /cds=(522,4811) | 1 | CTGGCTGTGTACAGGGGTGAGCCCC AAAATTGGGGTTCAGCGTGGGAGGC |
| 3211 | Table 3A | Hs.211576 | NM_005546 | 5031810 | IL2-inducible T-cell kinase (ITK), mRNA /cds=(2021,3883) | 1 | AATGGTCCCCTGTGTTGTAGAGAAC TCCCTTATACAGAGTTTTGGTTCT |
| 3212 | Table 3A | Hs.70266 | NM_014933 | 7662369 | yeast Sec31p homolog (KIAA0905), mRNA /cds=(53,3715) | 1 | TTCTTTCATGTCCTCCCTACTTCCCTCA GTGTCAATCAGATTAAAGTGTGT |
| 3213 | Table 3A | Hs.42959 | NM_014939 | 7662447 | KIAA1012 protein (KIAA1012), mRNA /cds=(57,4364) | 1 | TTTGAACCTTTGGTCAATAGAGTCTTCAT ATTTCAAGTATTTGGTGGTCCCTA |
| 3214 | Table 3A | Hs.24083 | NM_014950 | 7662437 | KIAA0997 protein (KIAA0997), mRNA /cds=(262,2196) | 1 | ACCCTAGAGTTACTCTCTTTTGGGAA CATAAGGAGGTATACAGAACTGCA |
| 3215 | Table 3A | Hs.323346 | NM_014953 | 7662443 | KIAA1008 protein (KIAA1008), mRNA /cds=(93,2879) | 1 | TTGATGTGTCAAAACATTAACATT TGATTTCCCCACCCCGCCCAAC |
| 3216 | Table 3A | Hs.10031 | NM_014959 | 7662403 | KIAA0955 protein (KIAA0955), mRNA /cds=(313,1608) | 1 | TCAGGGCGTTTGAATGTGAATTAGGA CCAGCGCAATGAATGCTCAAGTTG |
| 3217 | Table 3A | Hs.227133 | NM_014977 | 7662237 | KIAA0670 protein/acinus (KIAA0670), mRNA /cds=(327,4352) | 1 | AGTTCCCACTCTCTTCTGTCTGTCAG CCCTTGCCCTCTTCCCAAGGTTTC |
| 3218 | Table 3A | Hs.184627 | NM_014999 | 7661921 | KIAA0118 protein (KIAA0118), mRNA /cds=(255,932) | 1 | GTAGAATCAGGCACTGCTCGCAGAA GGAACACAGATTGTAGAGATTAAACA |
| 3219 | Table 3A | Hs.184245 | NM_015001 | 14790189 | SMART/HDAC1 associated repressor protein (SHARP), mRNA /cds=(204,11198) | 1 | TTTTCTCAGCGCAGTTTGTGTTGTGT GTCCATTGGATTACAAACTTTAT |
| 3220 | Table 3A | Hs.151411 | NM_015057 | 7662379 | KIAA0916 protein (KIAA0916), mRNA /cds=(146,14071) | 1 | TGCCTCATTATCTTGCAGCTGTAAC ATATTGGAATGTACATGTCAATAA |
| 3221 | Table 3A | Hs.132942 | NM_015071 | 7662207 | GTPase regulator associated with the focal adhesion kinase pp125(FAK); KIAA0621 protein (KIAA0621), mRNA /cds=(423,2867) | 1 | GCCATAGCCTGAATCTTTAGGGGTA TTAAGGTCAGCCTCTCACTCTTCC |
| 3222 | Table 3A | Hs.306117 | NM_015125 | 11056033 | capicua protein (CIC) mRNA, complete cds /cds=(40,4866) | 1 | AGCCGCCTTCCAGGCCCGCTATGCA GACATCTTCCCTCCAAGGTTTGTG |
| 3223 | Table 3A | Hs.79337 | NM_015148 | 8923825 | KIAA0135 protein (KIAA0135), mRNA /cds=(1803,3791) | 1 | AGCAGCTTCTTCTCAAGTCGCTCTTTA GCCCTTTGTGGTTAATCTCTCAGT |
| 3224 | Table 3A | Hs.11000 | NM_015344 | 7662509 | MY047 protein (MY047), mRNA /cds=(84,479) | 1 | TGCACTGATACAACATTACCATCTTTC TATGGAAAGAAAATTTTGATGA |
| 3225 | Table 3A | Hs.287586 | NM_015384 | 7661841 | cDNA FLJ13648 fis, clone PLACE1011340, weakly similar to IDN3-B mRNA /cds=UNKNOWN | 1 | ATAGAGGAGGAGGAGGAGTCAACGTATT GAGGCGGAGGAGGAGTCAACGTATT |
| 3226 | Table 3A | Hs.105460 | NM_015393 | 7661631 | DKFZP564O0823 protein (DKFZP564O0823), mRNA /cds=(170,904) | 1 | ATACCCACACAGCAACTGGTCCACTG CTTTACTGTCTGTTGGATAATGGC |
| 3227 | Table 3A | Hs.99843 | NM_015400 | 7661691 | DKFZP586N0721 protein (DKFZP586N0721), mRNA /cds=(726,1151) | 1 | AGATTTGTGTCCTCTCATTCCCTCTCT TCCTCTGTGAAGTGCCCTTCTAA |
| 3228 | Table 3A | Hs.75884 | NM_015416 | 7661659 | DKFZP586A011 protein (DKFZP586A011), mRNA /cds=(330,632) | 1 | GCACTGTTTTAAACCCCAAGTAAAGA CTGCTTGAAACCTGTTGATGGAAA |
| 3229 | Table 3A | Hs.64595 | NM_015423 | 7661649 | aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (AASDHPPT), mRNA /cds=(166,1095) | 1 | AGATTTCCCCTCAGTTTCCATTGACTT AGATCAGGTTACAGAGAAAGGCA |
| 3230 | Table 3A | Hs.48320 | NM_015435 | 13491169 | mRNA for ring-IBR-ring domain containing protein Dorfin, complete cds /cds=(317,2833) | 1 | AGATCGAGATCTTCAGTCTCTGCTT CATCTGTGAGCTTGCCCTCAGTCA |
| 3231 | Table 3A | Hs.12305 | NM_015509 | 7661639 | DKFZP566B183 protein (DKFZP566B183), mRNA /cds=(351,749) | 1 | AGTGACTAAATACTGGGAACCTATTT TCTCAATCTTCTCCATGTTGTGT |
| 3232 | Table 3A | Hs.6880 | NM_015530 | 7661569 | DKFZP434D156 protein (DKFZP434D156), mRNA /cds=(230,1384) | 1 | TGGCACTCTGTGGCTCCTTGTAGTAT TATAGCTATACTGGGAAAGCATAG |
| 3233 | Table 3A | Hs.187991 | NM_015626 | 7661595 | DKFZP564A122 protein (DKFZP564A122), mRNA /cds=(2570,2908) | 1 | TTGGTGAGTTGCCAAAGAAGCAATAC AGCATATCTGCTTTTGCCCTCTGT |
| 3234 | Table 3A | Hs.156764 | NM_015646 | 7661677 | RAP1B, member of RAS oncogene family (RAP1B), mRNA /cds=(148,702) | 1 | AATTGACCAACCTAATGTTACAACATA CTTTGAGGTGGCCAAATGTAACT |
| 3235 | Table 3A | Hs.44563 | NM_015697 | 7661549 | Homo sapiens, Similar to RIKEN cDNA 2310002F18 gene, clone MGC:10413 IMAGE:3954787, mRNA, complete cds /cds=(16,1131) | 1 | CTACTACGCTGCCCTGGGTGCTGTA GGAGCCCATCTGACTACCAGAAAT |
| 3236 | Table 3A | Hs.5324 | NM_015702 | 7661547 | hypothetical protein (CL25022), mRNA /cds=(157,1047) | 1 | AAGGCCTCAGTTTTAATTATTTCTTC CCAAAATAAATCACACATTTGGT |
| 3237 | Table 3A | Hs.110707 | NM_015726 | 7657147 | H326 (H326), mRNA /cds=(176,1969) | 1 | GGTGGGGTGATAGGGTGGGCTAAAA ACCATGCCTCTGGAATTTGTTGTA |
| 3238 | Table 3A | Hs.25674 | NM_015832 | 7710144 | methyl-CpG binding domain protein 2 (MBD2), transcript variant testis-specific, mRNA /cds=(229,1137) | 1 | AGAGGCAGCTTCTAGACAGAGTTGCT TAATGAAAGGGTTGTAATACTTT |
| 3239 | Table 3A | Hs.278573 | NM_015874 | 7706215 | H-2K binding factor-2 (LOC51580), mRNA /cds=(238,1500) | 1 | GCTCAGTTCCATATTTTCATCGTGAA AAACTTGCAATACGAGCAGTTTCA |
| 3240 | Table 3A | Hs.104640 | NM_015898 | 7705374 | HIV-1 inducer of short transcripts binding protein (FBI1), mRNA /cds=(0,1754) | 1 | CAACGGCCAGGAGAGCACTTTAAG GACGAGGACGAGGACGAGGACGTGG |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|---|
| 3241 | Table 3A | Hs.287414 | NM_015906 | 7706235 | transcriptional intermediary factor 1 gamma (TIF1GAMMA), transcript variant alpha, mRNA /cds=(84,3467) | 1 | ATACAGCCCCGGCAGAAACGCCTA AAGTCAGATGAGAGACCAGTACATA |
| 3242 | Table 3A | Hs.145956 | NM_015919 | 7706241 | zinc finger protein mRNA, complete cds /cds=(1073,3133) | 1 | ACCAGAACTTCAAATGTGTACAAAA AGATGAGCAGAACTATCCCCAGGT |
| 3243 | Table 3A | Hs.279813 | NM_015932 | 7705428 | hypothetical protein (HSPC014), mRNA /cds=(82,507) | 1 | AAAGCGAAGTCATGGGAGAGCCACA CTTGATGGTGGAAATAGAACTGGT |
| 3244 | Table 3A | Hs.171774 | NM_015933 | 7705430 | hypothetical protein (HSPC016), mRNA /cds=(38,232) | 1 | TCCCTGCCATAACATCTTTGCCACG TATAGCTGGAATTAAGTGTGTCT |
| 3245 | Table 3A | Hs.119908 | NM_015934 | 7706253 | nucleolar protein NOP5/NOP58 (NOP5/NOP58), mRNA /cds=(0,1589) | 1 | CTGGTGACTCCACACTTCCAACCTGC TCTAAAAACGCGAAATAGAACAG |
| 3246 | Table 3A | Hs.84038 | NM_015937 | 7706257 | CGI-06 protein (LOC51604), mRNA /cds=(6,1730) | 1 | TGTGTAGTGGATGGAGTTTACTGTTT GTGGAATAAAAAACGGCTGTTTCCG |
| 3247 | Table 3A | Hs.5798 | NM_015946 | 7705599 | pelota (Drosophila) homolog (PELO), mRNA /cds=(259,1416) | 1 | ACAGGGATTCTTCTTATGCTTGGCTA CACTAGATATTTTGTGATTGGCAA |
| 3248 | Table 3A | Hs.7236 | NM_015953 | 7705715 | eNOS interacting protein (LOC51070), mRNA /cds=(44,949) | 1 | AGGCCTGAGTGTGTGCGGGAGACCA AATAAACCGGCTTGGGTGCGCAAAA |
| 3249 | Table 3A | Hs.7104 | NM_015995 | 7706289 | mRNA; cDNA DKFZp761P06121 (from clone DKFZp761P06121) /cds=UNKNOWN | 1 | AAGAAAGAGAGAGAGAACTTGATGC CAAGTCCACGAAAAACAATTTTT |
| 3250 | Table 3A | Hs.6153 | NM_016001 | 7705764 | CGI-48 protein (LOC51096), mRNA /cds=(107,1672) | 1 | GATCCAGCTGTGCTTAAGAGCCAGTA ATGTCTTAATAAACATGTGGCAGC |
| 3251 | Table 3A | Hs.7194 | NM_016007 | 7706297 | CGI-74 protein | 1 | AAGCACTGTTTTATTTGTGTGTGGA GTATAAAGGCTACACCCATTATTG |
| 3252 | Table 3A | Hs.318725 | NM_016018 | 7705782 | CGI-72 protein (LOC51105), mRNA /cds=(69,1400) | 1 | CCTTTTCTACAGAATCATCAGGCAT GGGTAAGGTGGCTAACGCTGAGAT |
| 3253 | Table 3A | Hs.110803 | NM_016039 | 7706321 | CGI-99 protein (LOC51637), mRNA /cds=(161,895) | 1 | TGGGTATGTTCTAGAGATTTACCACC ATTGCTTATGCTTTTTTCTTTAA |
| 3254 | Table 3A | Hs.286131 | NM_016041 | 7705603 | CGI-101 protein (LOC51009), mRNA /cds=(6,635) | 1 | TCTTCTGATAGATGAGGCCATGGTG TAAATGGAAGTTTCAGAGAGGACA |
| 3255 | Table 3A | Hs.271614 | NM_016049 | 7705615 | CGI-112 protein (LOC51016), mRNA /cds=(158,784) | 1 | GTGGGTGGTCCCACTAATGGAATG GAAATGCCTGAGCCAGGCCAGCGG |
| 3256 | Table 3A | Hs.283670 | NM_016056 | 7706334 | CGI-119 protein (LOC51643), mRNA /cds=(0,776) | 1 | AATCTATTCTGCACCTGTTACGGTT TCTGGAAGCAGTTAATAAAAAAGTA |
| 3257 | Table 3A | Hs.181271 | NM_016057 | 7706336 | CGI-120 protein (LOC51644), mRNA /cds=(37,570) | 1 | GCATGGAGTCAGGAGAAAAACCCCTT CATAAACTGCTCTGTGCAAGAGAG |
| 3258 | Table 3A | Hs.27693 | NM_016059 | 7706338 | peptidylprolyl isomerase (cyclophilin)-like 1 (PPI1), mRNA /cds=(227,727) | 1 | ACAAATGCCCTGTTTATCAATAGGT GACTACTTACTACACATGGAACCA |
| 3259 | Table 3A | Hs.184542 | NM_016061 | 7706340 | CGI-127 protein (LOC51646), mRNA /cds=(125,490) | 1 | TGATTATATGCAGATTCTAGTAGCA TGCCCTACCTACAGCACTATGTGC |
| 3260 | Table 3A | Hs.32826 | NM_016063 | 7705623 | CGI-130 protein (LOC51020), mRNA /cds=(63,575) | 1 | GGTCATTGAGCCTCAGGTAGGGAATA TATCAACCCGATTTCCTCTCTCT |
| 3261 | Table 3A | Hs.5887 | NM_016090 | 9994184 | RNA binding motif protein 7 (RBM7), mRNA /cds=(21,821) | 1 | TTTCAAAGTGCCAGACTGTGTACAA AGACACATGTAATGGAGATTGTAC |
| 3262 | Table 3A | Hs.119503 | NM_016091 | 7705432 | HSPC025 (HSPC025), mRNA /cds=(33,1727) | 1 | AGGACCGAAGTGTTTCAAGTGATCT CAGTAAAGGATCTTTGGAGCCAGA |
| 3263 | Table 3A | Hs.7953 | NM_016099 | 7705820 | HSPC041 protein (LOC51125), mRNA /cds=(141,455) | 1 | AGTTTCACTGTCAGAGATATTGTAGG TGCTAATACTGGATTTCGTCTCAG |
| 3264 | Table 3A | Hs.27023 | NM_016106 | 7706370 | vesicle transport-related protein (RA410), mRNA /cds=(7,1929) | 1 | AGTTAGAAGAGCAATATGTTTCCTTC TCTGTAACAGTGTCTAACAGTGA |
| 3265 | db mining | Hs.306603 | NM_016115 | 7705830 | cDNA FLJ11517 fis, clone HEMBA1002337 /cds=UNKNOWN | 1 | AGCTGCCACTTCCCAGAACGCTACAT AATTATTGCTCTATGAAGACGTT |
| 3266 | Table 3A | Hs.142295 | NM_016123 | 7705840 | putative protein kinase NY-REN-64 antigen (LOC51135), mRNA /cds=(49,1431) | 1 | GCCACTAATAACATTGGGCTAATATC TGCTGTGCTTCTCTGACAGGTAGT |
| 3267 | Table 3A | Hs.279921 | NM_016127 | 7706384 | HSPC035 protein (LOC51669), mRNA /cds=(16,1035) | 1 | AGCATGCAGTTCTCTGTGAAATCTCA AATATTGTTGTAATAGTCTGTTTC |
| 3268 | Table 3A | Hs.102950 | NM_016128 | 11559928 | coat protein gamma-cop (LOC51137), mRNA /cds=(15,2639) | 1 | TGAATCTATCCCCAAGAAACCATCT TATCCCTGTAAGTATGATCTGAGT |
| 3269 | Table 3A | Hs.272398 | NM_016135 | 7706730 | transcription factor ets (TEL2), mRNA /cds=(75,1100) | 1 | GTGCTTCCAGGCGGCACTGACAGCC TCAGTAACAATAAAAAACATGGTAG |
| 3270 | Table 3A | Hs.108969 | NM_016145 | 7706664 | PTD008 protein (PTD008), mRNA /cds=(233,553) | 1 | GTCCATGTTTCTAGGGGTATTTCATT GCTTTCTCGTTGAAACCTGTTGTT |
| 3271 | Table 3A | Hs.279901 | NM_016146 | 7706666 | PTD009 protein (PTD009), mRNA /cds=(257,916) | 1 | TAGGTCCATAAATGTTGTAATAAATAT TCCTTTGATCTTGGTGTTCGCT |
| 3272 | Table 3A | Hs.306706 | NM_016154 | 7706672 | cDNA: FLJ21192 fis, clone COL00107, highly similar to AF165522 ras-related GTP-binding protein 4b (RAB4B) mRNA /cds=UNKNOWN | 1 | GCTAGTACCTGTTATTATTACCTGG AGGCCTGTCCAGCACCCACCTAC |
| 3273 | Table 3A | Hs.279518 | NM_016160 | 4502146 | amyloid beta (A4) precursor-like protein 2 (APLP2), mRNA /cds=(72,2363) | 1 | CCCACTATGCACAGATTAACTTCAC CTACAAACTCCTTAATATGATCTG |
| 3274 | Table 3A | Hs.75251 | NM_016166 | 7706636 | DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1 (DDXB1), mRNA /cds=(96,2051) | 1 | TGTGCTCTGTTTTACCTTACTCTGTTT AGAAAAGTATACAAGCGTGTGTTT |
| 3275 | Table 3A | Hs.241578 | NM_016200 | 7706424 | U6 snRNA-associated Sm-like protein Lsm8 (LOC51691), mRNA /cds=(82,372) | 1 | TGAGTGTGTCTCTGGATTTTGACCCC TTATTGATTCATTGTAATATGTAA |
| 3276 | literature | Hs.135756 | NM_016218 | 7705343 | polymerase (DNA-directed) kappa (POLK), mRNA /cds=(172,2784) | 1 | ACATTTGTAAGGGCTCTCAAAGATTC ACACATGCCTATATTATCAAGA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|---|
| 3277 | Table 3A | Hs.7905 | NM_016224 | 7706705 | SH3 and PX domain-containing protein SH3PX1 (SH3PX1), mRNA /cds=(43,1830) | 1 | TCCGCATCCATTATTTAAACCAAGTGG AAATTGTCTCTATTTTGGAAAGT |
| 3278 | Table 3A | Hs.108636 | NM_016227 | 7705321 | membrane protein CH1 (CH1), mRNA /cds=(124,4341) | 1 | ACGGAGCTGTAGTGCCATTAGAAACT GTGAATTTCCAAATAAATCTGAAC |
| 3279 | Table 3A | Hs.5741 | NM_016230 | 7705898 | flavohemoprotein b5+b5R (LOC51187), mRNA /cds=(6,1469) | 1 | AGCCTTCAGTTCTTCTTAAATGAAATCAA ATGTTCTCTCAGTACAGGTAAC |
| 3280 | Table 3A | Hs.127561 | NM_016239 | 7705900 | myosin XVA (MYO15A), mRNA /cds=(338,10930) | 1 | CCAGACCCCATCACTTGTATGGGGCC ACACAAGTTTGAGAGTGGTACAAGG |
| 3281 | Table 3A | Hs.250646 | NM_016252 | 10442821 | baculoviral IAP repeat-containing 6 (BIRC6), mRNA /cds=(0,14489) | 1 | TCAGGTTAAACCCAGCAGCAGCAAAAG AACTCCCAAGTGACTTCCAGTTAT |
| 3282 | Table 3A | Hs.107740 | NM_016270 | 7706468 | Kruppel-like factor (LOC51713), mRNA /cds=(84,1151) | 1 | GGTGGGCATTTTGGGGCTACCTGGTT CGTTTTTATAAGATTTTGCTGGGT |
| 3283 | Table 3A | Hs.8148 | NM_016275 | 7706470 | selenoprotein T (LOC51714), mRNA /cds=(138,629) | 1 | AGTGCAATAATACTGTATAGCTTTCC CCCACCTCCCAAAAATCACCCAG |
| 3284 | Table 3A | Hs.279586 | NM_016283 | 7706211 | adrenal gland protein AD-004 (LOC51578), mRNA /cds=(341,859) | 1 | AATCATGTTGCAGAACCCAGCAGGTGG ATAGTATATAGGTTTATGCCTGGG |
| 3285 | Table 3A | Hs.6406 | NM_016289 | 7706480 | MO25 protein (LOC51719), mRNA /cds=(53,1078) | 1 | GGTGCAGCGTGTGACACACAACATTC ATGTTACTCTTACATTGGAATCTG |
| 3286 | literature | Hs.182366 | NM_016292 | 7706484 | heat shock protein 75 (TRAP1), mRNA /cds=(4,2118) | 1 | GGACTGACACACAGATGACAGCCC CACCTCCTTGAGCTTTATTACCTA |
| 3287 | Table 3A | Hs.14770 | NM_016293 | 7706486 | bridging integrator 2 (BIN2), mRNA /cds=(38,1735) | 1 | ACGACCCATTTTGAAGACTTAAAGC CGGAAGAACACATTTTCAGATTGT |
| 3288 | Table 3A | Hs.284164 | NM_016301 | 9994188 | protein x 0004 (LOC51184), mRNA /cds=(31,885) | 1 | AGGAATTAAGCTTAACAAAATGTAT GTCCGAAGGGAAAAAGCTGCAAGG |
| 3289 | Table 3A | Hs.102897 | NM_016302 | 10047097 | CGI-47 protein (LOC51095), mRNA /cds=(131,1348) | 1 | TCCTGTGGAATCTGATATGTCTGGTA GCATGTCAATGATGGGACATGAAG |
| 3290 | Table 3A | Hs.284162 | NM_016304 | 10047101 | 60S ribosomal protein L30 isolog (LOC51187), mRNA /cds=(143,634) | 1 | ATGGCACTAGGCAGCATTGTATAGT AACTAATGGCAAAAATTCATGGCT |
| 3291 | Table 3A | Hs.334811 | NM_016312 | 7706500 | Npw38-binding protein NpwBP (LOC51729), mRNA /cds=(143,2068) | 1 | ATTTGATTAAATTTATTTCCCATGAC CTTAACCTTTGAGTTTGTGGG |
| 3292 | literature | Hs.110347 | NM_016316 | 7706680 | REV1 (yeast homolog)- like (REV1L), mRNA /cds=(212,3967) | 1 | AAAGCAAGTGTGTTGTACATTTCTTTT CAAAAAGTGCCAAATTTGTCACT |
| 3293 | Table 3A | Hs.83761 | NM_016325 | 7706506 | zinc finger protein 274 (ZNF274), mRNA /cds=(401,2266) | 1 | AATCTGCACATGATATTACATCCACAG TACCACAGTATTTATGTGTATGAA |
| 3294 | Table 3A | Hs.16085 | NM_016334 | 7706703 | putative G-protein coupled receptor (SH120), mRNA /cds=(103,1470) | 1 | ATGGTAGCTGAGCCAAACAGTAGG ATTTCCGTTTTAAGGTTTACATGGA |
| 3295 | Table 3A | Hs.279918 | NM_016391 | 7705450 | hypothetical protein (HSPC111), mRNA /cds=(62,598) | 1 | AAGCCAGAACCTGCTGTTTTACGGGT GGGTGATGTAATATAGTGTGTAC |
| 3296 | Table 3A | Hs.239720 | NM_016398 | 7705464 | CCR4-NOT transcription complex, subunit 2 (CNOT2), mRNA /cds=(115,1737) | 1 | TGACAAATTAGAGAACGGCCTCACC TGCCATCCACCTTCAACTACAACC |
| 3297 | Table 3A | Hs.334788 | NM_016406 | 7705480 | hypothetical protein FLJ14639 (FLJ14639), mRNA /cds=(273,689) | 1 | TCCTTCTGGTTTCTGGAGATAACCCA TCAATAAAGAGCTGCTTCTCTGGT |
| 3298 | Table 3A | Hs.98289 | NM_016440 | 7705992 | VRK3 for vaccinia related kinase 3 (LOC51231), mRNA /cds=(118,1542) | 1 | GGGACCCCTCCTCAACCTTGACTCTC TGTGCTTTGGTAATAAATGTTTT |
| 3299 | Table 3A | Hs.3059 | NM_016451 | 7705368 | coatamer protein complex, subunit beta (COPB), mRNA /cds=(178,3039) | 1 | GTCTGTAATGCTGTCTCTCAAGTATA TAATGTTTCATGTACCAAGACCTC |
| 3300 | Table 3A | Hs.172918 | NM_016466 | 7706006 | hypothetical protein (LOC51239), mRNA /cds=(0,527) | 1 | GACATCTGCTCCCTCCTGCTGCAACA CAGCCAGCCCTGAAGGCCATCCG |
| 3301 | Table 3A | Hs.171566 | NM_016468 | 7706010 | hypothetical protein (LOC51241), mRNA /cds=(0,320) | 1 | TGGGAAGATCCTGACCTCCTCCAAG GAAGAAATCCAGAAAGCCTTAAGAC |
| 3302 | Table 3A | Hs.75798 | NM_016470 | 7705508 | hypothetical protein (HSPC207), mRNA /cds=(0,620) | 1 | AGCCAGTGATCTCTGACTTTCAAT CAGTTTCCAAGCTTAACAGGGCA |
| 3303 | Table 3A | Hs.55847 | NM_016497 | 7706044 | hypothetical protein (LOC51258), mRNA /cds=(0,386) | 1 | AAACGCATCCGCTATCTCTACAAACA CTTTAACCCGACATGGGAAGTTTCG |
| 3304 | Table 3A | Hs.278429 | NM_016520 | 7706556 | hepatocellular carcinoma-associated antigen 59 (LOC51759), mRNA /cds=(27,896) | 1 | TCCTCCAGCTGACAGAAAAATCCAGG ATGAGATCAGAAGGATACTGGTGT |
| 3305 | Table 3A | Hs.183125 | NM_016523 | 7705573 | killer cell lectin-like receptor subfamily F, member 1 (KLRF1), mRNA /cds=(64,759) | 1 | TTCCAGGCTTTTGCTACTCTTCACTC AGCTACAATAAACATCTGAATGT |
| 3306 | Table 3A | Hs.75425 | NM_016525 | 8394498 | ubiquitin associated protein (UBAP), mRNA /cds=(172,1680) | 1 | ACACCTAGTCATAGAAATCAGTCTCT CTGGTTTGTGTTGATTATGTTGT |
| 3307 | Table 3A | Hs.239208 | NM_016533 | 7706622 | ninjurin 2 (NINJ2), mRNA /cds=(56,484) | 1 | CACTGCTTCTCTGCTCCAGGGCTC AATTTTCCCTCTTGTGTAATGGA |
| 3308 | Table 3A | Hs.10071 | NM_016551 | 7706574 | seven transmembrane protein TM7SF3 (TM7SF3), mRNA /cds=(37,1749) | 1 | ACTTTCCGAGGGAGTTTATTATTGAG TCTTTATCTGTGACAGTATTGGA |
| 3309 | Table 3A | Hs.179152 | NM_016562 | 7706092 | toll-like receptor 7 (LOC51284), mRNA /cds=(135,3284) | 1 | ATAGAGAGGTAATTAATGCTGGAG CCAACATTTTCACAACTCTGTAA |
| 3310 | Table 3A | Hs.18552 | NM_016565 | 7706098 | E2IG2 protein (LOC51287), mRNA /cds=(131,421) | 1 | GTTCCACCAAGTATTTACCAGGAAAAAC AAGAATGTGTGAAGGGATGCTCC |
| 3311 | Table 3A | Hs.267182 | NM_016569 | 7706728 | T-box 3 (ulnar mammary syndrome) (TBX3), mRNA /cds=(116,1906) | 1 | TGCTATTTCTTATTTTACCACAAATTG GGGAAGGAGTGCCACTTTCAGC |
| 3312 | Table 3A | Hs.14896 | NM_016598 | 7706132 | DHHC1 protein (LOC51304), mRNA /cds=(214,1197) | 1 | TGCTGCCACTTTTCAATTCTGTCACT GCTTCCACATGGAAACAAAATGCA |
| 3313 | Table 3A | Hs.24125 | NM_016604 | 7706598 | putative zinc finger protein (LOC51780), mRNA /cds=(744,4997) | 1 | TCACTTTCTGTATTTTAAATTTGTGTA AGGCTGATTGGGATTTCCATGT |
| 3314 | Table 3A | Hs.46847 | NM_016614 | 7705261 | TRAF and TNF receptor-associated protein (AD022), mRNA /cds=(16,1104) | 1 | GCATGAAGAGACATAGCCTTTTATGT TTGCTAATTGTGAAATGGAAATGC |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|---|
| 3315 | Table 3A | Hs.107139 | NM_016619 | 7706157 | hypothetical protein (LOC51316), mRNA /cds=(101,448) | 1 | TGTTGTCCCTGAACCTAGCTAAATGG |
| 3316 | db mining | Hs.106826 | NM_016621 | 7706159 | cDNA FLJ13196 fis, clone NT2RP3004428, weakly similar to CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 4 /cds=(385,2289) | 1 | TGCAACTAGTTTCTCCTTGCTTT TCATAGTGTGAGGTGCCGTGAG TCTTTGTAGTCTTGTGTCATCG |
| 3317 | Table 3A | Hs.92918 | NM_016623 | 7705303 | hypothetical protein (BM-009), mRNA /cds=(385,1047) | 1 | GTGCGTAGAATATTACGTATGCATGT |
| 3318 | Table 3A | Hs.70333 | NM_016628 | 7706169 | mRNA for KIAA1844 protein, partial cds /cds=(0,1105) | 1 | TCATGTCTAAAGAATGGCTGTTGA CGTGGTTGTGGGAGGGGAAAGAGGA AACAGAGCTAGTCAGATGTGAATTG |
| 3319 | Table 3A | Hs.71475 | NM_016630 | 13699804 | acid cluster protein 33 (ACP33), mRNA /cds=(176,1102) | 1 | GGACATTGGTTATTTTATGCTTTCTTG |
| 3320 | Table 3A | Hs.278027 | NM_016733 | 8051617 | LIM domain kinase 2 (LIMK2), transcript variant 2b, mRNA /cds=(315,2168) | 1 | GATATAACCATGATCAGAGTGCC GCAAGTGTAGGAGTGGTGGGCTGA ACTGGGCCATTGATCAGACTAAATA |
| 3321 | literature | Hs.342801 | NM_016734 | 9951919 | paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA /cds=(448,1623) | 1 | AATCAGAAGAGCCTGGAAGAACCT AGCCCAACTCCCTTGTTGGGAAAC |
| 3322 | Table 3A | Hs.324470 | NM_016824 | 9943847 | adducin 3 (gamma) (ADD3), transcript variant 1, mRNA /cds=(31,2151) | 1 | TCAACAAAGGGGATTTTGTACACATA ACATGGGTATTATTAGTTAACTCT |
| 3323 | Table 3A | Hs.77273 | NM_016936 | 9055373 | ras homolog gene family, member A (ARHA), mRNA /cds=(151,732) | 1 | CTTTTGTGCAGCGACTATGTTGGTGT |
| 3324 | Table 3A | Hs.159565 | NM_016952 | 8393083 | surface glycoprotein, Ig superfamily member (CDO), mRNA /cds=(0,3722) | 1 | TAGGGTGGTGTGGAGATTGTTAA ATTTATGCCCTTAATGTTTTCTTCCCC ATTCCTTCCTCCCCCTCGGTAGG |
| 3325 | Table 3A | Hs.9082 | NM_017426 | 8393857 | nucleoporin p54 (NUP54), mRNA /cds=(25,1542) | 1 | TTTGTATTTGTAACATCATGTGGG AGGAGTAAAGAAAATCCAAAGCA CCCCCGTGGCATGGACCACCTTTAT |
| 3326 | Table 3A | Hs.83551 | NM_017459 | 9665258 | microfibrillar-associated protein 2 (MFAP2), transcript variant 1, mRNA /cds=(114,665) | 1 | TTTATACAAAATTAACAAAGTT |
| 3327 | Table 3A | Hs.85100 | NM_017491 | 9257256 | WD repeat domain 1 (WDR1), transcript variant 1, mRNA /cds=(202,2022) | 1 | ACTGTAACTAATCTGTCATTGTTTT ACCTTCCTTTCTTTTCAGTGC |
| 3328 | Table 3A | Hs.139262 | NM_017523 | 8923794 | XIAP associated factor-1 (HSXIAPAF1), mRNA /cds=(0,953) | 1 | TACTTGCTGTGGTGGTCTTGTAAG GTGATGGGTTTTATCGTTGGGCT |
| 3329 | Table 3A | Hs.119018 | NM_017544 | 8923943 | transcription factor NRF (NRF), mRNA /cds=(653,1819) | 1 | AAAGAATTAGTGTATGCTTCTGAAT AAAAAGAGGCAAGTTGATCAGA AGGGGGTGATTTTGTCTTGTCTCTG |
| 3330 | Table 3A | Hs.306195 | NM_017601 | 8922168 | over-expressed breast tumor protein (OBTP), mRNA /cds=(0,224) | 1 | AGAAAATACAGTGCTGTTTTAAAA AGCTTAAGGTTTTAAAAATGTTGCC GTAGTTTGAACGCTGTCTGTTAGA |
| 3331 | Table 3A | Hs.32922 | NM_017632 | 8923039 | hypothetical protein FLJ20036 (FLJ20036), mRNA /cds=(162,1904) | 1 | GGATGCACGTACAGAATACATTCAGC CGTCAGGTAATACATGAAGCAGT GGACAGTTCTATTGCTTTTCTTTT |
| 3332 | Table 3A | Hs.246875 | NM_017644 | 8923060 | hypothetical protein FLJ20059 (FLJ20059), mRNA /cds=(25,1290) | 1 | TCCATCCCTCCCTACCATCAAA AGACTTACATTACTGCTTTAACGTGA TATCACTGGGCATCCCCAAGGGC |
| 3333 | Table 3A | Hs.7942 | NM_017657 | 8923087 | hypothetical protein FLJ20080 (FLJ20080), mRNA /cds=(315,3044) | 1 | GTCAAGTTAGGTCAAAGCCAGGGAG TGACAGAATCTGGGAATCAACAA CCTCTTGATGCCAAGCAGGTGAAGCA |
| 3334 | Table 3A | Hs.26369 | NM_017746 | 8923268 | hypothetical protein FLJ20287 (FLJ20287), mRNA /cds=(131,2920) | 1 | GATGCTAAGCTGATTTCTCCAA TGGATCTGTCAAACTAACACTTATGC CTTTAGTCTCATTGTATGAGGTGT |
| 3335 | Table 3A | Hs.8928 | NM_017748 | 8923270 | hypothetical protein FLJ20291 (FLJ20291), mRNA /cds=(117,1394) | 1 | ACCTGCCATCTTGGTCTTTACTAAG TGAAGTGACTCTTTCTTTTAAACA GCTGCCAAGCTAGTAATGATGCTTT |
| 3336 | Table 3A | Hs.7862 | NM_017761 | 8923294 | hypothetical protein FLJ20312 (FLJ20312), mRNA /cds=(133,552) | 1 | TAATAAAAGTGACCATGATATGC ACTGTTGTCCCCCACCCTTTTTTCC TTAAATAAAGTAAATGACACCC |
| 3337 | Table 3A | Hs.126721 | NM_017762 | 8923296 | hypothetical protein FLJ20313 (FLJ20313), mRNA /cds=(344,1699) | 1 | TGTGAATACTGTGTAGCAGGATCTTG AGAGTCCTTGTCTTACATAGGCA AAGAGGCTTCCATCCCTCCTTCCTC |
| 3338 | Table 3A | Hs.306668 | NM_017774 | 8923317 | cDNA FLJ14089 fis, clone MAMMA1000257 /cds=UNKNOWN | 1 | TTTCTCCTACAGTGCTGAGCAAA GTTGAATTGGGTGGATGGGGGGAG CAAGCATAATTTTAAAGTGTGAAGC |
| 3339 | Table 3A | Hs.105461 | NM_017780 | 8923329 | hypothetical protein FLJ20357 (FLJ20357), mRNA /cds=(35,2083) | 1 | TCACCAGCTGATGACACTTCCAAGA GATTAGTCACTTTCTCCTAGGC |
| 3340 | Table 3A | Hs.6631 | NM_017792 | 8923351 | hypothetical protein FLJ20373 (FLJ20373), mRNA /cds=(268,849) | 1 | CCCCTGAAGTCTTTGGGTAGCTCTT AAGCCATAACTAAGGAGCAGCATT AGTGACGAGGAGGAAGTGGCCTACA |
| 3341 | Table 3A | Hs.283685 | NM_017801 | 8923369 | hypothetical protein FLJ20396 (FLJ20396), mRNA /cds=(107,658) | 1 | CGGGTTAGCTGCCAGTAGGCATC |
| 3342 | Table 3A | Hs.14220 | NM_017827 | 8923420 | hypothetical protein FLJ20450 (FLJ20450), mRNA /cds=(27,1583) | 1 | AACAGAAGCTCAAGAGAATACAGCA ACTTGCTGCATGAGTAAGGTGGCT TTTTCCCTGCTATTGAGGAAGTATTT |
| 3343 | Table 3A | Hs.132071 | NM_017830 | 8923426 | ovarian carcinoma immunoreactive antigen (OCIA), mRNA /cds=(167,904) | 1 | GCCTTCCCTACTCACTGAGAACT CGGAACCAGAATTTGATCTCAACTAT GTTCCACTAAAGGCACAGGAATGG |
| 3344 | Table 3A | Hs.5811 | NM_017835 | 8923436 | chromosome 21 open reading frame 59 (C21ORF59), mRNA /cds=(360,776) | 1 | |
| 3345 | Table 3A | Hs.5080 | NM_017840 | 8923447 | mitochondrial ribosomal protein L16 (MRPL16), mRNA /cds=(111,866) | 1 | |
| 3346 | Table 3A | Hs.39850 | NM_017859 | 8923486 | hypothetical protein FLJ20517 (FLJ20517), mRNA /cds=(44,1690) | 1 | |
| 3347 | Table 3A | Hs.44344 | NM_017867 | 8923502 | hypothetical protein FLJ20534 (FLJ20534), mRNA /cds=(20,1060) | 1 | |
| 3348 | Table 3A | Hs.107213 | NM_017892 | 8923548 | hypothetical protein FLJ20585 (FLJ20585), mRNA /cds=(99,746) | 1 | |
| 3349 | Table 3A | Hs.55781 | NM_017897 | 8923558 | hypothetical protein FLJ20604 (FLJ20604), mRNA /cds=(99,1478) | 1 | |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|-----------------------------|
| 3350 | Table 3A | Hs.18791 | NM_017899 | 8923562 | hypothetical protein FLJ20607 (FLJ20607), mRNA /cds=(48,698) | 1 | CGCACCTTGTGTCTTGTAGGGTATGG |
| 3351 | Table 3A | Hs.52184 | NM_017903 | 8923570 | hypothetical protein FLJ20618 (FLJ20618), mRNA /cds=(318,725) | 1 | TATGTGGGACTTCGCTGTTTTTAT |
| 3352 | Table 3A | Hs.49376 | NM_017917 | 8923599 | hypothetical protein FLJ20644 (FLJ20644), mRNA /cds=(276,1637) | 1 | AGCAGTTATATTGCCCTTGCTTTTA |
| 3353 | Table 3A | Hs.234149 | NM_017918 | 8923601 | hypothetical protein FLJ20647 (FLJ20647), mRNA /cds=(90,836) | 1 | TTCAGTTTAACTACTGTTTCCAA |
| 3354 | Table 3A | Hs.180201 | NM_017924 | 8923614 | hypothetical protein FLJ20671 (FLJ20671), mRNA /cds=(72,494) | 1 | AGCAAAATCCTCAGAAATGGTCTAAA |
| 3355 | Table 3A | Hs.48712 | NM_017948 | 8923662 | hypothetical protein FLJ20736 (FLJ20736), mRNA /cds=(130,1851) | 1 | TAAAAACATTGATATGCCTAGAGA |
| 3356 | Table 3A | Hs.279937 | NM_014960 | 7662439 | KIAA1001 protein (KIAA1001), mRNA /cds=(458,2035) | 1 | TGATTTTGCAACTTAGGATGTTTTGA |
| 3357 | Table 3A | Hs.280978 | NM_018114 | 8922464 | hypothetical protein FLJ10496 (FLJ10496), mRNA /cds=(13,429) | 1 | GTCCCATGGTTCATTTTGATTGT |
| 3358 | Table 3A | Hs.55024 | NM_018053 | 8922341 | hypothetical protein FLJ10307 (FLJ10307), mRNA /cds=(28,462) | 1 | TTACCTGGATTCCATTGGCTGGTTTT |
| 3359 | Table 3A | Hs.100895 | NM_018099 | 8922433 | hypothetical protein FLJ10462 (FLJ10462), mRNA /cds=(147,1694) | 1 | ACCACCTCATCATGATGTAGTGT |
| 3360 | Table 3A | Hs.4997 | NM_018107 | 8922449 | hypothetical protein FLJ10482 (FLJ10482), mRNA /cds=(149,1369) | 1 | CTCTTTGCCCTCATCTGAGTAAGT |
| 3361 | Table 3A | Hs.236844 | NM_018169 | 8922572 | hypothetical protein FLJ10652 (FLJ10652), mRNA /cds=(50,1141) | 1 | AATGGACATCTTCTCATGCAAGGT |
| 3362 | Table 3A | Hs.66048 | NM_018174 | 8922582 | chromosome 19 open reading frame 5 (C19orf5), mRNA /cds=(175,2193) | 1 | GCCACAGAATGGTCACCCAGCTTATT |
| 3363 | Table 3A | Hs.8083 | NM_018210 | 8922653 | hypothetical protein FLJ10769 (FLJ10769), mRNA /cds=(14,1186) | 1 | TAGGTGTAGACAAGATGACACAG |
| 3364 | Table 3A | Hs.59838 | NM_018227 | 8922683 | hypothetical protein FLJ10808 (FLJ10808), mRNA /cds=(180,1559) | 1 | GCCACAGAGGCTCCAATACCTGGGA |
| 3365 | Table 3A | Hs.18851 | NM_018253 | 8922730 | hypothetical protein FLJ10875 (FLJ10875), mRNA /cds=(100,2037) | 1 | ATGTTCCACAAAGTCATCAACTGGAA |
| 3366 | Table 3A | Hs.8739 | NM_018255 | 8922734 | hypothetical protein FLJ10879 (FLJ10879), mRNA /cds=(10,2490) | 1 | AGAATGTGTGTGCTGTGGGTCTCTA |
| 3367 | Table 3A | Hs.143954 | NM_018270 | 8922763 | hypothetical protein FLJ10914 (FLJ10914), mRNA /cds=(71,685) | 1 | CAAGTGACAGATGTGTGTTTTTCA |
| 3368 | Table 3A | Hs.6118 | NM_018285 | 8922793 | mitochondrial ribosomal protein S4 (MRPS4), mRNA /cds=(47,601) | 1 | TCCAAATTGTTTCTTAACATTCTATTT |
| 3369 | Table 3A | Hs.302981 | NM_018295 | 8922813 | hypothetical protein FLJ11000 (FLJ11000), mRNA /cds=(223,780) | 1 | TATGCCCTTTCGCTATTAACCGTG |
| 3370 | Table 3A | Hs.30822 | NM_018326 | 8922872 | hypothetical protein FLJ11110 (FLJ11110), mRNA /cds=(44,1033) | 1 | GCCTCTACTGTGGCCTCAACCCTGG |
| 3371 | Table 3A | Hs.105216 | NM_018331 | 8922883 | hypothetical protein FLJ11125 (FLJ11125), mRNA /cds=(203,712) | 1 | CAATTATAGTACTCCCATCCCTTA |
| 3372 | Table 3A | Hs.8033 | NM_018346 | 8922910 | hypothetical protein FLJ11164 (FLJ11164), mRNA /cds=(56,1384) | 1 | AACCTGACACAAATTTGGGACACGCT |
| 3373 | Table 3A | Hs.184465 | NM_018370 | 8922957 | hypothetical protein FLJ11259 (FLJ11259), mRNA /cds=(87,485) | 1 | TTAAACATTACTTTTCTACTTTGA |
| 3374 | Table 3A | Hs.11260 | NM_018371 | 8922959 | hypothetical protein FLJ11264 (FLJ11264), mRNA /cds=(362,1189) | 1 | CTCAGCCGACGCCGCTGTCCTTAG |
| 3375 | Table 3A | Hs.26194 | NM_018384 | 8922984 | hypothetical protein FLJ11296 (FLJ11296), mRNA /cds=(303,1226) | 1 | ATTCAGCCACATCAGAAATAAAGT |
| 3376 | literature | Hs.266514 | NM_018394 | 8923000 | hypothetical protein FLJ11342 (FLJ11342), mRNA /cds=(10,930) | 1 | ACTGTGCCATGGACATTTTCTCTCTG |
| 3377 | Table 3A | Hs.183656 | NM_018399 | 9055235 | VNN3 protein (HSA238982), mRNA /cds=(45,1550) | 1 | GGGAATTAACTACTTAATCTCGT |
| 3378 | Table 3A | Hs.123090 | NM_018450 | 8922086 | BRG1-Associated Factor 250a (BAF250a) mRNA, complete cds /cds=(378,7235) | 1 | ACAACGCTCTTAGAGAATCCGTGAAT |
| 3379 | Table 3A | Hs.7731 | NM_018453 | 8922092 | uncharacterized bone marrow protein BM036 (BM036), mRNA /cds=(95,796) | 1 | GTGAACAGACAAATGTGGCTAACCC |
| 3380 | Table 3A | Hs.6375 | NM_018471 | 8923807 | uncharacterized hypothalamus protein HT010 (HT010), mRNA /cds=(226,1419) | 1 | GTGTAAGATCAGACTGTGCAACTTT |
| 3381 | Table 3A | Hs.334370 | NM_018476 | 8923715 | brain expressed, X-linked 1 (BEX1), mRNA /cds=(171,548) | 1 | CGTGAAGATGCTGATATAATATAG |
| 3382 | Table 3A | Hs.274369 | NM_018477 | 8923711 | uncharacterized hypothalamus protein HARP11 (HARP11), mRNA /cds=(80,1333) | 1 | AATGGGATTACTCTGCTTTACCA |
| 3383 | db mining | Hs.10669 | NM_018482 | 8923867 | mRNA for KIAA1249 protein, partial cds /cds=(0,2850) | 1 | AGCTAATTATCTCTTTGAGTCTTGCT |
| 3384 | Table 3A | Hs.102652 | NM_018489 | 8922080 | hypothetical protein ASH1 (ASH1), mRNA /cds=(309,9218) | 1 | TCTGTTTGCTCACTTGTCAAGTCA |
| 3385 | Table 3A | Hs.160271 | NM_018490 | 8923700 | G protein-coupled receptor 48 (GPR48), mRNA /cds=(444,3299) | 1 | TCCTACTATTAAAGCTATTGAGCTC |
| 3386 | Table 3A | Hs.7535 | NM_018491 | 13236498 | COBW-like protein (LOC55871), mRNA /cds=(64,1251) | 1 | CGGGTCTCTTCTACCTGCATTCT |
| 3387 | Table 3A | Hs.104741 | NM_018492 | 8923876 | PDZ-binding kinase; T-cell originated protein kinase (TOPK), mRNA /cds=(154,1122) | 1 | AGTGATTGCCACTTAATGCAAGAC |

Table 8

| | | | | | | | |
|------|-----------|-----------|-----------|----------|--|---|---|
| 3388 | Table 3A | Hs.283330 | NM_018507 | 8924082 | hypothetical protein PRO1843 (PRO1843), mRNA /cds=(964,1254) | 1 | TCCAATGCAGTCCCATTCTTTATGGC CTATAGTCTCACTCCCACTACCCC |
| 3389 | Table 3A | Hs.186874 | NM_018519 | 8924144 | hypothetical protein PRO2266 (PRO2266), mRNA /cds=(258,626) | 1 | GGTGTCTGACTTAATGACTCCTGCTG AAGTTGAATTGTGAGATGTTATCC |
| 3390 | Table 3A | Hs.343477 | AF119911 | 7770258 | PRO2975 mRNA, complete cds /cds=UNKNOWN | 1 | CATTTGTCTGGAAATGCTGCCGGGAG CCTATTGTGTAATGTAGGTATTT |
| 3391 | Table 3A | Hs.147644 | NM_018555 | 10092612 | zinc finger protein 331; zinc finger protein 463 (ZNF361), mRNA /cds=(376,1767) | 1 | GCGGGAAGGCATGTAACCACTAAA CCATCTCCGAGAACATCAGAGGATC |
| 3392 | Table 3A | Hs.300496 | NM_018579 | 8924027 | mitochondria solute carrier protein (MSCP) mRNA, complete cds, alternatively spliced /cds=(44,511) | 1 | CAGGTCAACCCCCACCGGACCTACA ACCCGCAGTCCCACATCATCTCAGG |
| 3393 | Table 3A | Hs.300496 | NM_018579 | 8924027 | mitochondria solute carrier protein (MSCP) mRNA, complete cds, alternatively spliced /cds=(44,511) | 1 | CAGGTCAACCCCCACCGGACCTACA ACCCGCAGTCCCACATCATCTCAGG |
| 3394 | Table 3A | Hs.52891 | NM_018607 | 13699864 | hypothetical protein PRO1853 (PRO1853), mRNA /cds=(472,771) | 1 | TTTAGGGTTGTGACTGGCTTTGGTGC AAATGTGTGCTCAAGCTAATAAGT |
| 3395 | Table 3A | Hs.103657 | NM_018623 | 8924137 | PRO2219 mRNA, complete cds /cds=(823,1056) | 1 | ACTTGTGTTTTGTTTGGGGGCTGGGA AATGTATTTTACATTGTAGCCAA |
| 3396 | Table 3A | Hs.241576 | NM_018630 | 8924181 | hypothetical protein PRO2577 (PRO2577), mRNA /cds=(491,664) | 1 | AACATTGTGCTCTAACAGTATGACTA TTCTTTCCCCCACTTTAAACAGT |
| 3397 | Table 3A | Hs.283022 | NM_018643 | 8924261 | triggering receptor expressed on myeloid cells 1 (TREM1), mRNA /cds=(47,751) | 1 | CCAAGGGAGGAGGGAGGAGTAAAA GGCAGGGAGTTAATAACATGAATTA |
| 3398 | Table 3A | Hs.14317 | NM_018648 | 8923941 | nucleolar protein family A, member 3 (H/ACA small nucleolar RNPs) (NOLA3), mRNA /cds=(97,291) | 1 | TACTCTTTGGCATCCAGTCTCTCGTG GCGATTGATTATGCTGTGTGAGG |
| 3399 | Table 3A | Hs.195292 | NM_018666 | 8924241 | putative tumor antigen (SAGE), mRNA /cds=(167,2881) | 1 | CCTTCCAGAAGCTACGAAAAAGGGA GCTGTTTAAATTTAATAAATCTCTG |
| 3400 | Table 3A | Hs.8117 | NM_018695 | 8923908 | erbB2-interacting protein ERBIN (ERBB2IP), mRNA /cds=(323,4438) | 1 | AAGTGCCATAGAAAGCAATAACTGT TTAGTTGAGGCTAGTCTGGAACCT |
| 3401 | Table 3A | Hs.78825 | NM_018834 | 10047081 | matrin 3 (MATR3), mRNA /cds=(254,2800) | 1 | TGGATTCAAGTTACTGAAGTGAATAC CAATAAAAAGAAAACCTTAGGCCA |
| 3402 | Table 3A | Hs.44163 | NM_018838 | 10092656 | 13kDa differentiation-associated protein (LOC55967), mRNA /cds=(53,490) | 1 | AGGAGTGGATCCCACCTTCAACACCT TACAAGTAAAGACAATGAAGAACA |
| 3403 | Table 3A | Hs.183842 | NM_018955 | 11024713 | ubiquitin B (UBB), mRNA /cds=(94,783) | 1 | CAGTAATAGCTGAACCTGTTCAAAAT GTTAATAAAGGTTTTCGTTGCATGG |
| 3404 | db mining | Hs.44234 | NM_018965 | 9507202 | triggering receptor expressed on myeloid cells 2 (TREM2), mRNA /cds=(94,786) | 1 | AGGGAGTGGGAGGTGGTAAGAACA CCTGACAACCTCTGAATATTGGACA |
| 3405 | Table 3A | Hs.274428 | NM_018975 | 9507032 | TRF2-interacting telomeric RAP1 protein (RAP1), mRNA /cds=(138,1034) | 1 | AAAATTAGTGGATTGACTCCACTTTG TTGTGTTGTTTCATTGTTGAAAA |
| 3406 | Table 3A | Hs.61053 | NM_018986 | 9506676 | hypothetical protein (FLJ20356), mRNA /cds=(91,3285) | 1 | AATGGAGGCACGAACGCAGGGGCCA AATAGCAATAAATGGGTTTTGTTTT |
| 3407 | Table 3A | Hs.80618 | NM_018996 | 9506648 | hypothetical protein (FLJ20015), mRNA /cds=(31,522) | 1 | TGTTTTGATTGTTTTGCAAGGAAGAA AGACAATGGAATAACATACCTTCA |
| 3408 | Table 3A | Hs.83954 | NM_019006 | 9506852 | protein associated with PRK1 (AWP1), mRNA /cds=(244,804) | 1 | TCATTGCTGTCTACAGGTTTCTTCCA GATTATGTTTCATGGGTTTGTGTGT |
| 3409 | Table 3A | Hs.98324 | NM_019044 | 9506632 | hypothetical protein (FLJ10996), mRNA /cds=(135,857) | 1 | GAAAACAGACCTTGTGCTGAGGACAC GTCAATAAAAATTATACCTTCCCC |
| 3410 | db mining | Hs.110746 | NM_019052 | 9506772 | HCR (a-helix coiled-coil rod homologue) (HCR), mRNA /cds=(79,2427) | 1 | GGGATACCAGCTGAGTCTGAATCTCTG CTCTAAATAAAGCAGCTACAGAG |
| 3411 | Table 3A | Hs.274248 | NM_019059 | 9506858 | hypothetical protein FLJ20758 (FLJ20758), mRNA /cds=(464,1308) | 1 | TGGCTCGGATAAGAGATGGGACATC ATTCACTCACTAGTTGGATGGCACA |
| 3412 | Table 3A | Hs.124835 | NM_019062 | 9506662 | hypothetical protein (FLJ20225), mRNA /cds=(177,860) | 1 | AACCTTGATGAAAGTATTGCAGTATTG ATGCCATTGTAGAATAGAAGTGA |
| 3413 | Table 3A | Hs.30909 | NM_019081 | 11464998 | KIAA0430 gene product (KIAA0430), mRNA /cds=(0,3599) | 1 | TTTGTGTGTTGGGACCAACAGTTGT CAATAAACTTTACAGCGAGCATC |
| 3414 | Table 3A | Hs.76807 | NM_019111 | 9506780 | major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA /cds=(26,790) | 1 | CATGGGGCTCTCTGTGTACTTATTG TTTAAGGTTTCTCAAACCTGTGAT |
| 3415 | Table 3A | Hs.25951 | NM_019555 | 9506400 | Rho guanine nucleotide exchange factor (GEF) 3 (ARHGEF3), mRNA /cds=(127,1707) | 1 | AGGTGGTCAATGAATGTTTTGATGAA ATGAATGTTTTGTATAATGGCCT |
| 3416 | Table 3A | Hs.278857 | NM_019597 | 14141155 | heterogeneous nuclear ribonucleoprotein H2 (H') (HNRPH2), mRNA /cds=(78,1427) | 1 | ACGGGACAATTTTAAGATGTAATACC AATACTTTAGAAGTTTGGTCGTGT |
| 3417 | Table 3A | Hs.159523 | NM_019604 | 9624976 | class-I MHC-restricted T cell associated molecule (CRTAM), mRNA /cds=(0,1181) | 1 | ACAGCAAACCTTGGCATTATGTGGA GCATTCTCATTGTTGGAATCTGA |
| 3418 | Table 3A | Hs.159523 | NM_019604 | 9624976 | class-I MHC-restricted T cell associated molecule (CRTAM), mRNA /cds=(0,1181) | 1 | ACAGCAAACCTTGGCATTATGTGGA GCATTCTCATTGTTGGAATCTGA |
| 3419 | Table 3A | Hs.324743 | NM_019853 | 9790172 | protein phosphatase 4 regulatory subunit 2 (PPP4R2), mRNA /cds=(417,1778) | 1 | ACTTTTATGTAAAAAAGTGACACCTTA GTTTTACAAGTAAAGCAGGTTGT |
| 3420 | Table 3A | NA | NM_019997 | 9910435 | Mus musculus cDNA sequence AB041581 (AB041581), mRNA. | 1 | TCTTAATAATAATGAAGACGACTTACC CTGTGGAATTGAACACACTGGTG |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|---|
| 3421 | Table 3A | Hs.5392 | NM_020122 | 10047127 | potassium channel modulatory factor (DKFZP434L1021), mRNA /cds=(53,1198) | 1 | GCTGCTGTGTGATTTATGAATATTAA TGAATAAAAACTGCTTGGATGGT |
| 3422 | Table 3A | Hs.8203 | NM_020123 | 10047129 | endomembrane protein emp70 precursor isolog (LOC56889), mRNA /cds=(19,1779) | 1 | ACCGTGTAAGTGGGGATGGGGTAA AAGTGTTTAACTACTGTTGGATCA |
| 3423 | Table 3A | Hs.236828 | NM_020135 | 9910349 | putative helicase RUVBL (LOC56897), mRNA /cds=(238,1575) | 1 | TAAATTTATTTATTTATGAAAAACCT CGTGCCGAATTCCTGGCCTCGAG |
| 3424 | Table 3A | Hs.110796 | NM_020150 | 9910541 | GTP-binding protein SAR1 (SAR1) mRNA, complete cds /cds=(124,720) | 1 | GGGTTTCCGCTGGCTCTCCCAAGTATA TTGACTGATGTTTGGACGGTGAAA |
| 3425 | Table 3A | Hs.334775 | NM_020151 | 9910251 | Homo sapiens, Similar to RIKEN cDNA 1200014H14 gene, clone IMAGE:3139657, mRNA, partial cds /cds=(0,523) | 1 | GTACAGTTACTCATGTCATTGTAATG ATTTCACTCCTAACTGTGACATTT |
| 3426 | literature | Hs.21320 | NM_020165 | 14550404 | postreplication repair protein hRAD18p (RAD18), mRNA /cds=(77,1564) | 1 | ACTGAGTTGTGAGAAATTATGTCAAA ATGAAAACTGTTTGTTCATGACA |
| 3427 | Table 3A | Hs.6879 | NM_020188 | 9910183 | DC13 protein (DC13), mRNA /cds=(175,414) | 1 | ACCTGACTTCACCATGTTTATTCCTT TGCCTACAACGAGTTAATATCTG |
| 3428 | Table 3A | Hs.7045 | NM_020194 | 9910247 | GL004 protein (GL004), mRNA /cds=(72,728) | 1 | TCATGCGTGAACAATTTAAAAACGA CAGAAATAAGGTACAAGTGTAGTGT |
| 3429 | literature | Hs.9822 | NM_020196 | 9910259 | HCNP protein; XPA-binding protein 2 (HCNP), | 1 | CCCATCCCCCTCCCCACCCCATC CCCAATACAGCTACGTTTGTACATC |
| 3430 | Table 3A | Hs.283611 | NM_020217 | 9910199 | hypothetical protein DKFZp547I014 (DKFZp547I014), mRNA /cds=(1774,2166) | 1 | CCAACAAAATTGGGATCATCCAACT GAGTCCATCTGGCTAATCTAAAT |
| 3431 | Table 3A | Hs.79457 | NM_017860 | 8923488 | hypothetical protein FLJ20519 (FLJ20519), mRNA /cds=(74,604) | 1 | TGACTGGAAGTGAAGTAAATTGGGA ATGTATGACCAATCTTAGACCCCTG |
| 3432 | Table 3A | Hs.4859 | NM_020307 | 9945319 | cyclin L ania-6a (LOC57018), mRNA /cds=(54,1634) | 1 | TGTTTAAATGATGGTGAATCTTCTT AACACTGGTTTGTCTGCATGTGT |
| 3433 | Table 3A | Hs.283728 | NM_020357 | 9966826 | PEST-containing nuclear protein (pcnp), mRNA /cds=(18,554) | 1 | ACCTAAGGTCAAGCTGGGAGAGAGA AATGACTGAGATGAATGCTTTACT |
| 3434 | Table 3A | Hs.322901 | NM_020368 | 9966798 | disrupter of silencing 10 (SAS10), mRNA /cds=(161,1600) | 1 | GCTTAGGGAAATTTACAGTTCATTG TGGAGTGTAAACTTAGAACATGT |
| 3435 | Table 3A | Hs.111988 | NM_020382 | 9966854 | PR/SET domain containing protein 07 (SET07), mRNA /cds=(150,1331) | 1 | TGTTACAGGTTTCCAAGGTGGACTTG AACAGATGGCCTTATATTACAAA |
| 3436 | Table 3A | Hs.12450 | NM_020403 | 14589940 | protocadherin 9 (PCDH9), mRNA /cds=(118,3729) | 1 | TGTTACTGCTTTGCCAGTCTACGTT ATTTACAATTATTCAGCTCTTGCA |
| 3437 | Table 3A | Hs.286233 | NM_020414 | 14251213 | sperm autoantigenic protein 17 (SPA17), mRNA /cds=(1210,1665) | 1 | TTTCTGTATTGCAAGTGTATAGGCTT CTTGTTGTGTAAACTTGATTTCA |
| 3438 | Table 3A | Hs.287369 | NM_020525 | 10092624 | interleukin 22 (IL22), mRNA /cds=(71,610) | 1 | AACTAACCCCTTTCCCTGCTAGAAA TAACAATTAGATGCCCAAGCGA |
| 3439 | Table 3A | Hs.81328 | NM_020529 | 10092618 | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA /cds=(94,1047) | 1 | GTTTGTGTTACCCTCCTGTAATGGT GTACATAATGTATTGTTGGTAATT |
| 3440 | Table 3A | Hs.78888 | NM_020548 | 10140852 | diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein) (DBI), mRNA /cds=(0,314) | 1 | GCTCACCATACGGCTCTAACAGATTA GGGGCTAAAACGATTACTGACTTT |
| 3441 | literature | Hs.247302 | NM_020648 | 10190663 | twisted gastrulation (TSG), mRNA /cds=(13,684) | 1 | CGGCTGATGGGACAGGAATTGAAGA AGAGAATTGACTCGTATGAACAGGA |
| 3442 | literature | Hs.149342 | NM_020661 | 10190699 | activation-induced cytidine deaminase (AICDA), mRNA /cds=(76,672) | 1 | TGGTGCTACGAAGCCATTTCCTTGA TTTTAGTAACTTTTATGACAGC |
| 3443 | Table 3A | Hs.295231 | NM_020666 | 10190705 | CLK4 mRNA, complete cds /cds=(153,1514) | 1 | TGAGAAACTGTTTGACCTGGTTCGAA GAATGTTAGAATATGATCCAACCTC |
| 3444 | Table 3A | Hs.105052 | NM_020979 | 10280625 | adaptor protein with pleckstrin homology and src homology 2 domains (APS), mRNA /cds=(127,2025) | 1 | GGTGGGACACGCAAGCTCTTCACT GAAGACACGATGTTATTAAGCCCT |
| 3445 | Table 3A | Hs.104624 | NM_020980 | 11038652 | aquaporin 9 (AQP9), mRNA /cds=(286,1173) | 1 | TGCTTTGAAGCTACCTGGATATTTCC TATTTGAAATAAAATGTTTCGGTC |
| 3446 | Table 3A | Hs.211563 | NM_020993 | 10337612 | B-cell CLL/lymphoma 7A (BCL7A), mRNA /cds=(953,1648) | 1 | ATCGCCAAGAACCTGTTAGAGGCAT AAAGACCTTTTTTACCCTGTACCT |
| 3447 | Table 3A | Hs.6574 | NM_021008 | 10337616 | suppressin (nuclear deformed epidermal autoregulatory factor-1 (DEAF-1)-related) (SPN), mRNA /cds=(356,2011) | 1 | TGCTGCGACGCACATACATACGTGTT GTGCTGTCAATAAGTGTAATAA |
| 3448 | Table 3A | Hs.178391 | NM_021029 | 10445222 | ribosomal protein L44 (RPL44), mRNA /cds=(37,357) | 1 | TGGGAGGAGATAAGAAGAGAAAGGG CCAAGTGATCCAGTTCTAAGTGTC |
| 3449 | Table 3A | Hs.28578 | NM_021038 | 10518339 | muscleblind (Drosophila)-like (MBNL), mRNA /cds=(1414,2526) | 1 | TGCAGTAGTTGACTTTGCTGTATGGA AAAATAAAGTGAAATTGCCCTAAT |
| 3450 | literature | Hs.51011 | NM_021064 | 10800131 | H2A histone family, member P (H2AFP), mRNA /cds=(30,422) | 1 | GCTAAATAAGGAATACTCATGCCAAG ATCATCGAATTGTGCTCCTCCCT |
| 3451 | Table 3A | Hs.51299 | NM_021074 | 10835024 | NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD) (NDUFV2), mRNA /cds=(18,767) | 1 | ACCAAGGGACCTGGATTTGGTGTAC AAGCAGGCCCTTAATTTATATTGA |
| 3452 | Table 3A | Hs.63302 | NM_021090 | 10835108 | myotubularin related protein 3 (MTMR3) | 1 | GGAGTCAGTCAGTGCTCTATATTTT TCATTTTTTGTCAAGCAAGAAGT |
| 3453 | Table 3A | Hs.324406 | NM_021104 | 10863874 | ribosomal protein L41 (RPL41), mRNA /cds=(83,160) | 1 | TTTGTGGCCGAGTGTAACAACCATAT AATAAATCACCTCTTCCGCTGTTT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|------------------------------|
| 3454 | Table 3A | Hs.198282 | NM_021105 | 10863876 | phospholipid scramblase 1 (PLSCR1), mRNA /cds=(256,1212) | 1 | TTCTACATGAAATGTTTAGCTCTTACA |
| 3455 | Table 3A | Hs.75968 | NM_021109 | 11056060 | thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(77,211) | 1 | CTCTATCCTTCCTAGAAAATGGT |
| 3456 | Table 3A | Hs.154890 | NM_021122 | 12669906 | fatty-acid-Coenzyme A ligase, long-chain 2 (FACL2), mRNA /cds=(13,2109) | 1 | GGACGACAGTGAATCTAGAGTAAAA |
| 3457 | Table 3A | Hs.96 | NM_021127 | 10863922 | phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), mRNA /cds=(173,337) | 1 | CCAAGCTGGCCCAAGTGTCTGCA |
| 3458 | Table 3A | Hs.71618 | NM_021128 | 14589956 | polymerase (RNA) II (DNA directed) polypeptide L (7.6kD) (POLR2L), mRNA /cds=(21,224) | 1 | TGTTTTGGGGTCTGTGAGAGTACATG |
| 3459 | Table 3A | Hs.184011 | NM_021129 | 11056043 | pyrophosphatase (inorganic) (PP), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,946) | 1 | TATTATACAAGCACACAGGGC |
| 3460 | Table 3A | Hs.267690 | NM_021130 | 10863926 | mRNA for KIAA1228 protein, partial cds /cds=(0,2176) | 1 | AGGAACAGTTAGTTCATCTAGAAT |
| 3461 | literature | Hs.84981 | NM_021141 | 12408650 | X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kD) (XRCC5), mRNA /cds=(33,2231) | 1 | GAAAGTCCATATATGCATTGGTG |
| 3462 | Table 3A | Hs.12743 | NM_021151 | 10863952 | carnitine O-octanoyltransferase (CROT), mRNA /cds=(136,1974) | 1 | TGTGTGTGTATCCCATACCCACTCT |
| 3463 | Table 3A | Hs.7137 | NM_021188 | 10863994 | clones 23667 and 23775 zinc finger protein (LOC57862), mRNA /cds=(182,1618) | 1 | GGAGGAACCATCCAGTAAAGGTC |
| 3464 | Table 3A | Hs.8185 | NM_021199 | 10864010 | CGI-44 protein; sulfide dehydrogenase like (yeast) (CGI-44), mRNA /cds=(76,1428) | 1 | GTGCAAGGGGAGCACATATTGGATG |
| 3465 | Table 3A | Hs.12152 | NM_021203 | 14917112 | APMCF1 protein (APMCF1), mRNA /cds=(16,831) | 1 | TATATGTTACCATATGTTAGGAAAT |
| 3466 | Table 3A | Hs.25726 | NM_021211 | 10864022 | transposon-derived Buster1 transposase-like protein (LOC58486), mRNA /cds=(468,2549) | 1 | TTTCCTTGTTCCCTCCCATGCCTAGC |
| 3467 | Table 3A | Hs.29417 | NM_021212 | 10864024 | HCF-binding transcription factor Zhangfei (ZF), mRNA /cds=(457,1275) | 1 | TGGATTGCAGAGTTAAGTTTATGA |
| 3468 | literature | Hs.274363 | NM_021257 | 10864064 | neuroglobin (NGB), mRNA /cds=(0,455) | 1 | ACCCAGTCACCTCTGTCTTCAGCACC |
| 3469 | Table 3A | Hs.19520 | NM_021603 | 11125763 | FXD domain-containing ion transport regulator 2 (FXD2), transcript variant b, mRNA /cds=(67,261) | 1 | CTCATAGTCGTCACATAATACACA |
| 3470 | Table 3A | Hs.104305 | NM_021621 | 14719827 | death effector filament-forming Ced-4-like apoptosis protein (DEFCAP), transcript variant B, mRNA /cds=(522,4811) | 1 | TGAATCACATTGTCAGAAATTTTTCCT |
| 3471 | Table 3A | Hs.17757 | NM_021622 | 11055985 | pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 1 (PLEKHA1), mRNA /cds=(66,1280) | 1 | CCTCGCTGTTCATTTTGTAGTT |
| 3472 | Table 3A | Hs.106747 | NM_021626 | 11055991 | serine carboxypeptidase 1 precursor protein (HSCP1), mRNA /cds=(32,1390) | 1 | AGATGCCTTGTTGCTTTGAAGAAGGG |
| 3473 | Table 3A | Hs.3826 | NM_021633 | 11056005 | cDNA FLJ14750 fis, clone NT2RP3002948, weakly similar to RING CANAL PROTEIN /cds=(200,1906) | 1 | AGTGATGCAATTCTCTGTTTACA |
| 3474 | Table 3A | Hs.155418 | NM_021643 | 11056053 | GS3955 protein (GS3955), mRNA /cds=(1225,2256) | 1 | CCATGTGGGCTACTCATGATGGGCTT |
| 3475 | Table 3A | Hs.279681 | NM_021644 | 14141158 | heterogeneous nuclear ribonucleoprotein H3 (2H9) (HNRPH3), transcript variant 2H9, mRNA /cds=(118,1158) | 1 | GATTCTTTGGGAATAATAAAATGA |
| 3476 | Table 3A | Hs.174030 | NM_021777 | 11496993 | a disintegrin and metalloproteinase domain 28 (ADAM28), transcript variant 1, mRNA /cds=(47,2374) | 1 | AAAAGTCTCTGTAGATTTCTGAAGT |
| 3477 | Table 3A | Hs.288906 | NM_021818 | 11141888 | WW Domain-Containing Gene (WW45), mRNA /cds=(215,1366) | 1 | GCATATTCATTGATGCCAAGAAAA |
| 3478 | Table 3A | Hs.10724 | NM_021821 | 11141894 | MDS023 protein (MDS023), mRNA /cds=(335,1018) | 1 | GGAGGAGTTTGCATGTCTCATGATAA |
| 3479 | Table 3A | Hs.154938 | NM_021825 | 11141900 | hypothetical protein MDS025 (MDS025), mRNA /cds=(5,769) | 1 | CCAAATGTAAGATGAAAAATAAAG |
| 3480 | literature | Hs.302003 | NM_021922 | 11345453 | Fanconi anemia, complementation group E (FANCE), mRNA /cds=(185,1795) | 1 | TTGGTGACTTAGTGATTTTGTCAATTTT |
| 3481 | Table 3A | Hs.7174 | NM_021931 | 11345467 | hypothetical protein FLJ22759 (FLJ22759), mRNA /cds=(2,2113) | 1 | TTACATCAACTTCATGGTCTTGT |
| | | | | | | 1 | CGCCCGGCAGCCCCCATCCATCTGT |
| | | | | | | 1 | GTCTGTCTGTTGGCCTGTATCTGTT |
| | | | | | | 1 | GGCATCGCCAACGCCTGCCTCGTGC |
| | | | | | | 1 | CACCTCATGCTTATAATAAAGCCGG |
| | | | | | | 1 | CTGGCTGTGTACAGGGTGAGCCCC |
| | | | | | | 1 | AAAATTGGGGTTCAGCGTGGGAGGC |
| | | | | | | 1 | GCCGTCCTCAGTTACCTTTTCATGAGG |
| | | | | | | 1 | CTTCTAGCCAAAGATGATAAAGGG |
| | | | | | | 1 | AGGATAAAATCATTGTCTCTGGAGGC |
| | | | | | | 1 | AATTTGGAAATTATTTCTGCTTCT |
| | | | | | | 1 | CGGGTGATTACAGGCACCACTGCAG |
| | | | | | | 1 | TGATGATTGTACTTATTTGACACAT |
| | | | | | | 1 | GCCTCTGGTGCTTTGTCTGTATTTG |
| | | | | | | 1 | GTTTAATGTTTTTGCTCAATCTC |
| | | | | | | 1 | TTGATGTGAATTCAGTTATTGAACCTG |
| | | | | | | 1 | TTACTTGTTTTGCCAGAAATGT |
| | | | | | | 1 | AAGCTTCGAACTCAAAATCATGGAAA |
| | | | | | | 1 | GGTTTTAAGATTGAGGTTGGTTT |
| | | | | | | 1 | CCCAGTTAGATATCAGTGAGTTTGA |
| | | | | | | 1 | TAAGTACACCTGTCAGCTGTTTCTTAC |
| | | | | | | 1 | CACCTCGATGGTTGTGATTAATTT |
| | | | | | | 1 | TGTTTGCTTGAAACAGTTGTGTAATC |
| | | | | | | 1 | ATACAGGATTTTGTGGGTATTGGT |
| | | | | | | 1 | TGACCTTCTGTGTTTTGTTTCTGACT |
| | | | | | | 1 | TGAATAATTTATCAATGGTGTG |
| | | | | | | 1 | CCAGGGCTGCTTTGCTGTGATGATGA |
| | | | | | | 1 | TTGCATTTCAACACATGCCAGATG |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|---|
| 3482 | Table 3A | Hs.89751 | NM_021950 | 11386186 | membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for, beta polypeptide) (MS4A2), mRNA /cds=(90,983) | 1 | GAGTTACCACACCCCATGAGGGAAGCTCTAAATAGCCAACACCCATCTGT |
| 3483 | Table 3A | Hs.2484 | NM_021966 | 11415027 | T-cell leukemia/lymphoma 1A (TCL1A), mRNA /cds=(45,389) | 1 | TTCTATCCTTGACTTAGATTCTGGTGAGAGAAAGTGAGAATAGGCAGCCC |
| 3484 | Table 3A | Hs.75569 | NM_021975 | 11496238 | v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA /cds=(38,1651) | 1 | TCTTGCTCTTTCTACTCTGAACATAAAGCTGTTGCCAAGCTGGACGGC |
| 3485 | literature | Hs.245342 | NM_021979 | 13676856 | hypothetical protein FLJ14642 (FLJ14642), mRNA /cds=(23,583) | 1 | TGCAAAACAAATGCATAAATGCAAAATGTAAAGTAAAGCTGAAATTGATCTC |
| 3486 | Table 3A | Hs.326801 | NM_021998 | 11527399 | DNA sequence from PAC 75N13 on chromosome Xq21.1. Contains ZNF6 like gene, ESTs, STSs and CpG islands /cds=(567,2882) | 1 | ATGCTACTTGGGAGAAAACCTCTCACTAACTGTCTCACCGGGTTTCAAAGC |
| 3487 | Table 3A | Hs.293970 | NM_021999 | 11527401 | methylmalonate-semialdehyde dehydrogenase (ALDH6A1), mRNA /cds=(42,1649) | 1 | TGCAATGGAATATAAATATCACAAAGTTGTTAACTAGACTGCGTGTGT |
| 3488 | Table 3A | Hs.82407 | NM_022059 | 11545764 | CXC chemokine ligand 16 (CXCL16), mRNA /cds=(423,1244) | 1 | TTTCACCTCCTCAGTCCCTTGCCCTACCCCAGTGAGAGTCTGATCTTGTTT |
| 3489 | Table 3A | Hs.136164 | NM_022117 | 11545834 | cutaneous T-cell lymphoma-associated tumor antigen se20-4 (SE20-4), mRNA /cds=(129,2210) | 1 | CGCCTCTCCCGTGGACCTGTGTAATCCCAATAAAATTCTGAGCAAGTTC |
| 3490 | Table 3A | Hs.24633 | NM_022136 | 11545870 | SAM domain, SH3 domain and nuclear localisation signals, 1 (SAMS1), mRNA /cds=(82,1203) | 1 | AGGATTGCGTGTGAAACAAGTTGTCCAAGCAATGTTATATTCATTTT |
| 3491 | Table 3A | Hs.184052 | NM_022152 | 11545897 | PP1201 protein (PP1201), mRNA /cds=(75,1010) | 1 | GGAAGGGGGACAAGGGTCAGTCTGTGCGGTGGGGGCAGAAATCAATCAG |
| 3492 | Table 3A | Hs.184052 | NM_022152 | 11545897 | PP1201 protein (PP1201), mRNA /cds=(75,1010) | 1 | GGAAGGGGGACAAGGGTCAGTCTGTGCGGTGGGGGCAGAAATCAATCAG |
| 3493 | literature | Hs.294030 | NM_022447 | 13937360 | topoisomerase-related function protein 4-2 (TRF4-2), mRNA /cds=(336,869) | 1 | TTTTTCCAGCTCGCCACAGAAATGGA TCATGAAGACTGACAACCTGCAAAA |
| 3494 | Table 3A | Hs.74899 | NM_022451 | 11967984 | hypothetical protein FLJ12820 (FLJ12820), mRNA /cds=(156,1451) | 1 | AGGAGTGGCCTAAGAAATGCGTGTTCAGTGACTAGATTATAAATATTCT |
| 3495 | Table 3A | Hs.15220 | NM_022473 | 11968022 | zinc finger protein 106 (ZFP106), mRNA /cds=(335,5986) | 1 | AGCTGTGAACCTCGTAACCTTTGTAAA GCAAGATATAAAGCAAAATACAAGA |
| 3496 | Table 3A | Hs.27556 | NM_022485 | 11968038 | hypothetical protein FLJ22405 (FLJ22405), mRNA /cds=(81,1334) | 1 | AGGAGGGATCACCTGCACTGAGAATGAGGCAGTTTGACACAGATCACAAA |
| 3497 | Table 3A | Hs.26367 | NM_022488 | 11968042 | PC3-96 protein (PC3-96), mRNA /cds=(119,586) | 1 | TGTTCCACTACCAGCCTTACTTGTTTAATAAAATCAGTGCAAGAGAAA |
| 3498 | Table 3A | Hs.22353 | NM_022494 | 11968052 | hypothetical protein FLJ21952 (FLJ21952), mRNA /cds=(424,1665) | 1 | ACCTCAGATTTTGTTACCTGTCTTTTA AAAATGCAGATTTTGTCAAAATCA |
| 3499 | Table 3A | Hs.23259 | NM_022496 | 11968056 | hypothetical protein FLJ13433 (FLJ13433), mRNA /cds=(35,1225) | 1 | TTAAGCGCTTCACTGGACAGCTTTTCC TTAGAAGGTAGTTTTGTGTGACTG |
| 3500 | Table 3A | Hs.275865 | NM_022551 | 14165467 | mRNA; cDNA DKFZp586A0618 (from clone DKFZp586A0618) /cds=UNKNOWN | 1 | ACCGTGGGTGTGTCCAAGAAGAAATA AGTCTGTAGGCCTTGCTGTTAAT |
| 3501 | Table 3A | Hs.161786 | NM_022570 | 13384603 | C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12 (CLECSF12), mRNA /cds=(71,676) | 1 | CCAATGGATATTTCTGTATTACTAGG GAGGCATTTACAGTCTCTAATGT |
| 3502 | literature | Hs.65328 | NM_022725 | 12232376 | Fanconi anemia, complementation group F (FANCF), mRNA /cds=(13,1137) | 1 | TAGCTTTAGAAAATAACAGTTTGTGAA CTTACTTCCTATATTTCAGCT |
| 3503 | Table 3A | Hs.63609 | NM_022727 | 12232380 | HpaII tiny fragments locus 9C (HTF9C), mRNA /cds=(235,1662) | 1 | CTTTGTGGACTAGCCAAGGCTGTGAG GGCCAGAATAAACAACTGCTCAAC |
| 3504 | Table 3A | Hs.7503 | NM_022736 | 12232392 | hypothetical protein FLJ14153 (FLJ14153), mRNA /cds=(30,1427) | 1 | GCCGAGCAATGACCCCTTTCAATTTCT TATTCTGTGTTACTGAGGACCC |
| 3505 | Table 3A | Hs.194477 | NM_022739 | 12232396 | E3 ubiquitin ligase SMURF2 (SMURF2), mRNA /cds=(8,2254) | 1 | GAAACATGTGGATTTGCTGTGGAATG ACAAGCTCAAGGATTTACCCAGG |
| 3506 | Table 3A | Hs.34516 | NM_022766 | 12232440 | mRNA for KIAA1646 protein, partial cds /cds=(0,1446) | 1 | TTTGATCTGAAATGTTTGAGAAGACA CGAATAAAGTTACTTGGGCAGAAA |
| 3507 | Table 3A | Hs.154057 | NM_022790 | 13027789 | matrix metalloproteinase 19 (MMP19), transcript variant rasi-3, mRNA /cds=(1642,1899) | 1 | TCCCATCAAAAAGGTATCAATGCCT TGGAAGCTCCCTGATCTACAAAA |
| 3508 | Table 3A | Hs.121849 | NM_022818 | 13699866 | microtubule-associated proteins 1A/1B light chain 3 (MAP1A/1BLC3), mRNA /cds=(84,461) | 1 | ATCTGACATTATTGTAACCTACCGTGT GATCAGTAAGATTCTGTAGAAA |
| 3509 | Table 3A | Hs.146123 | NM_022894 | 12597628 | hypothetical protein FLJ12972 (FLJ12972), mRNA /cds=(168,1076) | 1 | ACCTTGATACCATGGAACATGAAAA GAGTCTTAGAAGTAAAGAACAACA |
| 3510 | Table 3A | Hs.57987 | NM_022898 | 12597634 | B-cell lymphoma/leukaemia 11B (BCL11B), mRNA /cds=(267,2738) | 1 | AGCATGTGCTGCCATTTTCATTTGTA CGCTTGTTCAAAACCAAGTTTGT |
| 3511 | Table 3A | Hs.128003 | NM_022900 | 12597638 | hypothetical protein FLJ21213 (FLJ21213), mRNA /cds=(74,1042) | 1 | TGAGCTGTATTACCATAAGTAGAATTT TAAGTAAACTGGTGAATTTGGGC |

Table 8

| | | | | | | | |
|------|-----------------------|-----------|-----------|----------|--|---|---|
| 3512 | Table 3A | Hs.194688 | NM_023005 | 14670389 | bromodomain adjacent to zinc finger domain, 1B (BAZ1B), transcript variant 1, mRNA /cds=(352,4803) | 1 | GCCCCATTAAAGGGTGAACCTTGTAAT AAATTGGAATTTCAAATAAACCTC |
| 3513 | Table 3A | Hs.168232 | NM_023079 | 12751494 | hypothetical protein FLJ13855 (FLJ13855), mRNA /cds=(314,1054) | 1 | TGCCCTAATCTTGAGTTGAGGAAATA TATGCACAGGAGTCAAGAGATGT |
| 3514 | db mining | Hs.37026 | NM_024013 | 13128949 | interferon, alpha 1 (IFNA1), mRNA /cds=(67,636) | 1 | AACGTCATGTGCACCTTTACACTGTG GTTAGTGTAATAAAACATGTTCCCT |
| 3515 | Table 3A | Hs.302981 | NM_024033 | 8922813 | hypothetical protein FLJ11000 (FLJ11000), mRNA /cds=(223,780) | 1 | TTATTCATATATTCCTGTCCAAAGCCA CACTGAAAACAGAGGAGAGACA |
| 3516 | Table 3A | Hs.115960 | NM_024036 | 13128987 | hypothetical protein MGC3103 (MGC3103), mRNA /cds=(10,984) | 1 | GCAGCCACCCACTGGGAGTCTTGTTT TTATTTATAATAAAATTTGTTGGGG |
| 3517 | Table 3A | Hs.7392 | NM_024045 | 13129005 | nucleolar protein GU2 (GU2), mRNA /cds=(107,2320) | 1 | ATCCACCAAAAATTAGGTCATCATAG TTGAGGTATGTGTCTGCTATTGTC |
| 3518 | Table 3A | Hs.103834 | NM_024056 | 13129025 | hypothetical protein MGC5576 (MGC5576), mRNA /cds=(51,803) | 1 | CCATTGGCTGGAACATGGATTGGGG ATTTGATAGAAAAATAAACCTGCT |
| 3519 | Table 3A | Hs.115659 | NM_024061 | 13129035 | hypothetical protein MGC5521 (MGC5521), mRNA /cds=(163,708) | 1 | GTTCCCTACTCTGTCTTGATGGAGG GGAGAAGGGAGGGCAAAGAAGTTA |
| 3520 | Table 3A | Hs.267400 | NM_024095 | 13129097 | hypothetical protein MGC5540 (MGC5540), mRNA /cds=(77,943) | 1 | TGGTTTTCCCTTTGGGACGTGGTTAA CGGTCCAGAAGAATCCCTTCTAGA |
| 3521 | Table 3A | Hs.321130 | NM_024101 | 13129107 | hypothetical protein MGC2771 (MGC2771), mRNA /cds=(184,1986) | 1 | ACCCCTTTCACTCTTGGCTTCTTATG TTGCTTTCATGAATGGAATGGAA |
| 3522 | Table 3A | Hs.109701 | NM_024292 | 13236509 | ubiquitin-like 5 (UBL5), mRNA /cds=(65,286) | 1 | CCCATCCTCATCCCCACACTGGGAT AGATGCTTGTGTTGAAAACTCAC |
| 3523 | Table 3A | Hs.78768 | NM_024298 | 13236521 | malignant cell expression-enhanced gene/tumor progression-enhanc (LENG4), mRNA /cds=(1101,1700) | 1 | TCAGGCCGCCTAGCTGCCCTTTGTC CAGGTTAATAAAGCACTGACTTGTT |
| 3524 | Table 3A | Hs.323193 | NM_024334 | 13236586 | hypothetical protein MGC3222 (MGC3222), mRNA /cds=(149,1351) | 1 | AAGGATTTTAAATAACTGCCGACTTC AAAAGTGTTCTTAAACGAAAGAT |
| 3525 | Table 3A | Hs.15961 | NM_024348 | 13259513 | dynactin 3 (p22) (DCTN3), transcript variant 2, mRNA /cds=(16,546) | 1 | CACCCACCTCCCCCAATCAGTGTT CTTATTTCACTGACAATAAACCAT |
| 3526 | Table 3A | Hs.8121 | NM_024408 | 13249343 | Notch (Drosophila) homolog 2 (NOTCH2), mRNA /cds=(12,7427) | 1 | ATAGCTGGTGACAAACAGATGGTTGC TCAGGACAAAGGTGCTCTCAATG |
| 3527 | db mining | Hs.12315 | NM_024557 | 13375722 | hypothetical protein FLJ11608 (FLJ11608), mRNA /cds=(561,1184) | 1 | CATGGATATCATGTATCCTTCTCGGT GCTCACACACCTGTACCTTGTA |
| 3528 | Table 3A | Hs.337561 | NM_024567 | 13375737 | hypothetical protein FLJ21616 (FLJ21616), mRNA /cds=(119,1093) | 1 | GCTGTGTGACTTAGTAGATAAAATAC TGCTTCTGCTCTTGGGACCATGA |
| 3529 | db mining | Hs.236449 | NM_024898 | 13376352 | hypothetical protein FLJ22757 (FLJ22757), mRNA /cds=(92,2473) | 1 | ACTTCCATCTCAGCTAATGCACCCAC CAGCTCAAACACACCAATAAAGCT |
| 3530 | literature | Hs.72241 | NM_030662 | 13489053 | mitogen-activated protein kinase kinase 2 (MAP2K2), mRNA /cds=(263,1465) | 1 | GCTGCTGTGTGTGGTCTCAGAGGCT CTGCTTCTTAGGTTACAAAACAA |
| 3531 | Table 3A | Hs.196270 | NM_030780 | 13540550 | folate transporter/carrier (LOC81034), mRNA /cds=(128,1075) | 1 | ATTTATCGTAAACATCCACGAGTGCT GTTGCACTACCATCTATTGTTGT |
| 3532 | Table 3A | Hs.211458 | NM_030788 | 13540564 | DC-specific transmembrane protein (LOC81501), mRNA /cds=(51,1463) | 1 | CCCCACAATGGTCTCTTTTCTCCCTG CTCCCTTATTAAGAAGCTCTTTCT |
| 3533 | cytokine arrays | Hs.46468 | NM_031409 | 14043039 | chemokine (C-C motif) receptor 6 (CCR6), transcript variant 2, mRNA /cds=(551,1675) | 1 | CAGTGTCTCCATGATCTTCCCAT ATCTTTTGTCTCAGGCTCTGGC |
| 3534 | Table 3A | Hs.301183 | NM_031419 | 13899228 | molecule possessing ankyrin repeats induced by lipopolysaccharide (MAIL), homolog of mouse (MAIL), mRNA /cds=(48,2204) | 1 | CTTGATCTCTAAATATGGTGTGATAT GAACCAAGTCCATTACATTGGAA |
| 3535 | Table 3A | Hs.245798 | NM_031435 | 13899258 | hypothetical protein DKFZp564I0422 (DKFZP564I0422), mRNA /cds=(510,1196) | 1 | ACATAGATTTTCTGCCAACAAATCCT CTCTGCTGTTACATTATCCTTTG |
| 3536 | db mining | Hs.238730 | NM_031437 | 13899264 | hypothetical protein MGC10823 (MGC10823), mRNA /cds=(63,1235) | 1 | CAGAGGTGGGAGTAAGTCTGGTAG TGCTTCTTTGTTGTGTGCTCAG |
| 3537 | Table 3A | Hs.103378 | NM_031453 | 13899290 | hypothetical protein MGC11034 (MGC11034), mRNA /cds=(245,640) | 1 | TTAGAACCAAAGTTATTCTTAATAAAA ATCACCACATGCTTGGACCATGC |
| 3538 | Table 3A | Hs.281397 | NM_031480 | 13899339 | hypothetical protein AD034 (AD034), mRNA /cds=(195,1880) | 1 | GCTCTTACACTTCGTCTTAATGTTCT TTTTGGAGTTAGGACCTCTCAGT |
| 3539 | RG housekeeping genes | Hs.334691 | NM_032223 | 14149927 | hypothetical protein FLJ22427 (FLJ22427), mRNA /cds=(40,2631) | 1 | ACCTTGACATGGGTTGTCTAATAAAA CTCGGACCCTTCTTGTAATCAA |
| 3540 | Table 3A | NA | R11456 | 764191 | spleen 1NFLS cDNA clone IMAGE:129880 5' similar to | 1 | ATCCCAAGTGCACAGTGAGTTGTATAT CACAAATAGGAGGCCATCTCAGGA |
| 3541 | RG housekeeping genes | Hs.170222 | R14692 | 768965 | Na ⁺ /H ⁺ exchanger NHE-1 isoform [human, heart, mRNA, 4516 nt] /cds=(577,3024) | 1 | GAAGCTGTAGGGCAAGGACTGGCC TGGCTCCAGAATGTTGTTGCCTTTT |
| 3542 | Table 3A | Hs.100896 | R18757 | 772367 | yg17e04.r1 cDNA, 5' end /clone=IMAGE:32522 /clone_end=5' | 1 | GGGAAGGAAAGGGGTGTGGCAGCT GGGAGCGTTTATTATGTTCTTTCT |
| 3543 | RG housekeeping genes | Hs.82927 | AK025706 | 10438309 | cDNA: FLJ22053 fis, clone HEP09502, highly similar to HUMAMPD2 AMP deaminase (AMPD2) mRNA /cds=UNKNOWN | 1 | GAGTGGTGTTCAGTGTGGCTCCC AGAGCTTTGACCAGATTGTGATCCC |
| 3544 | RG housekeeping genes | Hs.240013 | R44202 | 822065 | mRNA; cDNA DKFZp547A166 (from clone DKFZp547A166) /cds=UNKNOWN | 1 | CTTTGCATTTAGGGACACAGCCGGA GCCGAGAAGGTGAGCAGGGAGCA |

Table 8

| | | | | | | | |
|------|-----------------------------|-----------|-----------|---------|---|---|---|
| 3545 | RG housekeeping genes | Hs.12163 | NM_003908 | 4503504 | DNA sequence from clone RP1-64K7 on chromosome 20q11.21-11.23. Contains the EIF2B2 gene for eukaryotic translation initiation factor 2 subunit 2 (beta, 38kD), a putative novel gene, the gene for heterogenous nuclear ribonucleoprotein RALY or autoantigen P542, an RPS2 (RPS4) (40S ribosomal protein S2) pseudogene, ESTs, STS, GSSs and two CpG islands /cds=(138,1139) | 1 | CATTGCCTACTTTAACACCTGTCAGA GAAACGTGATATGGGGTAAGGAGG |
| 3546 | RG housekeeping genes | Hs.26320 | R56088 | 826194 | mRNA for TRABID protein (TRABID gene) /cds=(406,2532) | 1 | GCAATCTGGGAGCAGCACATTGTTGA TGGAGTCCAAGTGAGCACATTTCA |
| 3547 | Table 3A | Hs.208603 | R64054 | 835933 | 7f01d11.x1 cDNA, 3' end /clone=IMAGE:3293397 /clone_end=3' | 1 | CTCTCCTGGACTGTTGCAGTTGGGTG TGGCTGATTTGAAATTGTGCTTCA |
| 3548 | Table 3A | Hs.181400 | R67739 | 840377 | 602650370T1 cDNA, 3' end /clone=IMAGE:4761353 /clone_end=3' | 1 | TAACAAGAATTGCATTGAGGAAACAA GGCTCCACAGGGCCAATCTTCTGG |
| 3549 | Table 3A | Hs.161043 | R84314 | 942720 | 602415728F1 cDNA, 5' end /clone=IMAGE:4523958 /clone_end=5' | 1 | AAGAAGTTACATCTTCAATGTCCAGG GATGATCGTTTGAAGAGAACCTCT |
| 3550 | Table 3A | NA | R85137 | 943543 | brain N2b4HB55Y cDNA clone IMAGE:180492 5' | 1 | AAAACATTGCCAGACCATTAGTCCT CTTGAAGGGCCTCTCCGGTGGGG |
| 3551 | Table 3A | Hs.134025 | R88126 | 946939 | UI-H-BI2-agp-a-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2724781 /clone_end=3' | 1 | AGGGATAATAAGGTTAGCTGTTAACC AAGCACTGAGCTTTTAACCAAAG |
| 3552 | Table 3A | Hs.85289 | S53911 | 264768 | CD34 antigen (CD34), mRNA /cds=(90,1076) | 1 | CAAGACACTGTGGACTTGGTCACCAG CTCCTCCCTTGTCTCTAAGTTCC |
| 3553 | Table 3A | Hs.246381 | S57235 | 298664 | CD68 antigen (CD68), mRNA /cds=(15,1079) | 1 | GCCAGGATTAAGATCCATGAGTT CTTAAAGTATATGTTTCAAATTGCCA |
| 3554 | Table 3A | Hs.75256 | S59049 | 299704 | regulator of G-protein signalling 1 (RGS1), mRNA /cds=(14,604) | 1 | TTGCTACTATTGCTTGTCCGGTGT CTCCTGTGACCGGCTTGTGACATTC |
| 3555 | Table 3A | Hs.279518 | S60099 | 300168 | amyloid beta (A4) precursor-like protein 2 (APLP2), mRNA /cds=(72,2363) | 1 | ACTCAGAAAGACCAACCAAGGA |
| 3556 | Table 3A | Hs.300697 | S62140 | 386156 | mRNA for immunoglobulin lambda heavy chain /cds=(65,1498) | 1 | GTCGGACTATGTAATTGTAACATAC CTCTGGTCCCATTAAGAGTGACC |
| 3557 | Table 3A | Hs.249247 | S63912 | 399757 | heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), mRNA /cds=(30,839) | 1 | GCTAGTGTGTAATATGCTCTCTTGT GCTCTAATTCTGTGCTCCGTGC |
| 3558 | Table 3A | Hs.155924 | S68271 | 545204 | cAMP responsive element modulator (CREM), mRNA /cds=(0,998) | 1 | AGAGGAACCTGAAACCTTGAAGACA TTTGTCTCCCAAACCTGATTACT |
| 3559 | Table 3A | Hs.89545 | S71381 | 551546 | proteasome (prosome, macropain) subunit, beta type, 4 (PSMB4), mRNA /cds=(23,817) | 1 | ACTGGGATATTGCCACATGATCAGT GGCTTTGAATGAAATACAGATGCA |
| 3560 | Table 3A | Hs.179526 | S73591 | 688296 | upregulated by 1,25-dihydroxyvitamin D-3 (VDUP1), mRNA /cds=(221,1396) | 1 | CCAGAAAGTGTGGGCTGAAGATGGT TGGTTTCATGTGGGGGTATTATGTA |
| 3561 | Table 3A | Hs.155396 | S74017 | 693841 | nuclear factor (erythroid-derived 2)-like 2 (NFE2L2), mRNA /cds=(39,1808) | 1 | TTTCTTAGGACACCATTTGGGCTAGT TTCTGTGTAAGTGTAATACTACA |
| 3562 | Table 3A | Hs.274401 | S75463 | 833998 | mRNA; cDNA DKFZp434P086 (from clone DKFZp434P086); partial cds /cds=(798,1574) | 1 | GAAGGGTGGCCTGCCTGGCTGGGG AGGTCAGTAACTTTGAATAGTAAG |
| 3563 | Table 3A | Hs.73090 | S76638 | 243420 | p50-NF-kappa B homolog [human, peripheral blood T cells, mRNA, 3113 nt] /cds=(250,2952) | 1 | TTAACACCCACACCCACCCCTCAGT TGGGACAAATAAGGATTCTCATG |
| 3564 | Table 3A | Hs.252136 | S80990 | 1911529 | ficolin (collagen/fibrinogen domain-containing) 1 (FCN1), mRNA /cds=(92,1072) | 1 | CAAGCCGCCACATGCCCACAACCTC ACCAGAGGGAGAATTATGTTTCTAA |
| 3565 | Table 3A | Hs.301497 | T77017 | 694220 | arginine-tRNA-protein transferase 1-1p (ATE1) mRNA, alternatively spliced product, partial cds /cds=(0,1544) | 1 | GTGTATTGATCCAAGTAGTCAAAGTG TCTTAAGGGCACCTATTTGTCTT |
| 3566 | Table 3A | Hs.158193 | T78173 | 696682 | yd79c05.r1 cDNA, 5' end /clone=IMAGE:114440 /clone_end=5' | 1 | AGTGCTTCCAAATGTGATTGTTCTG GGTGATGGGACATATGGGCAGTTG |
| 3567 | Table 3A | NA | T80378 | 698887 | 1NIB cDNA clone IMAGE:24693 5' | 1 | CGGGGAATAGGAGGAAACATGG CATGGAACAAACCAACATAAAGGT |
| 3568 | Table 3A | NA | T80654 | 703539 | spleen 1NFLS cDNA clone IMAGE:108950 5' | 1 | ACTAATTCTGCTCTTTGGACAAGTGC CTGACATCTGCTTCATTGGGTTTT |
| 3569 | Table 3A | Hs.189744 | T85880 | 714232 | qz25e11.x1 cDNA, 3' end /clone=IMAGE:2027948 /clone_end=3' | 1 | AGGAATAAAGTTAAGTATTTCCCACTT GGAAATTGTACCACTCTCTGGGGT |
| 3570 | Table 3A | Hs.327 | U00672 | 482802 | interleukin 10 receptor, alpha (IL10RA), mRNA /cds=(61,1797) | 1 | CCTCTGCCAAAGTACTCTTAGGTGCC AGTCTGGTAAGTGAAGTCCCTCTG |
| 3571 | Table 3A | Hs.184592 | U00946 | 405048 | protein kinase, lysine deficient 1 (PRKWKN1), mRNA /cds=(0,7148) | 1 | GTCTGGTAAGCCGATGCTAATGGCA GAAGCAATAGAAGTCCAAGGCACTA |
| 3572 | Table 3A | Hs.278857 | U01923 | 460085 | heterogeneous nuclear ribonucleoprotein H2 (H') (HNRPH2), mRNA /cds=(78,1427) | 1 | ACGGGACAATTTTAAGATGTAATACC AATACTTTAGAAGTTTGGTCGTGT |

Table 8

| | | | | | | | |
|------|----------|-----------|--------|---------|---|---|---|
| 3573 | Table 3A | Hs.303627 | U02019 | 433343 | heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA-binding protein 1, 37kD) (HNRPD), transcript variant 1, mRNA /cds=(285,1352) | 1 | CTCTCAGTCCCAAGATGGCCCCACA TTCCCATTTGTTTTCCCAAGAGAA |
| 3574 | Table 3A | Hs.239138 | U02020 | 404012 | pre-B-cell colony-enhancing factor (PBEF), mRNA /cds=(27,1502) | 1 | GGTTGTTGTATTGTACCAAGTGAATG CCAAATTTGAAAGGCCTGTACTGC |
| 3575 | Table 3A | Hs.172081 | U02882 | 433346 | rolipram-sensitive 3',5'-cyclic AMP phosphodiesterase mRNA, complete cds /cds=(108,1922) | 1 | TTGTTTGCCATCTGTTGATCAGGAAC TACTTCAGCTACTTGCATTTGATT |
| 3576 | Table 3A | Hs.75969 | U03105 | 476094 | proline-rich protein with nuclear targeting signal (B4-2), mRNA /cds=(113,1096) | 1 | AATCTACATTTTCTTACCAGGAGCAG CATTGAGGTTTTTGAGCATAGTAC |
| 3577 | Table 3A | Hs.89421 | U03644 | 476104 | CBF1 interacting corepressor (CIR), mRNA /cds=(0,1352) | 1 | ACAGAGAGCACCAGGAGGTACACA TACTAAAGTGACACAAAGAGAATGA |
| 3578 | Table 3A | Hs.154654 | U03688 | 501030 | cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1), mRNA /cds=(372,2003) | 1 | TGTGTGCATAATAGCTACAGTGCATA GTTGTAGACAAAGTACATTCTGGG |
| 3579 | Table 3A | Hs.75546 | U03851 | 433307 | capping protein alpha mRNA, partial cds /cds=(16,870) | 1 | AGCATGTTGTTTAATTTCTTTTAAAA ATCACTGTTGGGCTTTGAAAGCA |
| 3580 | Table 3A | Hs.196384 | U04636 | 496975 | prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2), mRNA /cds=(134,1948) | 1 | GCTGACAAACCTGGGAATTTGGGTT GTGTATGCCAATGTTTCAGTGCCT |
| 3581 | Table 3A | Hs.118962 | U05040 | 460151 | far upstream element (FUSE) binding protein 1 (FUBP1), mRNA /cds=(26,1960) | 1 | TCACTTTCCAAATGCCTGTTTTGTGCT TTACAATAATGATATGAAACCT |
| 3582 | Table 3A | Hs.79630 | U05259 | 452561 | MB-1 gene, complete cds | 1 | TTTATGCGTATTTAAGCCTTGGAAC ACAGGGACTATCTTGTGGATTGGG |
| 3583 | Table 3A | Hs.177559 | U05875 | 463549 | interferon gamma receptor 2 (interferon gamma transducer 1) (IFNGR2), mRNA /cds=(648,1661) | 1 | GTCTTGACTTTGGCAAATGAGCCGGA GCCCCCTGGGCAGGTACACAACC |
| 3584 | Table 3A | Hs.1197 | U07550 | 469170 | heat shock 10kD protein 1 (chaperonin 10) (HSP61), mRNA /cds=(41,349) | 1 | ACATCCAGTGCTCCAAAATGTTTC CTTGTAAGTATATAAACACTTCCA |
| 3585 | Table 3A | Hs.78909 | U07802 | 984508 | Tis11d gene, complete cds /cds=(291,1739) | 1 | GGTACAGTTGGAGCACTATATGTACT CTCTGGACTACTTTGGACAGAAGT |
| 3586 | Table 3A | Hs.173965 | U08316 | 475587 | ribosomal protein S6 kinase, 90kD, polypeptide 3 (RPS6KA3), mRNA /cds=(0,2222) | 1 | AAAATCACCTCAACAGCCCTGTGAAG TGACCTCAGTGAGATATTTGGATC |
| 3587 | Table 3A | Hs.170171 | U08626 | 551473 | glutamine synthetase pseudogene | 1 | TTAAAGTGCACCTTCCAAAATGTCTC CCATAAGTAGGTAAGACCAACCTG |
| 3588 | Table 3A | Hs.333513 | U10117 | 498909 | small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating) (SCYE1), mRNA /cds=(49,987) | 1 | AATGATGAGTGTGTGGCTACATACAA AGGAGTTCCTTTGAGGTGAAAGG |
| 3589 | Table 3A | Hs.40202 | U10485 | 505685 | lymphoid-restricted membrane protein (LRMP), mRNA /cds=(574,2241) | 1 | GGGAAAGTATAGCATGAAACCAGAG GTTCTCAGAAATGACCGTAAGATAGC |
| 3590 | Table 3A | Hs.79022 | U10550 | 762886 | GTP-binding protein overexpressed in skeletal muscle (GEM), mRNA /cds=(213,1103) | 1 | TGGTTGACCCCTTGATGTGCAGCTC TGCTCTATTTATTATTATTTTGA |
| 3591 | Table 3A | Hs.194778 | U11870 | 511804 | interleukin 8 receptor, alpha (IL8RA), mRNA /cds=(100,1152) | 1 | TTGTCCACAAGTAAAGGAAATCCTC CTCCAGGGAGTCTCAGCTTCACCC |
| 3592 | Table 3A | Hs.80561 | U12767 | 924281 | mitogen induced nuclear orphan receptor (MINOR) mRNA, complete cds /cds=(209,1972) | 1 | CATTGCTCTTTAGTGTGTGTTAACCT GTGGTTTGAAGAATGCTCTTGT |
| 3593 | Table 3A | Hs.184411 | U13044 | 531892 | albumin (ALB), mRNA /cds=(39,1868) | 1 | GTCTGGCTTAACATTTTTTGAAATAT AACTGTTTCCCCTCTCTGCTGCT |
| 3594 | Table 3A | Hs.78915 | U13045 | 531894 | GA-binding protein transcription factor, beta subunit 1 (53kD) (GABPB1), transcript variant beta, mRNA /cds=(169,1356) | 1 | AAAAGCAATTACCCTTAAACTGTACT CTGGCCTACTTTTCTATTTTGA |
| 3595 | Table 3A | Hs.1162 | U15085 | 557701 | major histocompatibility complex, class II, DM beta (HLA-DMB), mRNA /cds=(233,1024) | 1 | GGCTCTCAGTGTGCCATAGAGGACA GCAACTGGTGATTGTTTCAGAGAAA |
| 3596 | Table 3A | Hs.155596 | U15173 | 558843 | BCL2/adenovirus E1B 19kD-interacting protein 2 (BNIP2), mRNA /cds=(211,1155) | 1 | AAACTGTTTCTTTGGTGTCTTTACAT TGAAATAAATGTGTTTGTGCCT |
| 3597 | Table 3A | Hs.2128 | U15932 | 9911129 | dual specificity phosphatase 5 (DUSP5), mRNA /cds=(210,1364) | 1 | ACCCGTGTGAATGTGAAGAAAAGCAG TATGTTACTGGTTGTTGTTGTTGT |
| 3598 | Table 3A | Hs.64639 | U16307 | 1100927 | glioma pathogenesis-related protein (RTVP1), mRNA /cds=(128,928) | 1 | AGAGAGGGAACATCAAATGCTGGCA CTATATACATACGATCAGCCTGATT |
| 3599 | Table 3A | Hs.183105 | U17989 | 805094 | nuclear autoantigen (GS2NA), mRNA /cds=(204,2345) | 1 | GTCTTCCGAGAACTTTTCTGATCAG TTTGCGAGTTTGTGAGTTTGT |
| 3600 | Table 3A | Hs.155188 | U18062 | 642794 | TATA box binding protein (TBP)-associated factor, RNA polymerase II, F, 55kD (TAF2F), mRNA /cds=(740,1789) | 1 | GCTGCTGTTGCTGCTTTGTGATGACG TGAGATCAATAAGAAGAACCTAGT |

Table 8

| | | | | | | | |
|------|----------|-----------|--------|----------|--|---|---|
| 3601 | Table 3A | Hs.2488 | U20158 | 806765 | lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD), (LCP2), mRNA /cds=(207,1808) | 1 | AGGACTGAACTGAACCCCTCCCATG AACACAAGGGTTTTATCCTTTCTCT |
| 3602 | Table 3A | Hs.78913 | U20350 | 665580 | G protein-coupled receptor V28 mRNA, complete cds /cds=(87,1154) | 1 | GATGTGGTAACTGTTAAATTGCTGTG TATCTGATAGCTCTTTGGCAGTCT |
| 3603 | Table 3A | Hs.154230 | U22897 | 984286 | nuclear domain 10 protein (NDP52), mRNA /cds=(54,1394) | 1 | GATCAAAAGGGCTATGGGAAGGGCA GACCCCGCCAATGATTTCTTCTCAC |
| 3604 | Table 3A | Hs.2437 | U23028 | 806853 | eukaryotic initiation factor 2B-epsilon mRNA, partial cds /cds=(0,1925) | 1 | GAACAGCTTTGTGCTCCGGCTTTCCC TCAGGGAACAGCAGAGAGCAGTTG |
| 3605 | Table 3A | Hs.93304 | U24577 | 1314245 | phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma) (PLA2G7), mRNA /cds=(161,1486) | 1 | TCCAGGGACCAACATTAAACACAACCA ATCAACACATCATGTTACAGAACT |
| 3606 | Table 3A | Hs.278625 | U24578 | 1125049 | RP1 and complement C4B precursor (C4B) genes, | 1 | TATTAAAGGCTTTTGGCAGCAAAGTG TCAGTGTGGCAGCGAAGTGTCAG |
| 3607 | Table 3A | Hs.3144 | U26710 | 862406 | Cas-Br-M (murine) ectropic retroviral transforming sequence b (CBLB), mRNA /cds=(322,2634) | 1 | TTCAACAAGATGCTTTGAAGGTTCTGA TTTTCAACTGATCAAACTAATGCA |
| 3608 | Table 3A | Hs.1724 | U29607 | 903981 | interleukin 2 receptor, alpha (IL2RA), mRNA /cds=(159,977) | 1 | ACTAATTTGATGTTTACAGGTGGACA CACAAGGTGCAATCAATGCGTAC |
| 3609 | Table 3A | Hs.75981 | U30888 | 940181 | ubiquitin specific protease 14 (tRNA-guanine transglycosylase) (USP14), mRNA /cds=(91,1575) | 1 | ACTGTACAAATTTCTGAAGATGGTTATT AACACTGTGCTGTTAAGCATCCA |
| 3610 | Table 3A | Hs.845 | U31120 | 1045451 | interleukin-13 (IL-13) precursor gene, complete cds | 1 | CTGTGCTGTGGCACCACCCACACATCC ATGTCTCCCTCACAACCCAGGAGG |
| 3611 | Table 3A | Hs.64310 | U32324 | 975336 | interleukin 11 receptor, alpha (IL11RA), mRNA /cds=(5,1273) | 1 | CATGTATGTAGGTGCCTGGGAGTGT GTGTGGTCTCTGCTCTGGCCCTTTC |
| 3612 | Table 3A | Hs.41724 | U32659 | 1155222 | interleukin 17 (cytotoxic T-lymphocyte-associated serine esterase 8) (IL17), mRNA /cds=(53,520) | 1 | ATTCAATTCAGAGTAGTTTCAAGTTT CACATCGTAACCATTTTCGCCCG |
| 3613 | Table 3A | Hs.108327 | U32986 | 1136227 | damage-specific DNA binding protein 1 (127kD) (DDB1), mRNA /cds=(109,3531) | 1 | TCTTCGGAAGAAGAAGGTGGGAGG ATGTGAATTGTTAGTTTCTGAGTTT |
| 3614 | Table 3A | Hs.32970 | U33017 | 984968 | signaling lymphocytic activation molecule (SLAM), mRNA /cds=(133,1140) | 1 | ATCAAGCCTCTGTGCCTCAGTTTCTC TCTCAGGATAAAGAGTGAATAGAG |
| 3615 | Table 3A | Hs.2533 | U34252 | 1049218 | aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme) (ALDH9), mRNA /cds=(377,1858) | 1 | GCGATAGAGGAAATCTACTCCCTATC TTGGGTCTTGAACCTACAGCCTGC |
| 3616 | Table 3A | Hs.169476 | U34995 | 1497857 | Homo sapiens, glyceraldehyde-3-phosphate dehydrogenase, clone MGC:10926 IMAGE:3628129, mRNA, complete cds /cds=(2306,3313) | 1 | CTAGGGAGCCGCACCTTGTCATGTAC CATCAATAAAGTACCCTGTGCTCA |
| 3617 | Table 3A | Hs.289107 | U37547 | 1145292 | baculoviral IAP repeat-containing 2 (BIRC2), mRNA /cds=(1159,3015) | 1 | TTTCTCCCCCTAGTTTGTGAGAAACA TCTCAATAAAGTGCTTTCCAAAAA |
| 3618 | Table 3A | Hs.154057 | U38320 | 2228241 | matrix metalloproteinase 19 (MMP19), transcript variant rasi-3, mRNA /cds=(1642,1899) | 1 | TCCATCAAAAAGGTATCAAATGCCT TGGAAGCTCCCTGATCCTACAAAA |
| 3619 | Table 3A | Hs.151518 | U38847 | 1184691 | TAR (HIV) RNA-binding protein 1 (TARBP1), mRNA /cds=(0,4865) | 1 | TGCCAAAAGTTTGCCATGTGCCTTAA ACATATTACTATATATTTTCCCCT |
| 3620 | Table 3A | Hs.75916 | U41371 | 1173904 | splicing factor 3b, subunit 2, 145kD (SF3B2), mRNA /cds=(48,2666) | 1 | CAGTTCCCCAAGGACTTGTGATTTTCAT GTTCTTATTTTAGACCTGTTTTGT |
| 3621 | Table 3A | Hs.169531 | U41387 | 1230563 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21 (DDX21), mRNA /cds=(265,2412) | 1 | TTACCAAGAGGACTTAAGGGAGTAA GGGGCGCAGATTAGCATTGCTCAA |
| 3622 | Table 3A | Hs.57304 | U41654 | 2058395 | Ras-related GTP-binding protein (RAGA), mRNA /cds=(31,972) | 1 | GATATGCACATCAAAGCCTTTACCAG TATCTTCTGTATTCCGTATCAGA |
| 3623 | Table 3A | Hs.167503 | U43185 | 1151169 | signal transducer and activator of transcription 5A (STAT5A), mRNA /cds=(640,3024) | 1 | CTCTGAGGCGTGAGGACTCGCAGTC AGGGGCAGCTGACCATGGAAGATTG |
| 3624 | Table 3A | Hs.54460 | U46573 | 1280140 | small inducible cytokine subfamily A (Cys-Cys), member 11 (eotaxin) (SCYA11), mRNA /cds=(53,346) | 1 | CCTCTCTTCTCCCTGGAATCTTGTA AAGGTCCTGGCAAAGATGATCAGT |
| 3625 | Table 3A | Hs.279891 | U46751 | 3077821 | truncated calcium binding protein (LOC51149), mRNA /cds=(219,695) | 1 | GCCTCCTGGTCTCTTACCACCTGTAG TTCTCTCATTTCCAAACCATCAGC |
| 3626 | Table 3A | Hs.155637 | U47077 | 13570016 | DNA-dependent protein kinase catalytic subunit (DNA-PKcs) mRNA, complete cds /cds=(57,12443) | 1 | TTTTCTTCTAACACTTGTATTTGGAG GCTCTTCTGTATTTTGAGAAGT |
| 3627 | Table 3A | Hs.306359 | U50078 | 4220427 | clone 25038 mRNA sequence /cds=UNKNOWN | 1 | TGAATTGCCTGTTTCAGGGTTCCTTAT GCAGAGAAATAAGCAGATTACAGG |
| 3628 | Table 3A | Hs.173824 | U51166 | 1378106 | thymine-DNA glycosylase (TDG), mRNA /cds=(399,1631) | 1 | GGACATCCACTAGAGATGGGTTTGAG GATTTTCCAAGCGTGTAATAATGA |
| 3629 | Table 3A | Hs.78993 | U51903 | 1262925 | IQ motif containing GTPase activating protein 2 (IQGAP2), mRNA /cds=(222,4949) | 1 | TTGCACGCAGAGCCTTTAAGTGACTA AGGAACAACATAGATAGTAGCAT |
| 3630 | Table 3A | Hs.74170 | U52054 | 1377850 | 602708243F1 cDNA, 5' end /clone=IMAGE:4844914 /clone_end=5' | 1 | ACTTTAATCTGATCTTGTGTCTTAGAG AAGCCCCATACCTGGTAGAGCA |

Table 8

| | | | | | | | |
|------|----------|-----------|--------|---------|--|---|-----------------------------|
| 3631 | Table 3A | Hs.82132 | U52682 | 1378108 | interferon regulatory factor 4 (IRF4), mRNA /cds=(105,1460) | 1 | TGTAGGAAAGGATGCTTCACAACTG |
| 3632 | Table 3A | Hs.82132 | U52682 | 1378108 | interferon regulatory factor 4 (IRF4), mRNA /cds=(105,1460) | 1 | AGGTAGATAATGCTATGCTGTCGT |
| 3633 | Table 3A | Hs.183556 | U53347 | 1478280 | solute carrier family 1 (neutral amino acid transporter), member 5 (SLC1A5), mRNA /cds=(590,2215) | 1 | TGTAGGAAAGGATGCTTCACAACTG |
| 3634 | Table 3A | Hs.333527 | U53530 | 1314642 | cDNA FLJ13685 fis, clone PLACE2000039, highly similar to DYNEIN HEAVY CHAIN, CYTOSOLIC /cds=UNKNOWN | 1 | AGGTAGATAATGCTATGCTGTCGT |
| 3635 | Table 3A | Hs.58189 | U54559 | 2351379 | eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD) (EIF3S3), mRNA /cds=(5,1063) | 1 | CTGGGGAGAGGCTGAGGACAAATAC |
| 3636 | Table 3A | Hs.44585 | U58334 | 1399804 | tumor protein p53-binding protein, 2 (TP53BP2), mRNA /cds=(756,3773) | 1 | CTGCTGTCACTCCAGAGGACATTTT |
| 3637 | Table 3A | Hs.169191 | U58913 | 4204907 | small inducible cytokine subfamily A (Cys-Cys), member 23 (SCYA23), mRNA /cds=(71,433) | 1 | CATTACTTGTGAGCTGCTGAACAAAC |
| 3638 | Table 3A | Hs.11383 | U59808 | 4097420 | small inducible cytokine subfamily A (Cys-Cys), member 13 (SCYA13), mRNA /cds=(75,371) | 1 | AAGTCAAGGTGAGCCCGGACATGG |
| 3639 | Table 3A | Hs.79089 | U60800 | 1663566 | sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (SEMA4D), mRNA /cds=(87,2675) | 1 | AAGAAGTTAACATGAACCTCTTGAAGT |
| 3640 | Table 3A | Hs.238648 | U60805 | 1794210 | oncostatin M receptor (OSMR), mRNA /cds=(367,3306) | 1 | CACACCAGGGCAACTCTTGAAGA |
| 3641 | Table 3A | Hs.77256 | U61145 | 1575348 | enhancer of zeste (Drosophila) homolog 2 (EZH2), mRNA /cds=(57,2297) | 1 | GAAACTTGCTACAGACTTACCCGTAA |
| 3642 | Table 3A | Hs.30035 | U61267 | 1418285 | splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10 (SFRS10), mRNA /cds=(121,987) | 1 | TATTTGTCAAGATCATAGCTGACT |
| 3643 | Table 3A | Hs.155935 | U62027 | 1511643 | complement component 3a receptor 1 (C3AR1), mRNA /cds=(0,1448) | 1 | TGGACACACGGATCAAGACCAGGAA |
| 3644 | Table 3A | Hs.177584 | U62961 | 1519051 | 3-oxoacid CoA transferase (OXCT), nuclear gene encoding mitochondrial protein, mRNA /cds=(98,1660) | 1 | GAATTGAACCTTGTCAGGTGAAGGG |
| 3645 | Table 3A | Hs.75498 | U64197 | 1778716 | small inducible cytokine subfamily A (Cys-Cys), member 20 (SCYA20), mRNA /cds=(58,348) | 1 | TGCTAAATATGTTATTGTGGAAGAT |
| 3646 | Table 3A | Hs.73165 | U64198 | 1685027 | interleukin 12 receptor, beta 2 (IL12RB2), mRNA /cds=(640,3228) | 1 | GAATGCAATAGTAGGACTGCTGAC |
| 3647 | Table 3A | Hs.279939 | U65590 | 1794218 | mitochondrial carrier homolog 1 (MTCH1), nuclear gene encoding mitochondrial protein, mRNA /cds=(0,1118) | 1 | AGCAATAAACTCTGGATGTTTGTGCG |
| 3648 | Table 3A | Hs.73172 | U67369 | 1698691 | growth factor independent 1 (GFI1), mRNA /cds=(267,1535) | 1 | CGTGTGTGGACAGCTTATCTTCC |
| 3649 | Table 3A | Hs.84264 | U70439 | 1698782 | Homo sapiens, acidic protein rich in leucines, clone MGC:8650 IMAGE:2961642, mRNA, complete cds /cds=(211,966) | 1 | TCCTCTTTTCTTTCAAGAACTATAT |
| 3650 | Table 3A | Hs.82116 | U70451 | 1763090 | myeloid differentiation primary response protein MyD88 mRNA, complete cds /cds=(32,922) | 1 | AAATGACCTGTTTTACGCGGCC |
| 3651 | Table 3A | Hs.117005 | U71383 | 2411474 | sialic acid binding Ig-like lectin 5 (SIGLEC5), mRNA /cds=(142,1797) | 1 | AGCTGCAAAGTGTTTGTACCACTGA |
| 3652 | Table 3A | Hs.12045 | U72514 | 2276395 | Homo sapiens, Similar to gene rich cluster, C2f gene, clone MGC:16358 IMAGE:3927564, mRNA, complete cds /cds=(278,733) | 1 | ATTTTTGCAATAATGCAGTATGGT |
| 3653 | Table 3A | Hs.183684 | U73824 | 1857236 | eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2), mRNA /cds=(306,3029) | 1 | TTGCTTACCAAAGGAGGCCCAATTT |
| 3654 | Table 3A | NA | U75686 | 2801402 | Poly(A)-binding protein, cytoplasmic 4 (inducible form) | 1 | ACTCAAATGTTTTGAGAACTGTGT |
| 3655 | Table 3A | Hs.20191 | U76248 | 2673967 | hSIAH2 mRNA, complete cds /cds=(526,1500) | 1 | ACATAGTGAAAGTTTATAAGAGGATG |
| 3656 | Table 3A | Hs.81361 | U76713 | 1814273 | heterogeneous nuclear ribonucleoprotein A/B (HNRPAB), transcript variant 1, mRNA /cds=(224,1219) | 1 | AAGTGATATGGTGAGCAGCGGACT |
| 3657 | Table 3A | Hs.76507 | U77396 | 1684871 | LPS-induced TNF-alpha factor (PIG7), mRNA /cds=(233,919) | 1 | AACAGCCTTTCTGGCTGACCACATGG |
| 3658 | Table 3A | Hs.78103 | U77456 | 1679778 | nucleosome assembly protein 1-like 4 (NAP1L4), mRNA /cds=(149,1276) | 1 | TAAATGCATACCTTCCCAGTACT |
| 3659 | Table 3A | Hs.80205 | U77735 | 1750275 | pim-2 oncogene (PIM2), mRNA /cds=(185,1189) | 1 | TGTGCCTCACCTGGACTGTGCCAATT |
| | | | | | | | AATGAAGTTGATTTCATTGTCATC |
| | | | | | | | CTATAGATGAAGACATAAAGACACT |
| | | | | | | | GGTAAACACCAATGTAAAGGGCC |
| | | | | | | | AGCTGTTGATGCTGGTTGGACAGGTT |
| | | | | | | | TGAGTCAAATTGTACTTTGTGCCA |
| | | | | | | | TGGGAAGGAAGGCTCTGTCTTCAACT |
| | | | | | | | CTTTGACCCTCCATGTGTACCATA |
| | | | | | | | GATTCTTGCTGTAGCGTGGATAGCTG |
| | | | | | | | TGATTGGTGAGTCAACCGTCTGTG |
| | | | | | | | TGGGCATTTTAAAGCCATCTCAAGAG |
| | | | | | | | GCATCTTCTACATGTTTTGTACGC |
| | | | | | | | AAGTCAGGGACCACTTGCTGAAGCA |
| | | | | | | | CGAAGAGCCCTTGTTGGCAATGTTAA |
| | | | | | | | GACTGCTGGAAGATGATCTTCTGCA |
| | | | | | | | CTGAGACTGTGGAGTTTGGGGAAG |
| | | | | | | | TTGTGGGTGTGAAACAAATGGTGAGA |
| | | | | | | | ATTTGAATTGGTCCCTCTATTAT |
| | | | | | | | AATTCCAGCTGAGCGCCGGTGCCTA |
| | | | | | | | CCATTACCCTGGTCTTGGTGTCAA |
| | | | | | | | CCCCAACCCCTCAAATTAAGTAGAA |
| | | | | | | | CTATAGATCCACATGAACGCACGC |
| | | | | | | | AGCTTTTGAAATTAATTTTAAACCC |
| | | | | | | | CAAGCCTGGGTGAGTGTGGGAAA |
| | | | | | | | TCTGTAATCAAATGATTGGTGTCAATT |
| | | | | | | | TCCCATTTGCCAATGTAGTCTCA |
| | | | | | | | GCCCCACCATTCATCCTGTCTGAAGG |
| | | | | | | | TCCTGGGTTGGTGTGACCGCTTG |
| | | | | | | | TTCTGCCTGGATTATTTAAAGGCC |
| | | | | | | | ATGTGTGGAACCCACTATTTAAT |

Table 8

| | | | | | | | |
|------|----------|-----------|--------|---------|---|---|-----------------------------|
| 3660 | Table 3A | Hs.55481 | U78722 | 1699000 | zinc finger protein 165 (ZNF165), mRNA /cds=(567,2024) | 1 | AGCCTTCAGTCAGAGCTCAAACCTTA |
| 3661 | Table 3A | Hs.71848 | U79277 | 1710245 | clone 23548 mRNA sequence /cds=UNKNOWN | 1 | GTCAACACCAGAGAATTCACATGA |
| 3662 | Table 3A | Hs.173854 | U80735 | 2565045 | CAGF28 mRNA, partial cds /cds=(0,2235) | 1 | GAATTTTCAGTTTGTGCTTACATTTTC |
| 3663 | Table 3A | Hs.306094 | U80743 | 2565060 | mRNA for KIAA1818 protein, partial cds /cds=(0,3473) | 1 | TAACATTGGATGTTTGCTTTGGC |
| 3664 | Table 3A | Hs.181466 | U81002 | 4580010 | cDNA FLJ14502 fis, clone NT2RM1000244, highly similar to TRAF4 associated factor 1 mRNA /cds=UNKNOWN | 1 | TATGACTTTAAGAGCCCACATTAGGT |
| 3665 | Table 3A | Hs.161002 | U82828 | 2072424 | non-lens beta gamma-crystallin like protein (AIM1) mRNA, partial cds /cds=(0,4913) | 1 | TTTATGATTCAATTTGCCAGGTTTT |
| 3666 | Table 3A | Hs.334457 | U83115 | 2623760 | Aac11 (aac11) mRNA, complete cds /cds=(77,1663) | 1 | GGCGTGCCGTTGAGGGGGAAAAACGA |
| 3667 | Table 3A | Hs.80420 | U83857 | 1888522 | small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin) (SCYD1), mRNA /cds=(79,1272) | 1 | AGCCCAAGTATTGCTACTGTTTTTC |
| 3668 | Table 3A | Hs.154695 | U84487 | 2218086 | phosphomannomutase 2 (PMM2), mRNA /cds=(48,788) | 1 | CTCTTGGGCATAAAATCTCAGAGGAA |
| 3669 | Table 3A | Hs.50404 | U85773 | 2388626 | small inducible cytokine subfamily A (Cys-Cys), member 25 (SCYA25), mRNA /cds=(0,452) | 1 | GCTACTTAGACATCATCTTGGCC |
| 3670 | Table 3A | Hs.162808 | U86453 | 2317893 | phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds /cds=(195,3329) | 1 | TCTACAGTAGCCTGTGCTGAACTGAT |
| 3671 | Table 3A | Hs.74407 | U86602 | 1835785 | nucleolar protein p40; homolog of yeast EBNA1-binding protein (P40), mRNA /cds=(142,1062) | 1 | CTCTTAAATAAACTTGCTTCTGGT |
| 3672 | Table 3A | Hs.5181 | U87954 | 4099505 | proliferation-associated 2G4, 38kD (PA2G4), mRNA /cds=(97,1281) | 1 | TTCTCAAGTTTGATACTGAGTTGACT |
| 3673 | Table 3A | Hs.173334 | U88629 | 1946346 | ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA /cds=(0,1922) | 1 | GTTCCCTTATCCCTCACCCTGCC |
| 3674 | Table 3A | Hs.169963 | U90543 | 2062687 | butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA /cds=(210,1793) | 1 | AGACTTTTCCAACCTCATCACCAAC |
| 3675 | Table 3A | Hs.167741 | U90548 | 2062697 | butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA /cds=(171,1925) | 1 | GTCTGTGCCATTTTGATTTTACT |
| 3676 | Table 3A | Hs.284283 | U90552 | 2062705 | butyrophilin (BTF5) mRNA, complete cds /cds=(359,1900) | 1 | CCAGCGGCATCTTCTCTGTGCAATG |
| 3677 | Table 3A | Hs.83724 | U90904 | 1913882 | Homo sapiens, clone IMAGE:3451448, mRNA, partial cds /cds=(0,901) | 1 | ATACTGTAATGACCTTCCAAAGTG |
| 3678 | Table 3A | Hs.279948 | U93243 | 6649661 | HSPC205 mRNA, complete cds /cds=(190,681) | 1 | TCTGGTCATTCAAGGATCCCTCCCA |
| 3679 | Table 3A | Hs.7811 | U94855 | 2055430 | eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD) (EIF3S5), mRNA /cds=(6,1079) | 1 | AGGCTATGCTTTTCTATAACTTTT |
| 3680 | Table 3A | Hs.326248 | U96628 | 2343084 | cDNA: FLJ22071 fis, clone HEP11691 /cds=UNKNOWN | 1 | TGTGGGTTGAGACCAGCACTCTGTGA |
| 3681 | Table 3A | Hs.195175 | U97075 | 2253680 | mRNA for CASH alpha protein /cds=(481,1923) | 1 | AACCTTGAAATGAGAAGTAAAGGC |
| 3682 | Table 3A | Hs.308026 | V00522 | 32122 | major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), mRNA /cds=(29,829) | 1 | ATTTGACCAACAGCAAGCAGAGT |
| 3683 | Table 3A | Hs.25647 | V01512 | 29903 | cellular oncogene c-fos (complete sequence) | 1 | GACGCCTTACAAATGATGGAGGATTC |
| 3684 | Table 3A | Hs.44189 | W00466 | 1271875 | yz99f01.r1 cDNA, 5' end /clone=IMAGE:291193 /clone_end=5' | 1 | CAAAGAGTTTTGTTTATTTGGGT |
| 3685 | Table 3A | NA | W00491 | 1271910 | 2NbHM cDNA clone IMAGE:291255 5' similar to | 1 | CCTGGTCATTGGTGGATGTTAAACCC |
| 3686 | Table 3A | NA | W02600 | 1274578 | spleen 1NFLS cDNA clone IMAGE:296099 5' | 1 | ATATTCCTTCAACTGCTGCCTGC |
| 3687 | Table 3A | NA | W03955 | 1275820 | za62d04.r1 cDNA, 5' end /clone=IMAGE:297127 / | 1 | TGGTGGATGTTAAACCAATATTCTTT |
| 3688 | Table 3A | Hs.306117 | W16552 | 1290934 | capicua protein (CIC) mRNA, complete cds /cds=(40,4866) | 1 | CAACTGCTGCTAGGCAAAA |
| 3689 | Table 3A | Hs.17778 | W19201 | 1295429 | neuropilin 2 (NRP2), mRNA /cds=(0,2780) | 1 | CAGCTCTGGGAATAGAAGACTAGG |
| 3690 | Table 3A | Hs.235883 | W19487 | 1295576 | 602628774F1 cDNA, 5' end /clone=IMAGE:4753483 /clone_end=5' | 1 | GTTGTTCTTAAATTTAGCTCATGT |
| 3691 | Table 3A | Hs.340717 | W25068 | 1302933 | we58c01.x1 cDNA, 3' end /clone=IMAGE:2345280 /clone_end=3' | 1 | TGACTTATGAGCTGTGACTCAACTGC |
| 3692 | Table 3A | Hs.173334 | W47229 | 1331869 | ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA /cds=(0,1922) | 1 | TTCATTAAACATTCTGCATTGGGT |

Table 8

| | | | | | | | |
|------|-----------|-----------|--------|---------|--|---|---|
| 3693 | Table 3A | NA | W56487 | 1358345 | zc59c07.r1 Soares_parathyroid_tumor_NbHPA cDNA clone | 1 | TCAATTGAGGCCCTTCCCTAAGATT ACAACATTGATAACCTGTCTTTT |
| 3694 | Table 3A | Hs.21812 | W74397 | 1384683 | AL562895 cDNA /clone=CS0DC021YO20-(3-prime) | 1 | CAGCCCTCCGTCGCTTTTTATAAAAC TTTGTGTGAGAAGAATATATTGAT |
| 3695 | Table 3A | Hs.163846 | W79598 | 1390869 | putative N6-DNA-methyltransferase (N6AMT1), mRNA /cds=(29,673) | 1 | ACTTCAGATCCTTTTGTGTTTAAATAA AGGAAAAGCTGCACATCCAAAAA |
| 3696 | Table 3A | Hs.8294 | W80882 | 1391906 | KIAA0196 gene product (KIAA0196), mRNA /cds=(273,3752) | 1 | AGCCTACCTCCCTACCCAGCTGTCTG TTGAGAGCAGTGCTGACCCAGCA |
| 3697 | Table 3A | Hs.303157 | X00437 | 36748 | mRNA for T-cell specific protein /cds=(37,975) | 1 | GAAGAGCTGCTCTCACCTCTCTGCAT CCCAATAGATATCCCCCTATGTGC |
| 3698 | Table 3A | Hs.75514 | X00737 | 35564 | nucleoside phosphorylase (NP), mRNA /cds=(109,978) | 1 | GGGCTCAGTTCTGCCTTATCTAAATC ACCAGAGACCAACAAGGACTAAT |
| 3699 | Table 3A | Hs.1724 | X01057 | 33812 | interleukin-2 receptor | 1 | AAATACAAACATTCTAATTAAGGCTT TGCAACACATGCCTTGTCTGTTT |
| 3700 | Table 3A | Hs.95327 | X01451 | 36774 | CD3D antigen, delta polypeptide (TIT3 complex) (CD3D), mRNA /cds=(0,515) | 1 | GCCATTACCAACTGTACCTCCCTTC TTGCTCAGCCATAAATATATCCT |
| 3701 | Table 3A | Hs.1103 | X02812 | 37092 | transforming growth factor, beta 1 (TGFB1), mRNA /cds=(841,2016) | 1 | CACCAGGAACCTGCTTTAGTGGGGG ATAGTGAAGAAGACAATAAAGATA |
| 3702 | Table 3A | Hs.1217 | X02994 | 28379 | adenosine deaminase (ADA), mRNA /cds=(95,1186) | 1 | TGGGCATGGTTGAATCTGAACCCCTC CTTCTGTGGCAACTTGTACTGAAA |
| 3703 | Table 3A | Hs.2233 | X03656 | 31687 | gene for granulocyte colony-stimulating factor (G-CSF) | 1 | CTGGGGAGGAGGTCCAGGGAGGAG GAGGAAAGTTCTCAAGTTCGTCTGAC |
| 3704 | Table 3A | Hs.174142 | X03663 | 29899 | colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog (CSF1R), mRNA /cds=(300,3218) | 1 | AACTAACAGTCACGCCGTGGGATGTC TCTGTCCACATTAACTAACAGCA |
| 3705 | Table 3A | Hs.14376 | X04098 | 28338 | actin, gamma 1 (ACTG1), mRNA /cds=(74,1201) | 1 | GGTTTTCTACTGTTATGTGAGAACATT AGGCCCCAGCAACACGTCATTGT |
| 3706 | Table 3A | Hs.74451 | X04106 | 35327 | calpain 4, small subunit (30K) (CAPN4), mRNA /cds=(158,964) | 1 | TTTGCTATATTCCTGCTCCAGCCTG CCAGGCCAGGAGGAAATAAACATG |
| 3707 | Table 3A | Hs.198365 | X04327 | 29480 | 2,3-bisphosphoglycerate mutase (BPGM), mRNA /cds=(110,889) | 1 | TTCTCTTTGGCCACAAGAATAAGCA GCAAATAAACAACTATGGCTGTTG |
| 3708 | Table 3A | Hs.58685 | X04391 | 37186 | CD5 antigen (p56-62) (CD5), mRNA /cds=(72,1559) | 1 | CTCATCTAAAGACACCTTCCTTTCCA CTGGCTGTCAAAGCCACAGGGCACC |
| 3709 | Table 3A | Hs.93913 | X04430 | 32673 | interleukin 6 (interferon, beta 2) (IL6), mRNA /cds=(62,700) | 1 | GCAGTTTGAATATCCTTTGTTTCAGA GCCAGATCATTTCTTGGAAAGTGT |
| 3710 | Table 3A | Hs.2253 | X04481 | 34627 | complement component 2 (C2), mRNA /cds=(36,2294) | 1 | CCCTGGTTGACTTGACTCATGCTTGT TTCACCTTTCACATGGAATTTCCCA |
| 3711 | Table 3A | Hs.2247 | X04688 | 33835 | interleukin 5 (colony-stimulating factor, eosinophil) (IL5), mRNA /cds=(44,448) | 1 | TCAGAGGGAAAGTAAATATTTCAGGC ATACTGACACTTTGCCAGAAAGCA |
| 3712 | Table 3A | Hs.79015 | X05323 | 34742 | MRC OX-2 gene signal sequence | 1 | CACAAGGTAAAGAACTCAATTCCCC TGCTTGAGGCCAGCAACACAAAT |
| 3713 | Table 3A | Hs.78225 | X05908 | 34387 | annexin A1 (ANXA1), mRNA /cds=(74,1114) | 1 | TGTGGAGGAACTAAACATTCCCTTG ATGGTCTCAAGCTATGATCAGAAAG |
| 3714 | Table 3A | Hs.36972 | X06180 | 29819 | CD7 antigen (p41) (CD7), mRNA /cds=(0,722) | 1 | GGAGGAGACCAGTCCCCACCCAGC CGTACCAGAAATAAAGGCTTCTGTG |
| 3715 | Table 3A | Hs.81665 | X06182 | 34084 | v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog (KIT), mRNA /cds=(21,2951) | 1 | TGTGTAATACATAAGCCGCTGAAGT TTAAAGGATGTTGGTGTCCACGT |
| 3716 | Table 3A | Hs.173255 | X06347 | 37540 | small nuclear ribonucleoprotein polypeptide A (SNRPA), mRNA /cds=(125,973) | 1 | CGCTGTTAGGCCGGAATTAAGTGG CTTTTGTAGGTTTGGTTTTTACAA |
| 3717 | db mining | Hs.2014 | X06557 | 37003 | mRNA for T-cell receptor delta /cds=UNKNOWN | 1 | GGGGTTTATGTCTCTAAGCTCTTTGTA TGCTGTTTTATAGGGATAGAAG |
| 3718 | Table 3A | Hs.153003 | X06956 | 32014 | serine/threonine kinase 16 (STK16), mRNA /cds=(118,1050) | 1 | ACACCAACCTGCTTCCACTTTATTCTT GTTTACACATTCTCCTGCTCCCA |
| 3719 | Table 3A | Hs.77202 | X07109 | 35492 | protein kinase C, beta 1 (PRKCB1), mRNA /cds=(136,2151) | 1 | AAGATGTTTGGAATGTTCATTGTG ATCTGGATCTCTGTTATGTGCCA |
| 3720 | Table 3A | Hs.89751 | X07203 | 29775 | membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide) (MS4A2), mRNA /cds=(90,983) | 1 | GAGTTACCACACCCCATGAGGGAG CTCTAAATAGCCAACACCATCTGT |
| 3721 | Table 3A | Hs.77436 | X07743 | 35517 | pleckstrin (PLEK), mRNA /cds=(60,1112) | 1 | TTCTGGAAGCTGTTCCCACTCCAGAG TGGTTTTATCAATAGCCTAGAGGT |
| 3722 | Table 3A | Hs.318885 | X07834 | 36517 | superoxide dismutase 2, mitochondrial (SOD2), mRNA /cds=(4,672) | 1 | TACTTTGGGACTTGTAGGGATGCCT TTCTAGTCCTATTCTATTGCAGTT |
| 3723 | Table 3A | Hs.78056 | X12451 | 29714 | cathepsin L (CTSL), mRNA /cds=(288,1289) | 1 | TGGAATCTGTGATATTTTACAA ATATCCAATATTCGTGTGTGAGCAT |
| 3724 | Table 3A | Hs.193400 | X12830 | 33845 | interleukin 6 receptor (IL6R), mRNA /cds=(437,1843) | 1 | AGAAGTAACCTTACTTAGGTGTGGG TTGTTGACAACTGTGACTGTACCCAA |
| 3725 | Table 3A | Hs.856 | X13274 | 32691 | interferon, gamma (IFNG), mRNA /cds=(108,608) | 1 | ATGGAAGTAACCTATTGTTTAA AAGTTTCTCAGCTCCCATTTCTACTCT |
| 3726 | Table 3A | Hs.2299 | X13444 | 29826 | CD8 antigen, beta polypeptide 1 (p37) (CD8B1), mRNA /cds=(50,682) | 1 | CCCATGGCTTCATGCTTCTTTCA TCTCCATGTTGTCAAATCATGCCGT |
| 3727 | Table 3A | Hs.234489 | X13794 | 34314 | lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) | 1 | TTATAGCTATTTTACCTCAGTGG |

Table 8

| | | | | | | | |
|------|------------|-----------|--------|---------|---|---|---|
| 3728 | literature | Hs.89137 | X13916 | 34338 | low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor) (LRP1), mRNA /cds=(466,14100) | 1 | GCCCCGTTTTGGGGACGTGAACGTTT TAATAATTTTTGCTGAATTCCTTTA |
| 3729 | Table 3A | Hs.82120 | X14008 | 34433 | nuclear receptor subfamily 4, group A, member 2 (NR4A2), mRNA /cds=(317,2113) | 1 | AGGTGGGCACAAGTATTACACATCAG AAAATCCTGACAAAAGGGACACAT |
| 3730 | Table 3A | Hs.77424 | X14356 | 31331 | Fc fragment of IgG, high affinity Ia, receptor for (CD64) (FCGR1A), mRNA /cds=(0,1124) | 1 | GTTCAACAACACCAGAAGTGTGTGTC TCATGGTATGTAACCTCTAAAGCA |
| 3731 | Table 3A | Hs.87409 | X14787 | 37464 | thrombospondin 1 (THBS1), mRNA /cds=(111,3623) | 1 | TTGACCTCCCATTTTTACTATTTGCCA ATACCTTTTTCTAGGAATGTGCT |
| 3732 | Table 3A | Hs.289088 | X15183 | 32487 | heat shock 90kD protein 1, alpha (HSPCA), mRNA /cds=(60,2258) | 1 | AAAGCTGTTCAAATACTCGAGCCAG TCTTGTTGGATGGAAATGTAGTGCT |
| 3733 | Table 3A | Hs.339703 | X16277 | 35137 | zv26f06.r1 cDNA, 5' end /clone=IMAGE:754787 /clone_end=5' | 1 | CTTAAGTCTGACGGACCTGTCCGTGTC CAGGCCAGTGCCAGGGAAGGTGT |
| 3734 | Table 3A | Hs.50964 | X16354 | 37197 | mRNA for transmembrane carcinoembryonic antigen BGPα (formerly TM1-CEA) /cds=(72,1652) | 1 | TTTCTAACCCGTGACACGGACTGTGCA TACTTTCCCTCATCCATGCTGTGC |
| 3735 | Table 3A | Hs.154672 | X16396 | 35070 | methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,1110) | 1 | CAGCAGCTGCCTGCTTTTCTGTGATG TATGTATCCTGTTGACTTTTCCAG |
| 3736 | Table 3A | Hs.14601 | X16663 | 32054 | hematopoietic cell-specific Lyn substrate 1 (HCLS1), mRNA /cds=(42,1502) | 1 | TCCCTGAAGAAATATCTGTGAACCTT CTTTCTGTTCACTCCTAAAATTCG |
| 3737 | Table 3A | Hs.176663 | X16863 | 31321 | leukocyte IgG receptor (Fc-gamma-R) mRNA, complete cds /cds=(17,718) | 1 | ATGGGAGTAATAAGAGCAGTGGCAG CAGCATCTCTGAACATTTCTCTGGA |
| 3738 | Table 3A | Hs.271986 | X17033 | 33906 | integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) (ITGA2), mRNA /cds=(42,3587) | 1 | ACCCATTTCTACTTTTTGCACCTTATT TTCTCTGTTCTGAGCCCCACA |
| 3739 | Table 3A | Hs.1908 | X17042 | 32432 | proteoglycan 1, secretory granule (PRG1), mRNA /cds=(24,500) | 1 | TGTGTTTGACAGCTAGTGGATGTGT TTGTCTACAAGTATGATTGCTGTT |
| 3740 | Table 3A | Hs.342863 | X17094 | 31477 | tg48f06.x1 cDNA, 3' end /clone=IMAGE:2112035 /clone_end=3' | 1 | GGCCAGCATTGCTGGTTCTATTATA TGGACATGAGATAATGTTAGAGGT |
| 3741 | Table 3A | Hs.198951 | X51345 | 34014 | jun B proto-oncogene (JUNB), mRNA /cds=(253,1296) | 1 | TGAATATAATATATTTGTGATTTAAC AGGGAGGGGAAGAGGGGGCGATC |
| 3742 | Table 3A | Hs.3268 | X51757 | 35221 | heat shock 70kD protein 6 (HSP70B) (HSPA6), mRNA /cds=(0,1931) | 1 | TGGCACTTTAACTATGCTTTCACTTAT ATTTTGTGTACTTTGTATTCTTG |
| 3743 | Table 3A | Hs.76053 | X52104 | 35219 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD) (DDX5), mRNA /cds=(170,2014) | 1 | AGTAAATGTACAGTGATTGAAATAC AATAATGAAGGCAATGCATGGCCT |
| 3744 | Table 3A | Hs.323098 | X52142 | 30292 | cDNA: FLJ23458 fis, clone HSI07327 /cds=UNKNOWN | 1 | CTTAATGTGACCTAGCAATAGGCATA GCTACGTGGCACTATATTCTGGCC |
| 3745 | literature | Hs.99987 | X52221 | 31215 | ERCC2 gene, exons 1 & 2 (partial) /cds=UNKNOWN | 1 | AGGAGCACCTCACAGATGCCAACCT CAACCTGACCGTGACGAGGGTGTC |
| 3746 | Table 3A | Hs.278544 | X52882 | 311380 | acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase) (ACAT2), mRNA /cds=(37,1230) | 1 | CCACGACTTCTGCCATTCTCTCCAG TGTGTGAACAGGGTCACAAGAAT |
| 3747 | Table 3A | Hs.85266 | X53587 | 33950 | integrin, beta 4 (ITGB4), mRNA /cds=(126,5384) | 1 | GGCCCAAACCTATTTGTAACCAAAGA GCTGGGAGCAGCACAGGACCCAG |
| 3748 | Table 3A | Hs.117950 | X53793 | 28383 | multifunctional polypeptide similar to SAICAR synthetase and AIR carboxylase (ADE2H1), mRNA /cds=(24,1301) | 1 | GCGAGCAAGCATTTTGAACACATGGA TTTCCTTGAAGCAGGCTGACAAGA |
| 3749 | Table 3A | NA | X53795 | 35832 | R2 mRNA for an inducible membrane protein | 1 | TCGGATGGGCTGTTTAGATGTTATAT AATCCACAAAAGGTTTCATTGAGCT |
| 3750 | Table 3A | Hs.105938 | X53961 | 34415 | lactotransferrin (LTF), mRNA /cds=(294,2429) | 1 | GGATTGCCCATCCATCTGCTTACAAT TCCCTGCTGCTGCTTTAGCAAGAA |
| 3751 | Table 3A | Hs.55921 | X54326 | 31957 | glutamyl-prolyl-tRNA synthetase (EPRS), mRNA /cds=(58,4380) | 1 | AAAAATGAAGTCACACAGGACAATTAT TCTTATGCCTAAGTTAACAGTGGA |
| 3752 | Table 3A | Hs.789 | X54489 | 34625 | GRO1 oncogene (melanoma growth stimulating activity, alpha) (GRO1), mRNA /cds=(79,402) | 1 | GCCTTGTTTAAATGGTAGTTTACAGT GTTTCTGGCTTAGAACAAAGGGGC |
| 3753 | Table 3A | Hs.74085 | X54870 | 35062 | DNA segment on chromosome 12 (unique) 2489 expressed sequence (D12S2489E), mRNA /cds=(338,988) | 1 | AGTGCCTTCCCTGCCTGTGGGGGTC ATGCTGCCACTTTTAAATGGGTCTCT |
| 3754 | Table 3A | Hs.83758 | X54942 | 29978 | CDC28 protein kinase 2 (CKS2), mRNA /cds=(95,334) | 1 | TTCCAGTCAGTTTTTCTCTTAAGTGCC TGTTTTGAGTTTACTGAAACAGTT |
| 3755 | Table 3A | Hs.283330 | X55733 | 8924082 | hypothetical protein PRO1843 (PRO1843), mRNA /cds=(964,1254) | 1 | TCCAATGCAGTCCCATTTCTTTATGGC CTATAGTCTCACTCCCAACTACCC |
| 3756 | Table 3A | Hs.312670 | X55740 | 23896 | xn42c03.x1 cDNA, 3' end /clone=IMAGE:2696356 /clone_end=3' | 1 | TGGTATAAGAAATGACTTTGAACCAC TTTGCAATTGTAGATTCCCAACAA |
| 3757 | Table 3A | Hs.85112 | X57025 | 33007 | IGF-I mRNA for insulin-like growth factor I /cds=(166,627) | 1 | CCCCTGCTACTTTTGAACCAAGAAAAT AATGACTGGCCATTTCGTACATCT |

Table 8

| | | | | | | | |
|------|------------|-----------|--------|--------|--|---|---|
| 3758 | Table 3A | Hs.279920 | X57346 | 23113 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide (YWHAB), mRNA /cds=(372,1112) | 1 | TGATCTGTCCAGTGTCACTCTGTACC CTCAACATATATCCCTTGTGCGAT |
| 3759 | Table 3A | Hs.74405 | X57347 | 32463 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide (YWHAQ), mRNA /cds=(100,837) | 1 | AAAAGCCTTGTGAAAATGTTATGCC TATGTAACAGCAGAGTAACATAAA |
| 3760 | Table 3A | Hs.289110 | X57809 | 33714 | rearranged immunoglobulin lambda light chain mRNA /cds=(9,710) | 1 | CCACCACGGGAGACTAGAGCTGCAG GATCCCGGGGGAGGGGTCTCTCCTC |
| 3761 | Table 3A | Hs.289110 | X57812 | 33723 | rearranged immunoglobulin lambda light chain mRNA /cds=(9,710) | 1 | CAGTGGAAAGTCCCACAGAAGCTACA GCTGCCAGGTACGCATGAAGGGAG |
| 3762 | Table 3A | Hs.302063 | X58529 | 33480 | rearranged immunoglobulin mRNA for mu heavy chain enhancer and constant region /cds=UNKNOWN | 1 | CCCACACTGCTTTGCTGTGTATACGC TTGTTGCCCTGAAATAAATATGCA |
| 3763 | Table 3A | Hs.302063 | X58529 | 33480 | rearranged immunoglobulin mRNA for mu heavy chain enhancer and constant region /cds=UNKNOWN | 1 | CCCACACTGCTTTGCTGTGTATACGC TTGTTGCCCTGAAATAAATATGCA |
| 3764 | Table 3A | Hs.155101 | X59066 | 28937 | Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle | 1 | ACAAATTTCTTGCTGGATTGGAAGC TTAAACTCCTGTGGATTCACATCA |
| 3765 | Table 3A | Hs.83532 | X59405 | 34508 | H.sapiens, gene for Membrane cofactor protein /cds=UNKNOWN | 1 | AGAGACCAGTTTTCTCTGGAAGTTTG TTTAAATGACAGAAGCGTATATGA |
| 3766 | literature | Hs.861 | X60188 | 31220 | ERK1 mRNA for protein serine/threonine kinase /cds=(72,1211) | 1 | CGCCCTGCCACCTCCCTGACCCGT CTAATATATAATATAGAGATGTGT |
| 3767 | Table 3A | Hs.81634 | X60221 | 509290 | ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1), mRNA /cds=(32,802) | 1 | GCCAGTCAGATGTTTCTCATCCTTCT TGCTCTGCCCTTGAGTTGTTCCGT |
| 3768 | Table 3A | Hs.44926 | X60708 | 35335 | dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2) (DPP4), mRNA /cds=(75,2375) | 1 | AAATACTGATGTTCTAGTGAAAGAG GCAGCTTGAAACTGAGATGTGAAC |
| 3769 | Table 3A | Hs.81226 | X60992 | 29817 | CD6 mRNA for T cell glycoprotein CD6 /cds=(120,1526) | 1 | AGAAGCTGCACTAGGCCCGAGTCC CCATGTGTCTCCTGAATTGATGAG |
| 3770 | Table 3A | Hs.77054 | X61123 | 29508 | B-cell translocation gene 1, anti-proliferative (BTG1), mRNA /cds=(308,823) | 1 | AAGTCTTTTCCACAAACCACCATCTAT TTGTGAACCTTTGTAGTCATCT |
| 3771 | Table 3A | Hs.76913 | X61970 | 296739 | proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA /cds=(21,746) | 1 | AAATTTTATTTCCAGCTCCTGTTCCTT GGAAATCTCCATTGTATGTGCA |
| 3772 | Table 3A | Hs.276770 | X62466 | 29645 | CDW52 antigen (CAMPATH-1 antigen) (CDW52), mRNA /cds=(24,209) | 1 | CCTGAAACAGCTGCCACCATCACTCG CAAGAGAATCCCCTCCATCTTTGG |
| 3773 | Table 3A | Hs.80684 | X62534 | 32332 | high-mobility group (nonhistone chromosomal) protein 2 (HMG2), mRNA /cds=(190,819) | 1 | TTCTGTGTGTATGGTAGCACAGCAAA CTTGTAGGAATTAGTATCAATAGT |
| 3774 | Table 3A | Hs.172690 | X62535 | 30822 | diacylglycerol kinase, alpha (80kD) (DGKA), mRNA /cds=(103,2310) | 1 | ACACACATACACACACCCCAAAACAC ATACATTGAAAGTGCCTCATCTGA |
| 3775 | Table 3A | Hs.77522 | X62744 | 36062 | major histocompatibility complex, class II, DM alpha (HLA-DMA), mRNA /cds=(45,830) | 1 | GATCTCCTCTAGGGTAGAAGAAGTC TCTGGGACATCCCTGGGGTGTGTG |
| 3776 | Table 3A | Hs.296014 | X63563 | 36121 | polymerase (RNA) II (DNA directed) polypeptide B (140kD) (POLR2B), mRNA /cds=(43,3567) | 1 | GGCTGCCGCAATAAAACCCAGATTTT TTTGGTGCAATGCCTTACGCATG |
| 3777 | Table 3A | Hs.82359 | X63717 | 28741 | tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), mRNA /cds=(220,1227) | 1 | TCATCATCTGGATTAGGAATTGCTC TTGTCATACCCCCAAGTTTCTAAG |
| 3778 | db mining | Hs.2490 | X65019 | 33792 | caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase) (CASP1), mRNA /cds=(0,1151) | 1 | TGCCCCACCACTGAAAGAGTGACTTTG ACAAGATGTTTCTACCTCTTCCCA |
| 3779 | Table 3A | Hs.75248 | X68060 | 37230 | topoisomerase (DNA) II beta (180kD) (TOP2B), mRNA /cds=(0,4865) | 1 | TTTGATCAGGATTCAGATGTGGACAT CTTCCCCTCAGACTTCCCTACTGA |
| 3780 | Table 3A | Hs.652 | X68550 | 37269 | tumor necrosis factor (ligand) superfamily, member 5 (hyper-IgM syndrome) (TNFSF5), mRNA /cds=(39,824) | 1 | TCTACCTGCAGTCTCCATTGTTTCCA GAGTGAACCTGTAATTATCTTGT |
| 3781 | Table 3A | Hs.116774 | X68742 | 33949 | mRNA for integrin, alpha subunit /cds=UNKNOWN | 1 | CGGATTGTTGCTGTTAATGCTGCTCA TTTTAGCACTGTGGAAGATTGGAT |
| 3782 | Table 3A | Hs.77502 | X68836 | 36326 | Homo sapiens, methionine adenosyltransferase II, alpha, clone MGC:4537 IMAGE:3010820, mRNA, complete cds /cds=(116,1303) | 1 | TAGAGATTGTGAAGAAGAAATTCGAT CTCCGCCCTGGGGTCATTGTCAAG |
| 3783 | Table 3A | Hs.192760 | X69392 | 36114 | kinesin family member 5A (KIF5A), mRNA /cds=(148,3246) | 1 | CTCCTGTTGGGTAAGGGTGTGAGTG TGACTTGTGCTGAAAACCTGGTTC |

Table 8

| | | | | | | | |
|------|----------|-----------|-----------|----------|--|---|---|
| 3784 | Table 3A | Hs.83715 | X69804 | 1015499 | Sjogren syndrome antigen B (autoantigen La) (SSB), mRNA /cds=(72,1298) | 1 | AAAAGGAAAAACCGAATTAGGTCCACT TCAATGTCCACCTGTGAGAAAGGA |
| 3785 | Table 3A | Hs.309952 | X69819 | 32627 | mRNA; cDNA DKFZp434E0516 (from clone DKFZp434E0516) /cds=UNKNOWN | 1 | GGAAGAACCGTCCAGAGCTGAGTGA CGCTGGGATCCGGGATCAAAGTTGG |
| 3786 | Table 3A | Hs.170009 | X70340 | 37089 | transforming growth factor, alpha (TGFA), mRNA /cds=(31,513) | 1 | TGTGCATTGTTATTGAGTTGTAAGTGA CCTTATTGGGAAGGATGAAGGAA |
| 3787 | Table 3A | Hs.180610 | X70944 | 38457 | splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-associated) (SFPQ), mRNA /cds=(85,2208) | 1 | CCCATTCTCTGTTTTAAAGACCAAC AAATCTCAAGCCCTATAAATGGC |
| 3788 | Table 3A | Hs.106876 | X71490 | 313011 | Homo sapiens, clone MGC:15351 IMAGE:4126712, mRNA, complete cds /cds=(87,1142) | 1 | AGAAGCATGTCACTTTCATGTTCTCTC CCTAACTCCCTGACCTGAGAACCC |
| 3789 | Table 3A | Hs.251526 | NM_006273 | 13435401 | gene for monocyte chemotactic protein-3 (MCP-3) /cds=(0,329) | 1 | GGATGCTCCTCCCTTCTCTACCTCAT GGGGGTATTGTATAAGTCCTTGCA |
| 3790 | Table 3A | Hs.156110 | X72475 | 441418 | cDNA: FLJ21321 fis, clone COL02335, highly similar to HSA010442 mRNA for immunoglobulin kappa light chain /cds=UNKNOWN | 1 | GCACCATCTGTCTTCATCTTCCGCCA TCTGATGAGCAGTTGAAATCTGGA |
| 3791 | Table 3A | Hs.156110 | X72475 | 441418 | cDNA: FLJ21321 fis, clone COL02335, highly similar to HSA010442 mRNA for immunoglobulin kappa light chain /cds=UNKNOWN | 1 | GCACCATCTGTCTTCATCTTCCGCCA TCTGATGAGCAGTTGAAATCTGGA |
| 3792 | Table 3A | Hs.79081 | X74008 | 402777 | protein phosphatase 1, catalytic subunit, gamma isoform (PPP1CC), mRNA /cds=(154,1125) | 1 | AAAAGAAATCTGTTTCAACAGATGAC CGGTGACAATACCGTGTGGTGAAG |
| 3793 | Table 3A | Hs.331328 | X74262 | 397375 | intermediate filament protein syncoilin (SYNCOILIN), mRNA /cds=(168,623) | 1 | GGCCTGTACTCTCCATGACTAACTG TGTAAGTGCTTAAATGGAATAAA |
| 3794 | Table 3A | Hs.1708 | X74801 | 671526 | chaperonin containing TCP1, subunit 3 (gamma) (CCT3), mRNA /cds=(0,1634) | 1 | GGCAGCCCCAGTCCCTTTCTGTCC CAGCTCAGTTTTCCAAAAGACACTG |
| 3795 | Table 3A | Hs.44313 | X75042 | 402648 | v-rel avian reticuloendotheliosis viral oncogene homolog (REL), mRNA /cds=(177,2036) | 1 | TCTTGATACCACCTATATAGATGCAG CATTTTGTATTTGTCTAACTGGGG |
| 3796 | Table 3A | Hs.73965 | X75755 | 455418 | splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(155,820) | 1 | CGGGCCTTGCATATAAATAACGGAGC ATACAGTGAGCACATCTAGCTGAT |
| 3797 | Table 3A | Hs.74637 | X75861 | 456258 | testis enhanced gene transcript (TEGT), mRNA /cds=(40,753) | 1 | CTGTGCTTTTTGCTTGGGATAATGGA GTTTTCTTTAGAAACAGTGCCAA |
| 3798 | Table 3A | Hs.79362 | X75918 | 415822 | p130 mRNA for 130K protein /cds=(69,3488) | 1 | TTGAGGGGATTAATATGAAACTTAT GACCTCTTCTTTAGAGGGGAGTT |
| 3799 | Table 3A | Hs.79362 | X76061 | 416030 | p130 mRNA for 130K protein /cds=(69,3488) | 1 | TGTTAAACCCCTATAGCCACCTTTT GGGAATGTTTTAAATTTCTCCAGTT |
| 3800 | Table 3A | Hs.83347 | X76302 | 431952 | angio-associated, migratory cell protein (AAMP), mRNA /cds=(0,1358) | 1 | TGGCAGGCGTCAACCCCATTTTATTT GTCCTTATTCCTGTGGAAGCAGTA |
| 3801 | Table 3A | Hs.85226 | X76488 | 434305 | lipase A, lysosomal acid, cholesterol esterase (Wolman disease) (LIPA), mRNA /cds=(40,1239) | 1 | AATACACCTGCTTACGTCCTCATGT TGGGAAGTCCATATTGTCTGCTT |
| 3802 | Table 3A | Hs.334648 | X76770 | 556782 | PAP mRNA /cds=UNKNOWN | 1 | CAGGAAATGCAGCAACTTCAGGAAAT GCAGCAACAAAAATACCTACTCTCT |
| 3803 | Table 3A | Hs.76136 | X77584 | 453963 | thioredoxin (TXN), mRNA /cds=(63,380) | 1 | AAACCCAGTTGCCATCTGCGTGACAA TAAACAGTAATGCTAACACTTTT |
| 3804 | Table 3A | Hs.85155 | X79067 | 483524 | ERF-1 mRNA 3' end /cds=UNKNOWN | 1 | TGCTGTATTACTTCTGAAAAGACTGT GCAGTGTGTTAGTTGTTGGCTGAA |
| 3805 | Table 3A | Hs.153221 | X79201 | 531105 | synovial sarcoma translocation, chromosome 18 (SS18), mRNA /cds=(3,1178) | 1 | GTGTATGAGAGAGAGAGTGTGTGTTT GTGTGTTTCAAGGTCAGAACAGGT |
| 3806 | Table 3A | Hs.179943 | X79234 | 495125 | ribosomal protein L11 (RPL11), mRNA /cds=(0,536) | 1 | TGGTTCAGCAGAGATGATGGGGAT CATCCTTCTCGGCAAAATAATTCC |
| 3807 | Table 3A | Hs.74576 | X79353 | 695584 | GDP dissociation inhibitor 1 (GDI1), mRNA /cds=(80,1423) | 1 | TGTCCTCTTCCCACCTCTAGTGTA TTTCACAGAAAAACAACTCCCA |
| 3808 | Table 3A | Hs.7957 | X79448 | 2326523 | adenosine deaminase, RNA-specific (ADAR), transcript variant ADAR-a, mRNA /cds=(187,3867) | 1 | AGTCCAGTTTATGATTCTGCTTTTAT GTGTCCCTTGATAACAGTGACTT |
| 3809 | Table 3A | Hs.249495 | X79536 | 496897 | heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 2, mRNA /cds=(104,1222) | 1 | AAACTCATCTGTCCAAGTTCGTGGCA GAAAGGAACGTCCTTGTGAAGACC |
| 3810 | Table 3A | Hs.151134 | X80695 | 619490 | oxidase (cytochrome c) assembly 1-like (OXA1L), mRNA /cds=(0,1487) | 1 | AGAGCACTGGGTAGCCAAGTGATCTT CCCATTACAGAGATTAGTAAACCT |
| 3811 | Table 3A | Hs.77897 | X81789 | 551449 | splicing factor 3a, subunit 3, 60kD (SF3A3), mRNA /cds=(8,1513) | 1 | CCCCAGAGACCCCATTTGCCTCTCA ACACTCAGACCTTCAACTGTTTTT |
| 3812 | Table 3A | Hs.318501 | X82200 | 899299 | stimulated trans-acting factor (50 kDa) (STAF50), mRNA /cds=(122,1450) | 1 | CCAGTGACACCCCATATTTCATCACA AATTAAGCAAGAAGTCCATAGTA |
| 3813 | Table 3A | Hs.153961 | X82206 | 563882 | ARP1 (actin-related protein 1, yeast) homolog A (centractin alpha) (ACTR1A), mRNA /cds=(57,1187) | 1 | TGACACCAAGACCCACCCCAATCCAG ACTTCACACAGTATTCTCCGCCAC |

Table 8

| | | | | | | | |
|------|----------|-----------|--------|---------|--|---|---|
| 3814 | Table 3A | Hs.289103 | X83300 | 603028 | SMA4 mRNA /cds=(66,488) | 1 | GACTGCAAGTCACTCTTAGGGGCTGT ACTTCCTTAGTACTGGTAGCATT |
| 3815 | Table 3A | Hs.160483 | X85116 | 1161561 | epb72 gene exon 1 /cds=(61,927) | 1 | AAC TGAGCATCAGCAACCTGTTTGG CAGACTGAGGTCACGATGGAGGGG |
| 3816 | Table 3A | Hs.24143 | X86019 | 2760482 | Wiskott-Aldrich syndrome protein interacting protein (VASPIP), mRNA /cds=(108,1619) | 1 | TCCTCCATTGAAGAAGAATGTCAACA AGAAAGGAAAAATAGACAACTGG |
| 3817 | Table 3A | Hs.75410 | X87949 | 1143491 | mRNA for BiP protein /cds=(222,2183) | 1 | AAGTCTCGAATGTAATTGGAATCTTC ACCTCAGAGTGGAGTTGAACCTGCT |
| 3818 | Table 3A | Hs.2007 | X89102 | 887455 | tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), mRNA /cds=(157,1002) | 1 | CCATCGGTGAAACTAACAGATAAGCA AGAGAGATGTTTTGGGGACTCATT |
| 3819 | Table 3A | Hs.180433 | X89602 | 1150420 | rTS beta protein (HSRTSBETA), mRNA /cds=(17,1267) | 1 | ACAAAAATAGCTATATCAAGGGCTGG CACCTAGACATTAAACTGTACTTT |
| 3820 | Table 3A | Hs.13046 | X91247 | 1237037 | thioredoxin reductase 1 (TXNRD1), mRNA /cds=(439,1932) | 1 | GTCCACCAGTCTCTGAAATTAGAACA GTAGGCGGTATGAGATAATCAGGC |
| 3821 | Table 3A | Hs.335328 | X91348 | 1418768 | predicted non coding cDNA (DGCR5) /cds=UNKNOWN | 1 | GAAATGTAGCTGGAGTCATCATTTAG CAGAGCAGGTGTCCTGGGTTGG |
| 3822 | Table 3A | Hs.2726 | X92518 | 1225979 | mRNA for HMGI-C protein /cds=(848,1177) | 1 | GCCTCTGTGATCCCCATGTGTTTTGA TTCTGTCTTTGTACAGTTCCA |
| 3823 | Table 3A | Hs.78335 | X94232 | 1292867 | microtubule-associated protein, RP/EB family, member 2 (MAPRE2), mRNA /cds=(112,1095) | 1 | AAAACAAGAAACAAATGTGCCACCC CACTTTCGGTTAACTGAAAAGCT |
| 3824 | Table 3A | Hs.75841 | X94910 | 3413292 | chromosome 12 open reading frame 8 (C12orf8), mRNA /cds=(11,796) | 1 | GTA AAAAGGCTGTCTGTGATTTTCCA GGGTTTGGTGGGGGTAGGGAGGGG |
| 3825 | Table 3A | Hs.3416 | X97324 | 1806039 | adipose differentiation-related protein (ADFP), mRNA /cds=(0,1313) | 1 | CTGACTGAGTCTCAGAAATGCTCAGGA CCAAGGTGCAGAGATGGACAAGAG |
| 3826 | Table 3A | Hs.100555 | X98743 | 1498228 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 18 (Myc-regulated) (DDX18), mRNA /cds=(71,2083) | 1 | AGCTTCTTGGGTTCTTAATCTCTGGT GTTTAATAATTCTCTCCACGATCA |
| 3827 | Table 3A | Hs.139262 | X99699 | 1869900 | XIAP associated factor-1 (HSXIAPAF1), mRNA /cds=(0,953) | 1 | TACTTGCTGTGGTGGTCTTGTAAG GTGATGGGTTTTATTCGTTGGGCT |
| 3828 | Table 3A | Hs.170121 | Y00062 | 34275 | protein tyrosine phosphatase, receptor type, C (PTPRC), mRNA /cds=(86,4000) | 1 | ATTTCAGTGAGCTTATCATGTCTGTC TTTACATGGGTTTTCAATTTTGC |
| 3829 | Table 3A | Hs.51077 | Y00093 | 35175 | integrin, alpha X (antigen CD11C (p150), alpha polypeptide) (ITGAX), mRNA /cds=(58,3549) | 1 | TGCAGCTCACACGCCACAGGGGCAG AAGAGACCCAACCACTTCTATTTT |
| 3830 | Table 3A | Hs.169476 | Y00282 | 36048 | Homo sapiens, glyceraldehyde-3- phosphate dehydrogenase, clone MGC:10926 IMAGE:3628129, mRNA, complete cds /cds=(2306,3313) | 1 | ACTTACCCAGATGTTGCTTTTGAAAA GTTGAAATGTGAATGTTTGGGA |
| 3831 | Table 3A | Hs.76473 | Y00285 | 33054 | insulin-like growth factor 2 receptor (IGF2R), mRNA /cds=(147,7622) | 1 | TGTATATAGACTCTGGTGTCTATTG CTGAGAAGCAAACCGCCCTGCAGC |
| 3832 | Table 3A | Hs.172182 | Y00345 | 35569 | poly(A)-binding protein, cytoplasmic 1 (PABPC1), mRNA /cds=(502,2403) | 1 | ATGTCAGTCTGTTTTTAAGTAACAGAA TTGATAACTGAGCAAGGAAACGT |
| 3833 | Table 3A | Hs.180414 | Y00371 | 32466 | hsc70 gene for 71 kd heat shock cognate protein | 1 | TTGGAGCTAAGCTGCCACCTGGTTAA TTAAGGTCCCAACAGTGAGTTGTG |
| 3834 | Table 3A | Hs.233950 | Y00503 | 34038 | serine protease inhibitor, Kunitz type 1 (SPINT1), mRNA /cds=(175,1716) | 1 | CTTTGAGGGTGTCTTCTGGGTAGAG GGATGGGAAGGAAGGGACCCTTAC |
| 3835 | Table 3A | Hs.75716 | Y00630 | 35267 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2 (SERPINB2), mRNA /cds=(72,1319) | 1 | TGCCTTTAATTGTCTCATAATGAAGA ATAAGTAGGTACCCTCCATGCC |
| 3836 | Table 3A | Hs.79368 | Y07909 | 1542882 | epithelial membrane protein 1 (EMP1), mRNA /cds=(218,691) | 1 | ATTTGCATTACTCTGGTGGATTGTCT AGTACTGTATTGGGCTTCTTCGT |
| 3837 | Table 3A | Hs.113503 | Y08890 | 2253155 | Homo sapiens mRNA for Ran_GTP binding protein 5 (RanBP5(Importin5) gene) /cds=(236,3529) | 1 | TTTGGCTTAGTGTTTCATTGCAAAAT ATAATTGCTGTAGAGCCACACAC |
| 3838 | Table 3A | Hs.227817 | Y09397 | 1694788 | BCL2-related protein A1 (BCL2A1), mRNA /cds=(183,710) | 1 | TTGATGATGTAACCTTGACCTTCCAGA GTTATGGAAATTTTGTCCCCATGT |
| 3839 | Table 3A | Hs.43913 | Y09631 | 3925684 | PIBF1 gene product (PIBF1), mRNA /cds=(0,2276) | 1 | AACAAAAGATGAAGACCTAGTGTTTT GGATGGGAAGCACCTGTAGACCAT |
| 3840 | Table 3A | Hs.44499 | Y09703 | 4581462 | pinin, desmosome associated protein (PNN), mRNA /cds=(30,2261) | 1 | ACATGTGC AAAATAATGTGGCTTAGA CTTGTTGACTGCTTAAGACTAAA |
| 3841 | Table 3A | Hs.47007 | Y10256 | 1841433 | mitogen-activated protein kinase kinase kinase 14 (MAP3K14), mRNA /cds=(232,3075) | 1 | TCTGGGTTGTAGAGAACTCTTTGTAA GCAATAAAGTTTGGGGTGATGACA |
| 3842 | Table 3A | Hs.7879 | Y10313 | 2706510 | interferon-related developmental regulator 1 (IFRD1), mRNA /cds=(219,1580) | 1 | CGAACCAAGCTAGAAGCAAATGTGCG AGATAAGAGAGCAGATGTTGGAGA |
| 3843 | Table 3A | Hs.51957 | Y11251 | 1848180 | splicing factor, arginine/serine-rich 2, interacting protein (SFRS2IP), mRNA /cds=(1210,4656) | 1 | CACTCTTCACCTATTGTATGACCAAAT AAAGGTTATGCTGCTTGTTACGC |
| 3844 | Table 3A | Hs.129953 | Y11289 | 2808510 | Ewing sarcoma breakpoint region 1 (EWSR1), transcript variant EWS, mRNA /cds=(43,2013) | 1 | TGCTAGGTGATGGAGTAGAAATGGAT TCCCTCTGGGAATGGTTTCTTGGT |
| 3845 | Table 3A | Hs.106019 | Y13247 | 2117158 | protein phosphatase 1, regulatory subunit 10 (PPP1R10), mRNA /cds=(539,3361) | 1 | TATGAAAACAGTGGATTGGTTGGGTT TTGTGCAAGGCTCTTGGGTTAGAGC |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|--|---|--|
| 3846 | Table 3A | Hs.16530 | Y13710 | 2326515 | small inducible cytokine subfamily A (Cys-Cys), member 18, pulmonary and activation-regulated (SCYA18), mRNA /cds=(70,339) | 1 | TGCATGGATCAATCAGTGTGATTAGC TTTCTCAGCAGACATTGTGCCATA |
| 3847 | Table 3A | Hs.17883 | Y13936 | 2315201 | protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform (PPM1G), mRNA /cds=(24,1664) | 1 | CTCATCACCGGTTCTGTGCCTGTGCT CTGTTGTGTTGGAGGGAAGGACTG |
| 3848 | Table 3A | Hs.195175 | Y14039 | 2653415 | mRNA for CASH alpha protein /cds=(481,1923) | 1 | GCAGCACACTCTGAGAAAGAACTTA TCCTCTCCTACACATAAGAAACCA |
| 3849 | Table 3A | Hs.227913 | Y15906 | 5327056 | API5-like 1 (API5L1), mRNA /cds=(132,1646) | 1 | TGCAAGACACCGTGTATCATCTTGT TAAATGTAATGTCCCTTATGC |
| 3850 | Table 3A | Hs.85951 | Y16414 | 2924334 | exportin, tRNA (nuclear export receptor for tRNAs) (XPOT), mRNA /cds=(0,2888) | 1 | TCAACGCCAATATGTATTCTACAAA GAGAATGGTTTTAGGCTCCAGTGT |
| 3851 | Table 3A | Hs.271387 | Y16645 | 2916795 | mRNA for monocyte chemotactic protein-2 /cds=(472,771) | 1 | TGGATCATCAAGGTGAAACACTTTGG TATTCTTTGGCAATCAGTGCCTCT |
| 3852 | Table 3A | Hs.337737 | Y17829 | 4128042 | Homer, neuronal immediate early gene, 1B (SYN47), mRNA /cds=(75,1139) | 1 | GATACACTGTCTCTCTCATAGGACT GTTTAGGCTCTGCATCAAGATTGC |
| 3853 | Table 3A | Hs.247792 | Z00013 | 33149 | germline gene for the leader peptide and variable region of a kappa immunoglobulin (subgroup V kappa I) | 1 | AAGGCAGGGATCATGACACCTGAGG AGTCTAGTTTATGGCTTCAGTTGGA |
| 3854 | Table 3A | Hs.173936 | Z17227 | 393378 | mRNA for transmembrane receptor protein /cds=(43,1020) | 1 | ATGGATGGACTGATCTGAAAATCGAC CTCAACTCAAGGTTGGTACGCTCA |
| 3855 | Table 3A | Hs.211577 | Z22551 | 296163 | kinesin 1 (kinesin receptor) (KTN1), mRNA /cds=(83,3985) | 1 | TGCTAATGTAATCGGTTTTGTAAATG GCGTCACAAATAAAGGATGCTTA |
| 3856 | Table 3A | Hs.82401 | Z22576 | 397938 | CD69 antigen (p60, early T-cell activation antigen) (CD69), mRNA /cds=(81,680) | 1 | TGCAAGACATAGAATAGTGTGGAAA ATGTGCAATATGTGATGTGGCAAA |
| 3857 | Table 3A | Hs.74076 | Z22970 | 312145 | mRNA for M130 antigen cytoplasmic variant 2 /cds=(101,3571) | 1 | AAGTTTGTGATGTGACTACTTAGTG GTGATATGAGACTTTCAAGGGA |
| 3858 | Table 3A | Hs.146381 | Z23064 | 3256006 | RNA binding motif protein, X chromosome (RBMX), mRNA /cds=(11,1186) | 1 | CCATTTTGCCTTTCTGACATTTCCTTG GGAATCTGCAAGAACCTCCCTT |
| 3859 | Table 3A | Hs.225160 | Z23090 | 433597 | hypothetical protein FLJ13102 (FLJ13102), mRNA /cds=(80,1084) | 1 | CTGTGCCTCCCCGCCACCTGTGTG TTCTTTTGATACATTATCTTCTGT |
| 3860 | Table 3A | Hs.4934 | Z24724 | 505034 | polyA site DNA /cds=UNKNOWN | 1 | TGTATATTTATGGTGGGAGGTGGTTG GGAACCTTTAAACAAATGGGGTGT |
| 3861 | Table 3A | Hs.2236 | Z29067 | 479172 | nek3 mRNA for protein kinase /cds=(0,1379) | 1 | TCCTTTGGAAACAGAAATGAAGCAGAG GAAACTCTTAATACTTAAATCGT |
| 3862 | Table 3A | Hs.109918 | Z35227 | 609016 | ras homolog gene family, member H (ARHH), mRNA /cds=(579,1154) | 1 | TTGCCAGGCCAGTTAGAAAATCCCT TGGGGAACCTGTGATGAATATCCCA |
| 3863 | Table 3A | Hs.198427 | Z46376 | 587201 | hexokinase 2 (HK2), mRNA /cds=(1490,4243) | 1 | CTAGTCATAGAAATACCTCATTCCGCC TGTGGGAAGAGAAAGGGAAGCCTCT |
| 3864 | Table 3A | Hs.171626 | Z47087 | 860989 | transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L), mRNA /cds=(101,592) | 1 | ATGTGGTAAACCCAGAAAGCATCCA TCATGAATGCAAGATCTTTCAAT |
| 3865 | Table 3A | Hs.180877 | Z48950 | 761715 | clone PP781 unknown mRNA /cds=(113,523) | 1 | TGCTTGATTAAGATGCCAATAGTG CTGTATTGCAAGTGTGGCTAAGA |
| 3866 | Table 3A | Hs.83465 | Z49995 | 895841 | homeo box D1 (HOXD1), mRNA /cds=(223,1209) | 1 | TCTTCTGTTTCATCTGCGGTTCTGG AACCAGATTTTGACTTGCCTGTCA |
| 3867 | Table 3A | Hs.78683 | Z72499 | 1545951 | ubiquitin specific protease 7 (herpes virus-associated) (USP7), mRNA /cds=(199,3507) | 1 | CCTTCAGTTATCTTTCAATGACCTTT TGTGCATCTGTGAAGGCAAAACA |
| 3868 | Table 3A | Hs.51077 | M81695 | 487829 | integrin, alpha X (antigen CD11C (p150), alpha polypeptide) (ITGAX), mRNA /cds=(58,3549) | 1 | ATGCATCTACCGCTCCTTGGGAAATA ATCTGAAAGGTCTAAAAATAAAAA |
| 3869 | Table 3A | Hs.113029 | BF025727 | 10733439 | ribosomal protein S25 (RPS25), mRNA /cds=(63,440) | 1 | CGCAAGAAGCAGGAAGAGGAAAGAG AAGAAAAGCACACCGGGGAAAGATA |
| 3870 | Table 3A | Hs.150675 | BF028489 | 10736201 | polymerase (RNA) II (DNA directed) polypeptide K (7.0kD) (POLR2K), mRNA /cds=(66,242) | 1 | GTAGTGTGTTGCATCCCTCTCACCT CTGATCTTCGTGAGTCGTGTCATG |
| 3871 | Table 3A | Hs.74170 | BF028896 | 10736608 | 602708243F1 cDNA, 5' end /clone=IMAGE:4844914 /clone_end=5' | 1 | GAGGGAAACCCGGTAATAGGCTGGG AGTAATCCACACACGTGCTAACATT |
| 3872 | Table 3A | Hs.199061 | BF029654 | 10737366 | p300/CBP-associated factor (PCAF), mRNA /cds=(458,2956) | 1 | CACACACTGCTACGTGACGTACCACT ACTGCCAGCGCAGCACTAGCTCAC |
| 3873 | Table 3A | Hs.13268 | BF029796 | 10737508 | 602634117F1 cDNA, 5' end /clone=IMAGE:4779149 /clone_end=5' | 1 | GGATCGTGACACACCGGGTTACACA CTTCCACACCGTAATTCATCAAT |
| 3874 | Table 3A | Hs.149595 | BF029894 | 10737606 | 601557056F1 cDNA, 5' end /clone=IMAGE:3827172 /clone_end=5' | 1 | GGTTGCACCAAGGCTGCCTAGGAGA AGTGCCTGACTGGACTACCCCGATC |
| 3875 | Table 3A | Hs.118303 | BF030930 | 10738642 | 601558648F1 cDNA, 5' end /clone=IMAGE:3828706 /clone_end=5' | 1 | TCTGCCATCTGTCTATTTCCCAATTTT CCTTCTGACTGTTCTTTCTCTCT |
| 3876 | Table 3A | Hs.337986 | BF033741 | 10741453 | Homo sapiens, clone MGC:17431 IMAGE:2984883, mRNA, complete cds /cds=(1336,1494) | 1 | CTGTGATATTTTGGTCATGGGCTGGT CTGGTCGGTTTCCCAATTGTCTGG |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|---|---|---|
| 3877 | Table 3A | Hs.144559 | BF036686 | 10744746 | 601459771F1 cDNA, 5' end /clone=IMAGE:3863248 /clone_end=5' | 1 | TACGACATTTGCGAAATTCGCTAAAA ACAAGGGGGAGTTCACGCGGCCAT |
| 3878 | Table 3A | Hs.39457 | BF103848 | 10886287 | 602537152F1 cDNA, 5' end /clone=IMAGE:4656037 /clone_end=5' | 1 | GCGCAGGTTACCGGAACCCAAGGTC CTTTGAAATTCACAACTCTCTTTGG |
| 3879 | Table 3A | Hs.279009 | BF105172 | 10887698 | matrix Gla protein (MGP), mRNA /cds=(46,357) | 1 | AGCTGTGGAAGGGCAACCTGTGGT TTCTCTGTACTGGTGTTTAATGGGG |
| 3880 | Table 3A | Hs.95388 | BF107010 | 10889635 | 602619064F1 cDNA, 5' end /clone=IMAGE:4733030 /clone_end=5' | 1 | CACAAACACCCGCCGAGCAACCAC AGACACAGGACACGACACCACACAC |
| 3881 | Table 3A | Hs.171595 | BF130300 | 10969340 | HIV TAT specific factor 1 (HTATSF1), mRNA /cds=(57,2321) | 1 | AAAGGGTTACTTTTCAAACAGTCTC CTTTCGACCGGGGTCAGGGTGGCC |
| 3882 | Table 3A | Hs.129872 | BF131060 | 10970089 | sperm associated antigen 9 (SPAG9), mRNA /cds=(110,2410) | 1 | GGTGGACAGTATAAGGCGGTAAAGT CCGTTGATGGCGAAGGTGAGAATG |
| 3883 | Table 3A | Hs.75428 | BF131654 | 10970694 | superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult)) (SOD1), mRNA /cds=(0,464) | 1 | GACAGAGCGAGTAGACGGGAGGCGG AGAAGGAAGAGGAGACGAGACGAGG |
| 3884 | Table 3A | Hs.9614 | BF131656 | 10970696 | nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), mRNA /cds=(0,884) | 1 | CAAGACACAGAGGCAACGGAGAGAC ACGCAGACAAGCAAGGCCACGGAAC |
| 3885 | Table 3A | NA | BF184881 | 11063302 | ESTs | 1 | AGGGATAGGATAATTACAGAGGTACT GAGACTCTGGCGTGGGTGACTCT |
| 3886 | Table 3A | Hs.160954 | BF207290 | 11100876 | 602759615F1 cDNA, 5' end /clone=IMAGE:4895042 /clone_end=5' | 1 | CCCATCATGAAAAACGCCTTAGGAG CCGAAGAAGAAAACCTCGGGAAAA |
| 3887 | Table 3A | Hs.76064 | BF214146 | 11107732 | ribosomal protein L27a (RPL27A), mRNA /cds=(22,468) | 1 | GACACAGCGAGAGTCCAGGAACAGG CAGACAAGCGAGAAAGAGGAGAAGC |
| 3888 | Table 3A | Hs.169248 | BF214508 | 11108094 | 601845758F1 cDNA, 5' end /clone=IMAGE:4076510 /clone_end=5' | 1 | GTAGGAGGCGAGAAGGAAGAACAAAG GCACACCGAAGGAGCAAGACCAGAC |
| 3889 | Table 3A | Hs.75968 | BF217687 | 11111273 | thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(77,211) | 1 | CAAGAAGCAGAAGCAGCAACCAGAG ACAGAGAGACAAACGCAGAACACA |
| 3890 | Table 3A | Hs.111611 | BF219474 | 11113299 | ribosomal protein L27 (RPL27), mRNA /cds=(17,427) | 1 | CAACAAGCAGACGAACAACAACAAAT ATCAACGAGGCGCAGCAGCTCAA |
| 3891 | Table 3A | Hs.112318 | BF237710 | 11151628 | cDNA FLJ14633 fis, clone NT2RP2000938 /cds=UNKNOWN | 1 | AACACACAAGAGAAACATAACCACTA AATCACTACAACACACACAGAAAT |
| 3892 | Table 3A | Hs.182937 | BF242969 | 11156897 | peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA /cds=(44,541) | 1 | AAACGAATCTTCTGCACCTGAGAGTGT CACAGCGCCACTTCTCTCTCTCTC |
| 3893 | Table 3A | Hs.171774 | BF243010 | 11156938 | hypothetical protein (HSPC016), mRNA /cds=(38,232) | 1 | CGAGAAGCAGAAGATGACAGCAGAG CGAAAGCAGAGAACGAACAGACAAG |
| 3894 | Table 3A | Hs.296251 | BF243724 | 11157654 | programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), mRNA /cds=(84,1493) | 1 | TTGGATTATTAAAGTCCCTTTGGAA GTCTTCTACCATTACTGTAGACCA |
| 3895 | Table 3A | Hs.109697 | BF244603 | 11158534 | 601862620F1 cDNA, 5' end /clone=IMAGE:4080412 /clone_end=5' | 1 | TCACATACCCTATGCCGACTGAGTGG AACGAGCCGACTATCACACAGAGC |
| 3896 | Table 3A | Hs.294110 | BF245076 | 11159008 | 601863910F1 cDNA, 5' end /clone=IMAGE:4082235 /clone_end=5' | 1 | CACATGCGCAATAAACCCGGCGAAG ACGCCACTCTGCGGCAAGGACACA |
| 3897 | Table 3A | Hs.182825 | BF245224 | 11159156 | ribosomal protein L35 (RPL35), mRNA /cds=(27,398) | 1 | CCGCAGACACGAAAGCACCAACCAC CGACCGCCACCAGAAGGAACAACAG |
| 3898 | Table 3A | Hs.199248 | BF245892 | 11159734 | prostaglandin E receptor 4 (subtype EP4) (PTGER4), mRNA /cds=(388,1854) | 1 | GGGCACTTAAATGGTCACCTGTGTAA CAGTTTGGTGTAACCTCCAGTAT |
| 3899 | Table 3A | Hs.108124 | BF303895 | 11250572 | cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN | 1 | ACAACACGAAAAACGAACGAAGA AAGAAAACGGACACGAGCGAACCA |
| 3900 | Table 3A | Hs.296251 | BF303931 | 11250608 | programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), mRNA /cds=(84,1493) | 1 | TTGGATTATTAAAGTCCCTTTGGAA GTCTTCTACCATTACTGTAGACCA |
| 3901 | Table 3A | NA | BF306204 | 11253289 | cDNA clone IMAGE:4138980 5' | 1 | CAGCCATGTCCATGACAACCAGAGC CTGGGAGGAGCTGGATGGCGGCTG |
| 3902 | Table 3A | Hs.5174 | BF307213 | 11254322 | ribosomal protein S17 (RPS17), mRNA /cds=(25,432) | 1 | AAACACACAGCAAGAACCACGAAAAG AGCAACCCAAATAGGAAAAGCGG |
| 3903 | Table 3A | Hs.84883 | BF307871 | 11255039 | mRNA for KIA0864 protein, partial cds /cds=(0,3656) | 1 | ACAGCGTGGATATAAGGACCAAGAG ACTAGGGCGCATACTATGATTCCGA |
| 3904 | Table 3A | Hs.63908 | BF309911 | 11257388 | hypothetical protein MGC14726 (MGC14726), mRNA /cds=(21,653) | 1 | ATGGACACGAGGACGGAACCTGGGG TACTAGAACACCCCTTCTCTGAAAA |
| 3905 | Table 3A | Hs.292457 | BF310166 | 11257703 | Homo sapiens, clone MGC:16362 IMAGE:3927795, mRNA, complete cds /cds=(498,635) | 1 | AGACCAAACGAGAAGGAGAAAAAGC AAGACCACAAAAGACAACAACAGCG |
| 3906 | Table 3A | NA | BF313856 | 11261925 | 601902261F1 5' end /clone=IMAGE:4134998 | 1 | AAAAAATCGGGCTTTTCTGGGGGAA AGGGAAGGGCGGGGAATGCTGGCC |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|---|---|---|
| 3907 | Table 3A | NA | BF315059 | 11263244 | 601899090F1 5' end /clone=IMAGE:4128334 | 1 | CTACAACAATACAGCACACAGCATAA GCGCACAGGGCATAGACTAGGCAA |
| 3908 | Table 3A | Hs.99858 | BF315159 | 11263380 | ribosomal protein L7a (RPL7A), mRNA /cds=(31,831) | 1 | CAAGAGAGTGGAGACGAGTACGCGA GAACGCACGACACAGAGCGCAAGAA |
| 3909 | Table 3A | Hs.268177 | BF339088 | 11285508 | phospholipase C, gamma 1 (formerly subtype 148) (PLCG1), mRNA /cds=(76,3948) | 1 | TCTGCTGCCCTCTTAAGATCTGACTG CCAAATAAATCATCCTCATGTCCT |
| 3910 | Table 3A | Hs.296317 | BF340402 | 11286776 | mRNA for KIAA1789 protein, partial cds /cds=(3466,4899) | 1 | GATGAGAAACAACCACAAGGAAGAG GGCAGCGCCGGAGACCTACAGAAAG |
| 3911 | Table 3A | Hs.116567 | BF341330 | 11287821 | 602013274F1 cDNA, 5' end /clone=IMAGE:4149066 /clone_end=5' | 1 | GCGGGGGCACTGGCTCTTCACATTT GGTTGCGAGTTGCACACACCACAAC |
| 3912 | Table 3A | Hs.2554 | BF341359 | 11287850 | sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) (SIAT1), mRNA /cds=(310,1530) | 1 | GGGGGAAGCGGAAGGGTTGGATTGG GTGAAAAAGAATTGTTCGTGTTTA |
| 3913 | Table 3A | Hs.28788 | BF341640 | 11288136 | 602016073F1 cDNA, 5' end /clone=IMAGE:4151706 /clone_end=5' | 1 | ATAATAGAGGAGAGATATTGTAAATA GAGACTGGCAGCAGTTTCCACAAA |
| 3914 | Table 3A | Hs.33905 | BF342246 | 11289148 | 602041247F1 cDNA, 5' end /clone=IMAGE:4179250 /clone_end=5' | 1 | AGTGGCAGGTGCAATTGTGCGTTCCG ATTTGTGTTCCCAACAGTCTGAAAT |
| 3915 | Table 3A | Hs.127863 | BF342439 | 11289452 | 601898969F1 cDNA, 5' end /clone=IMAGE:4128112 /clone_end=5' | 1 | GAGCCACGCGGAAGGGAACCCAGC AACACGGAAATAAGTTGGACCGATC |
| 3916 | Table 3A | Hs.205442 | BF377518 | 11339543 | 601439689F1 cDNA, 5' end /clone=IMAGE:3924407 /clone_end=5' | 1 | ACAACCTGAGAAATAATTCCGTCAAT ACCAGACTCCAACATTCCTGATCT |
| 3917 | Table 3A | Hs.319825 | BF380732 | 11369857 | 602021477F1 cDNA, 5' end /clone=IMAGE:4156915 /clone_end=5' | 1 | GTCTATTACAAAGTAAAGAGAGTCAA TTACTCCAGGAGGAGAATTGCAGG |
| 3918 | Table 3A | Hs.5174 | BF381953 | 11363256 | ribosomal protein S17 (RPS17), mRNA /cds=(25,432) | 1 | ACCAGACACGGACACACACGAACAC AAGAAAACACAAACAAGAGCAACC |
| 3919 | Table 3A | Hs.112237 | BF525720 | 11613081 | 602321076F1 cDNA, 5' end /clone=IMAGE:4424130 /clone_end=5' | 1 | CGGTTGGGTCTCAAAATATGCCTGT TTGGTTAACAAAAGCGGTTGTGAA |
| 3920 | Table 3A | Hs.136537 | BF526066 | 11613527 | 602071176F1 cDNA, 5' end /clone=IMAGE:4214059 /clone_end=5' | 1 | GATAAAGAAGGGGCGCGGGAACAG CGAGGGAAGGACGGGCTGGGAGAAC |
| 3921 | Table 3A | Hs.274472 | BF526421 | 11613784 | high-mobility group (nonhistone chromosomal) protein 1 (HMG1), mRNA /cds=(52,699) | 1 | ATCTCTGGCAACTACTGTCTGATTACG GGGGTGATGCCGACGGTTAAAAAC |
| 3922 | Table 3A | Hs.334825 | BF530382 | 11617745 | cDNA FLJ14752 fis, clone NT2RP3003071 /cds=(205,1446) | 1 | GAACACAAAAACCTCTTCTATAACG GGGACACACGCCAAGGGGACAAAGT |
| 3923 | Table 3A | Hs.255390 | BF531016 | 11618379 | 602072345F1 cDNA, 5' end /clone=IMAGE:4215251 /clone_end=5' | 1 | TTGGGTGCAACAACCAATACACTTAT ACTTGGAAACCACGGGCCATATTA |
| 3924 | Table 3A | Hs.146428 | BF569545 | 11642925 | pro-alpha-1 (V) collagen mRNA, complete cds /cds=(229,5745) | 1 | AGGAGGAACAAAAACCGCAGCGTGG ATTTCAAATTTCTGGAAGTAAGTCT |
| 3925 | Table 3A | Hs.22265 | BF571362 | 11645074 | pyruvate dehydrogenase phosphatase (PDP), mRNA /cds=(131,1855) | 1 | AAATTCGCGCACCCCTTTGTTTTATTG CCCCGGTTACAAGTTTGAACATG |
| 3926 | Table 3A | Hs.301183 | BF572855 | 11646567 | molecule possessing ankyrin repeats induced by lipopolysaccharide (MAIL), homolog of mouse (MAIL), mRNA /cds=(48,2204) | 1 | CGGGCCAGTATGAATGTAGGGTCAA GGAACGCCGAGGGTTTACAAAAGG |
| 3927 | Table 3A | Hs.79530 | BF663116 | 11937011 | M5-14 protein (LOC51300), mRNA /cds=(186,1043) | 1 | CTCAGTGTAGGGCAGAGAGGTCTAA CACCAACATAAGGTACTAGCAGTGT |
| 3928 | Table 3A | Hs.11356 | BF665055 | 11938950 | 602119656F1 cDNA, 5' end /clone=IMAGE:4276860 /clone_end=5' | 1 | AGAATATATGTAATTTTGAAGGAAAG GACTTGGGGATTTTACAGGGCA |
| 3929 | Table 3A | Hs.3585 | BF666961 | 11940856 | 602121608F1 cDNA, 5' end /clone=IMAGE:4278768 /clone_end=5' | 1 | GAGACTCTCGTTGTCTCCTCTTCTGC TCTCTTCTCTGTTGGAGGGGAGGA |
| 3930 | Table 3A | Hs.46677 | BF667621 | 11941516 | PRO2000 protein (PRO2000), mRNA /cds=(650,1738) | 1 | AGGTTGTGGGGAGTATGTTTGACCA AAAAATTTAAATTTGTTGGGAGGGA |
| 3931 | Table 3A | Hs.343615 | BF668050 | 11941945 | 602621493F1 cDNA, 5' end /clone=IMAGE:4755166 /clone_end=5' | 1 | GACCTTACCTGGTGGTTTTGTGTTTT GTTCTCCCGAAAAATGCGGGGTTT |
| 3932 | Table 3A | Hs.12035 | BF668230 | 11942125 | 602122419F1 cDNA, 5' end /clone=IMAGE:4279300 /clone_end=5' | 1 | CACCCTGGGTTTTAAAGTGTGGGAGA AAAGCGCCCGGAAGAAGGAAACAA |
| 3933 | Table 3A | Hs.324342 | BF668584 | 11942479 | 602123634F1 cDNA, 5' end /clone=IMAGE:4280408 /clone_end=5' | 1 | GAGGGGACCGGCCATCTGGGCAAGC AGATATGCTAATTGGGAATTATAGG |
| 3934 | Table 3A | Hs.285729 | BF670567 | 11944559 | 602013364F1 cDNA, 5' end /clone=IMAGE:4149351 /clone_end=5' | 1 | ATGACTTGTGAATACCTGAGTTATAC TTCCCAACAGATGTGCCTAACAC |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|--|---|---|
| 3935 | Table 3A | Hs.27590 | BF671020 | 11944915 | histone acetyltransferase (MORF), mRNA /cds=(315,6536) | 1 | TGATAGCTCACTTAGTTAATTGTTTTG AAGCAAATTTTGGGTGGATGGG |
| 3936 | Table 3A | Hs.99858 | BF673951 | 11947846 | ribosomal protein L7a (RPL7A), mRNA /cds=(31,831) | 1 | GACACAGAAGAGAGACAGAAGAGAA ACGGTCGAGGAGAAGAAGCAGGAGC |
| 3937 | Table 3A | Hs.96566 | BF673956 | 11947851 | 602137338F1 cDNA, 5' end /clone=IMAGE:4274048 /clone_end=5' | 1 | AAAGACCAGAGACAGGGAGACACGG CAGACAGAGCGCCGACAAAGAAGAG |
| 3938 | Table 3A | Hs.181357 | BF676042 | 11949937 | laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA /cds=(85,972) | 1 | CAAGCGCAGATGGGAGAGCGAGAAG GCTAGGAGGACGACAGACAAGGAAA |
| 3939 | Table 3A | Hs.122406 | BF677944 | 11951839 | 602084766F1 cDNA, 5' end /clone=IMAGE:4248905 /clone_end=5' | 1 | GAATTTTGGGGAGGTTACTGGTCGG GGGAAATAACAGGGTTGGACAAACG |
| 3940 | Table 3A | Hs.131887 | BF678298 | 11952193 | 602415255F1 cDNA, 5' end /clone=IMAGE:4523725 /clone_end=5' | 1 | CTCCACATATGGGTAACACACTCGGT CCTTACAAGCACCTAGTCACCTCC |
| 3941 | Table 3A | Hs.205319 | BF679831 | 11953640 | 602154415F1 cDNA, 5' end /clone=IMAGE:4295595 /clone_end=5' | 1 | GGGACCAGACTGCTTTCTAAATGCAC AGCTCTTTCATATCAGAATGTGT |
| 3942 | Table 3A | Hs.34549 | BF680988 | 11954883 | 602620663F1 cDNA, 5' end /clone=IMAGE:4746422 /clone_end=5' | 1 | TGTGGTCACTTGGGAAATAAATTCCA TCTGGCTTACCCAATGGGTGGTGG |
| 3943 | Table 3A | Hs.10702 | BF684382 | 11969790 | hypothetical protein DKFZp761H221 (DKFZp761H221), mRNA /cds=(776,1714) | 1 | CCACAGCCACAACACCAGACAAGCC GACCAACAGACAGATACAGACCACC |
| 3944 | Table 3A | Hs.164675 | BF689700 | 11975108 | 602186609F1 cDNA, 5' end /clone=IMAGE:4298402 /clone_end=5' | 1 | ACCACAGCAAGACAACAAGGACGAG AAAGAGAACAGACAATGAGCAACGA |
| 3945 | Table 3A | Hs.71331 | BF691178 | 11976586 | hypothetical protein MGC5350 (MGC5350), mRNA /cds=(189,995) | 1 | ACTACTGCTTGCGTACCTCTCCGCTT TCCCTCTCCTTACTATCGACCATA |
| 3946 | Table 3A | Hs.173965 | BF691895 | 11977303 | ribosomal protein S6 kinase, 90kD, polypeptide 3 (RPS6KA3), mRNA /cds=(0,2222) | 1 | TCCGTTTATATTAGCACTGTATCCCTT GTGCCATCCAACATTTTGTATGT |
| 3947 | Table 3A | Hs.233936 | BF694761 | 11980263 | myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB), mRNA /cds=(114,629) | 1 | CGGGCGCAGGACAGTAGCAGAGAAG AGAGGTGGAGAGCCGACAACGCAG |
| 3948 | Table 3A | Hs.318782 | BF696330 | 11981738 | 602808469F1 cDNA, 5' end /clone=IMAGE:4940633 /clone_end=5' | 1 | CTTCAGTCATTATGGGCTCAGTTTCC TCACTATTGGTTCCTCGCAAGGGA |
| 3949 | Table 3A | Hs.103180 | BF698884 | 11984292 | 602126455F1 cDNA, 5' end /clone=IMAGE:4283340 /clone_end=5' | 1 | AAGAGCAACAACGAGGCGAAGAGGA AGGAGGAGGCAAGACAGAAGAGGAA |
| 3950 | Table 3A | Hs.252723 | BF698920 | 11984328 | ribosomal protein L19 (RPL19), mRNA /cds=(28,618) | 1 | GAGGAGCAACGACCAGAGAGACGAA CTGACATCAACCATAGAAGACGACA |
| 3951 | Table 3A | Hs.323662 | BF700502 | 11985910 | hypothetical protein MGC14595 (MGC14595), mRNA /cds=(101,850) | 1 | AAGCATGAAGAAGACCTGGATGAGG CTCAGGGAGGTTCCCCAGTTTAAA |
| 3952 | Table 3A | Hs.253550 | BF750565 | 12077241 | RC1-BN0410-261000-014-f11 cDNA | 1 | ATCAGTCAATCAGTCAGCTTCTCAGA GTAGCAATCCATGTGTCCAGAGGA |
| 3953 | Table 3A | Hs.10957 | BF793378 | 12098432 | 602254823F1 cDNA, 5' end /clone=IMAGE:4347076 /clone_end=5' | 1 | AAATCCAATCCTTCGGAGAGGGGAATG GGCGGTATTAATTAAGGGAAGTCC |
| 3954 | Table 3A | Hs.293658 | BF794089 | 12099143 | 602255649F1 cDNA, 5' end /clone=IMAGE:4338732 /clone_end=5' | 1 | ATGACAAGACAAGCCAGACGAAGAA GACAAACAAGGGAGACACAGCAGAC |
| 3955 | Table 3A | Hs.206761 | BF794256 | 12099310 | 602255454F1 cDNA, 5' end /clone=IMAGE:4338949 /clone_end=5' | 1 | TGCGCCCCAATATTTGTGGAACAGCG TTTTGTTGGAATAAACGATCGGT |
| 3956 | Table 3A | Hs.246818 | BF796642 | 12101696 | 602259846F1 cDNA, 5' end /clone=IMAGE:4343171 /clone_end=5' | 1 | CTCGAGGTGTAACCTCAGGAAGGCCT AGCGAATCCCGACTCGGATGGTGTC |
| 3957 | Table 3A | Hs.54452 | BF797348 | 12102402 | zinc finger protein, subfamily 1A, 1 (Ikaros) (ZNFN1A1), mRNA /cds=(168,1727) | 1 | TTCACCTACTCTGTTCTTTTCATCCAT CCCCTGAGTCAGTTGGTTGGAGG |
| 3958 | Table 3A | NA | BF821451 | 12160669 | RT0038 cDNA | 1 | CTGTTGTCTGGAGTGTGGAGTCTCTT GTCTGGATTGTGGAGTCTCTTGTCT |
| 3959 | Table 3A | NA | BF889206 | 12280465 | RC6-TN0073-041200-013-H02 cDNA /gb=BF889206 | 1 | CAAGATGATGCTTGCTGTCTTTTCTCT CTCGGCTACCCAGAATGGCATTG |
| 3960 | Table 3A | Hs.38664 | BF892532 | 12283991 | IL0-MT0152-061100-501-e04 cDNA | 1 | AGTACTCATGACTTGAGAGACGTGGA CGGAGCCAGCTTCTACCTTGCTTG |
| 3961 | Table 3A | Hs.337534 | BF965068 | 12332283 | 602268833F1 cDNA, 5' end /clone=IMAGE:4356776 /clone_end=5' | 1 | GGTCCGACCAATTAATGACTCCATGA TCGGCCTCGGTTTTACAAACCTT |
| 3962 | Table 3A | Hs.334691 | BF965438 | 12332653 | hypothetical protein FLJ22427 (FLJ22427), mRNA /cds=(40,2631) | 1 | AGACAAAGAGAGCATAAATATAGCTC TACTCATGGGTACCATACCAGTGT |
| 3963 | Table 3A | Hs.133864 | BF965766 | 12332981 | 602276890F1 cDNA, 5' end /clone=IMAGE:4364495 /clone_end=5' | 1 | TTACATTTGTGGACCATGTTACAGTTA AAGAAAAATCCTGTTTCAGTCTCT |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|--|---|--|
| 3964 | Table 3A | Hs.279681 | BF965960 | 12333175 | heterogeneous nuclear ribonucleoprotein H3 (2H9) (HNRPH3), transcript variant 2H9, mRNA /cds=(118,1158) | 1 | GCAGGTTATCGCAAGATGTCTTAGAG TAGGGTTAAGGTTCTCAGTGACAC |
| 3965 | Table 3A | Hs.5324 | BF966028 | 12333243 | hypothetical protein (CL25022), mRNA /cds=(157,1047) | 1 | ATTTTAAATGGCTTTACCAAACATTG TCAGTACCTTTACGTGTTAGAAG |
| 3966 | Table 3A | Hs.179902 | BF966049 | 12333264 | transporter-like protein (CTL1), mRNA /cds=(0,1964) | 1 | CTTTCCACAGCAATTGTTTTGTACGA GGGGCCTTACAGCGCGGTCCACTT |
| 3967 | Table 3A | Hs.48320 | BF966269 | 12333484 | mRNA for ring-IBR-ring domain containing protein Dorfin, complete cds /cds=(317,2833) | 1 | TTCTACAGCACGATGCCTGGATCTAC TGACCTGTCAACCACGAATCTTGA |
| 3968 | Table 3A | Hs.171802 | BF966361 | 12333576 | RST31551 cDNA | 1 | GAAACAGCAACAAGCAAACAGGATCT CAGCATTACCAACAGCCAGCAGCTA |
| 3969 | Table 3A | Hs.22790 | BF968270 | 12335485 | 602269653F1 cDNA, 5' end /clone=IMAGE:4357740 /clone_end=5' | 1 | TGAGCCTGAACCTTTTTCAGCAATAT TATTCTCAGTTTCCATTACCTGT |
| 3970 | Table 3A | NA | BF968628 | 12335843 | cDNA clone IMAGE:4359351 5' | 1 | CCTTCCAAAGCGGTACCTGATAGG GAAGTCTTACGGCTAGGAAGTTACA |
| 3971 | Table 3A | Hs.5064 | BF968963 | 12336178 | 602490910F1 cDNA, 5' end /clone=IMAGE:4619835 /clone_end=5' | 1 | GAATGGTGGGGAGAAAAAGGGGGG CACAGTCATGATCGGCTCTTATAAT |
| 3972 | Table 3A | Hs.24143 | BF969990 | 12337205 | Wiskott-Aldrich syndrome protein interacting protein (WASPIP), mRNA /cds=(108,1619) | 1 | GTCACATAATCCGGGGACCCAAAGAA AGTTCTCCAGAGTGGTTTCACGAG |
| 3973 | Table 3A | Hs.23703 | BF970427 | 12337642 | 602272760F1 cDNA, 5' end /clone=IMAGE:4360767 /clone_end=5' | 1 | ACAACAACACATCACGTAACCACAAC ACGCATAAACAGCAAATCATCCTA |
| 3974 | Table 3A | Hs.102647 | BF970875 | 12338090 | 602271536F1 cDNA, 5' end /clone=IMAGE:4359609 /clone_end=5' | 1 | CAGAACACCAACAAGCAGGGACGGA AGCCGACCGAGCAAAACAGCGAAGGG |
| 3975 | Table 3A | Hs.321477 | BF970928 | 12338143 | 602270204F1 cDNA, 5' end /clone=IMAGE:4358425 /clone_end=5' | 1 | GTGGACGGCCTGGGAATGTGCCCCC CGGTGTAACATCGAGCCCAATAGG |
| 3976 | Table 3A | Hs.79101 | BF971075 | 12338290 | cyclin G1 (CCNG1), mRNA /cds=(187,1074) | 1 | AGGATTAGGAGAGGGTACAGAACA GAAAGCAGATTACACTTGGGATGGA |
| 3977 | Table 3A | Hs.33026 | BF971984 | 12339199 | mRNA for FLJ00037 protein, partial cds /cds=(3484,3921) | 1 | CTCTGTTTGTCTGGCCGCTCCGTGA TCAAACCGTGTCTGTCGGCGTGTTC |
| 3978 | Table 3A | Hs.146550 | BF976590 | 12343805 | DNA sequence from clone RP1-68O2 on chromosome 22 Contains the 5' end of the APOL2 gene for apolipoprotein L 2, the APOL gene for apolipoprotein L, the MYH9 gene for nonmuscle type myosin heavy chain 9. ESTs, STSs and GSSs /cds=(0,5882) | 1 | GGCTTGACATTGCTCTCAAGAAGAT TAAGAACCCTGGAGGAACACTAGG |
| 3979 | Table 3A | Hs.7905 | BF981080 | 12383892 | 602310311F1 cDNA, 5' end /clone=IMAGE:4401411 /clone_end=5' | 1 | TGTACAGCTAAATTTCTCCAAAGCAC TTTTTCAAAACCAAAAAAGAAAAA |
| 3980 | Table 3A | Hs.182740 | BF981263 | 12384075 | ribosomal protein S11 (RPS11), mRNA /cds=(33,509) | 1 | TTTGACACTGAACACTTACAGATGT GGCAGATGTGAAATTTGTCATCAA |
| 3981 | Table 3A | Hs.289721 | BF981634 | 12384446 | cDNA: FLJ22193 fis, clone HRC01108 /cds=UNKNOWN | 1 | ACAGAGAGTCACCCGCGAGTACGAA ACAGGCACATTTTAGAAACTCACA |
| 3982 | Table 3A | Hs.83583 | BG024761 | 12410861 | actin related protein 2/3 complex, subunit 2 (34 kD) (ARPC2), mRNA /cds=(84,986) | 1 | AGGTTCTTACCACCATTGTTGTGCCC ATCTTCCCTTCGTTCCCAATGTG |
| 3983 | Table 3A | Hs.1432 | BG026279 | 12413729 | protein kinase C substrate 80K-H (PRKCSH), mRNA /cds=(136,1719) | 1 | CCGGGGTGGCCCTCTCAAAATTTGGC ATGGGGTCTCTTTCAATGTTGTGG |
| 3984 | Table 3A | Hs.279009 | BG028577 | 12417672 | matrix Gla protein (MGP), mRNA /cds=(46,357) | 1 | CACGAGCGGCTGGAGGACACCCATT TTGTGCAGTGCCCGTCCGCTTC |
| 3985 | Table 3A | Hs.5122 | BG028906 | 12418001 | 602293015F1 cDNA, 5' end /clone=IMAGE:4387778 /clone_end=5' | 1 | GCCCTATGGCGTTGTAAACACGAGC GTATGCTAGTAAGTATCATTCATA |
| 3986 | Table 3A | Hs.143554 | BG033028 | 12424903 | Pur-beta (PURB) mRNA, complete cds /cds=(13,951) | 1 | GGTGTGTCTCGCGGCTGGCCAGTC TATTCTCGGTGTTTATCTTCATCAC |
| 3987 | Table 3A | Hs.118787 | BG033294 | 12425446 | transforming growth factor, beta-induced, 68kD (TGFB1), mRNA /cds=(47,2098) | 1 | GACAACGGAACTCTGTCTCTACCAC CATGTGACAGACGCGTTGATGCGT |
| 3988 | Table 3A | Hs.103902 | BG033732 | 12426494 | 602301101F1 cDNA, 5' end /clone=IMAGE:4402465 /clone_end=5' | 1 | CAAGACACAAACAGCAGACTCACAC AGAGAAAGCAACCATGCCGAGGAG |
| 3989 | Table 3A | Hs.306155 | BG033909 | 12426670 | chorionic somatomammotropin hormone 1 (placental lactogen) (CSH1), transcript variant 2, mRNA /cds=(116,886) | 1 | CGCGTCGAACTTCGGGACATTCGCG TAAACCACAAACAGATAAAGAATTA |
| 3990 | Table 3A | Hs.332404 | BG033953 | 12426761 | CDA02 protein (CDA02), mRNA /cds=(2,1831) | 1 | GCGTAAAGTGATCAAAAGGCCCTGAA GGGGAAATGATAAAACCCGTGGT |
| 3991 | Table 3A | Hs.12396 | BG034192 | 12427253 | 602302446F1 cDNA, 5' end /clone=IMAGE:4403866 /clone_end=5' | 1 | AGAGGAAGCGTGTGAATACAACATC TAAAAGGAGGAGAGGTCGAGCAC |
| 3992 | Table 3A | Hs.125819 | BG034799 | 12428456 | putative dimethyladenosine transferase (HSA9761), mRNA /cds=(78,1019) | 1 | ACACATTCCCATACCATTTTCGTGTT ATTACATTCCCGTACCATTCT |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|--|---|---|
| 3993 | Table 3A | Hs.16488 | BG035120 | 12428935 | calreticulin (CALR), mRNA /cds=(68,1321) | 1 | TAAAAGGGGGTGGCGGCTGTAGTA AGGAGGACGAGTAATGTATAGCAC |
| 3994 | Table 3A | Hs.17719 | BG035218 | 12429131 | EBP50-PDZ interactor of 64 kD (EPI64), mRNA /cds=(24,1550) | 1 | CCATGACGAGGCGCAACCATAACAG TTAGAGACGGCACACAGCACGACAC |
| 3995 | Table 3A | Hs.319825 | BG036101 | 12430901 | 602021477F1 cDNA, 5' end /clone=IMAGE:4156915 /clone_end=5' | 1 | ACTCACGCAAGAGCAGGGGGACTAT AACAGAAATAACAAGTAAATAAAT |
| 3996 | Table 3A | Hs.192965 | BG036938 | 12432665 | 602287708F1 cDNA, 5' end /clone=IMAGE:4375153 /clone_end=5' | 1 | TACACAGGCAGCTATGCGGATCATCA GACGAGCACATAATTCTAACAGAGA |
| 3997 | Table 3A | Hs.144924 | BG037042 | 12432874 | serine/threonine protein kinase SSTK (SSTK), mRNA /cds=(122,943) | 1 | CGTCGCCGTAGGACGCCTCCGTCGT CGTCTGGTCTGTCTCCTGCATCGAG |
| 3998 | Table 3A | Hs.318893 | BG106948 | 12600794 | 602291361F1 cDNA, 5' end /clone=IMAGE:4386159 /clone_end=5' | 1 | AAAGGCAAGAGTCCGGGGTGGCAGA AGAGTGAAAAATGAAAGAGAGAAGG |
| 3999 | Table 3A | Hs.109007 | BG110599 | 12604105 | 602342214F1 cDNA, 5' end /clone=IMAGE:4452602 /clone_end=5' | 1 | TTCTGCCAGAGTGATTTGTGAAGA GTCTCTTATATTATGTTTGTGGA |
| 4000 | Table 3A | Hs.173737 | BG110835 | 12604341 | ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) (RAC1), transcript variant Rac1b, mRNA /cds=(0,635) | 1 | GTGCGAATGTGGAGTGTTTTACATTG ATCTTTGCTAATGAATTAGCATCA |
| 4001 | Table 3A | Hs.323950 | BG111212 | 12604718 | zinc finger protein 6 (CMPX1) (ZNF6), mRNA /cds=(1265,3361) | 1 | CATTACGCATATTGGTAAGACGCAAA ATGAGACAGATCGACACTGGGACG |
| 4002 | Table 3A | Hs.34906 | BG111773 | 12605279 | 601820448F1 cDNA, 5' end /clone=IMAGE:4052578 /clone_end=5' | 1 | CACAACGGGTCTTAATGACGACGGAA AGATACATCCATCGGTATGAACGC |
| 4003 | Table 3A | Hs.74313 | BG112085 | 12605591 | mRNA for KIAA1265 protein, partial cds /cds=(66,2573) | 1 | ACCAGCAATCCGCAGCAGATCATAA GTGGGGTAGGTGATATGTACTAAC |
| 4004 | Table 3A | Hs.320972 | BG112503 | 12606009 | 602282105F1 cDNA, 5' end /clone=IMAGE:4369633 /clone_end=5' | 1 | GAAAAACAAGCTAACAAACACACAC GCCACACCAACATGCCAGAACGC |
| 4005 | Table 3A | Hs.7589 | BG112505 | 12606011 | 602282107F1 cDNA, 5' end /clone=IMAGE:4369729 /clone_end=5' | 1 | TGAACATGGGTGGGTTTGATCACGAG GATTCGGCTGAAAAGATTAGAGGG |
| 4006 | Table 3A | NA | BG118529 | 12612035 | cDNA clone IMAGE:4443519 5' | 1 | CGCGTTCATAACGGCGTGGACTGTTT TTGTGCTGCTGTTATCTATACTAT |
| 4007 | Table 3A | NA | BG121288 | 12614797 | cDNA clone IMAGE:4450407 5' | 1 | GGGACCAGACTACACGGGAATACCAG AGTTGAAGAAAATTAAGATTAAAGC |
| 4008 | Table 3A | Hs.285729 | BG163237 | 12669951 | 602013364F1 cDNA, 5' end /clone=IMAGE:4149351 /clone_end=5' | 1 | TATACTGAGAGTGAAGGTCTGGGTGC CAACTTGAGACAGGTGGTCTAGGA |
| 4009 | Table 3A | Hs.111554 | BG164898 | 12671532 | ADP-ribosylation factor-like 7 (ARL7), mRNA /cds=(14,592) | 1 | CCCCTGGTTTTCTCGTTCTGCCTCCT TTGGACCTGTGTTTGTCTTCTGCT |
| 4010 | Table 3A | Hs.193482 | BG165998 | 12672701 | cDNA FLJ11903 fis, clone HEMBB1000030 /cds=UNKNOWN | 1 | CCCTTAGAATGGTTACTGCCCTTGAA TTAAGTTGACACAAGTTGGGTTGG |
| 4011 | Table 3A | NA | BG166279 | 12672982 | cDNA clone IMAGE:4455496 5' | 1 | CGAATAATCCCTATTGATTACCTCA GAAAAGTTTTGCTCTCCGCCAAGG |
| 4012 | Table 3A | Hs.87113 | BG168139 | 12674842 | 602341526F1 cDNA, 5' end /clone=IMAGE:4449343 /clone_end=5' | 1 | TTGACCCCAAGGTAAGGCGGATAT TGTTGGGACGTTCCGGGAGTGTAT |
| 4013 | Table 3A | Hs.182695 | BG170647 | 12677350 | mitochondrial ribosomal protein 63 (MRP63), mRNA /cds=(215,523) | 1 | AATTACGTTCCGAGGTATATAAAAAAG GGATCGGCGCAGTGGATAGGGGGT |
| 4014 | Table 3A | Hs.204959 | BG180098 | 12686801 | hypothetical protein FLJ14886 (FLJ14886), mRNA /cds=(111,1169) | 1 | GGAGATCCACAGTGATCTCAGGCCCC TGGACCGGAAAAGGCAGCAAGATCA |
| 4015 | Table 3A | NA | BG249224 | 12759040 | cDNA clone IMAGE:4470038 5' | 1 | AAGACGAGTACACCAAGACCAAGA GCGCCAACGAGCAGACCGAGTGAA |
| 4016 | Table 3A | Hs.6682 | BG254117 | 12763933 | solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA /cds=(235,1740) | 1 | AACGCCGACTAGACGTCAAAAGACT TAATAAGAAACACACTGATATCCA |
| 4017 | Table 3A | NA | BG254292 | 12764108 | cDNA clone IMAGE:4477042 5' | 1 | CGCAACATTATCCATTTAAACCCCTG CATAACCCATTACCAAGCCCTCT |
| 4018 | Table 3A | Hs.30724 | BG260954 | 12770770 | 602372562F1 cDNA, 5' end /clone=IMAGE:4480647 /clone_end=5' | 1 | GGCACCCTCAATCCCGGCAAAAACA TTTGTTAACTCTTGGAATTTCTT |
| 4019 | Table 3A | Hs.217493 | BG282346 | 13031273 | annexin A2 (ANXA2), mRNA /cds=(49,1068) | 1 | CTCGTCTGCACCGGAGTCTCACAAT TTAGCATCTGGGTCTTGAGCATT |
| 4020 | Table 3A | Hs.71243 | BG283002 | 13032445 | 602406192F1 cDNA, 5' end /clone=IMAGE:4518214 /clone_end=5' | 1 | CCCTCCGGGGTCTCTATACCCACAAC CTTCTATCACTCAATCAGTTGGTA |
| 4021 | Table 3A | Hs.322653 | BG283132 | 13032707 | 602406784F1 cDNA, 5' end /clone=IMAGE:4518957 /clone_end=5' | 1 | AACAAGATAGAGAGAAGACGAAGATC GACACAGACAAACAACCAACCGG |
| 4022 | Table 3A | Hs.246818 | BG283706 | 13033918 | 602259846F1 cDNA, 5' end /clone=IMAGE:4343171 /clone_end=5' | 1 | TGTTGGGACCCCTCATCTCACGGGTC ATTTCCACCACTAAACGCCCTTTT |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|--|---|--|
| 4023 | Table 3A | Hs.151239 | BG286500 | 13039430 | 602382992F1 cDNA, 5' end /clone=IMAGE:4500527 /clone_end=5' | 1 | CCCTGAAATCCTAAATTCGGTCACCC CTCCAACATGACCATAAAAGTCCC |
| 4024 | Table 3A | Hs.323950 | BG286649 | 13039715 | zinc finger protein 6 (CMPX1) (ZNF6), mRNA /cds=(1265,3361) | 1 | GACCACGTTATGTGCGCTGACTTCGAG GACACCCCTCTCTGGTTTGGTATTT |
| 4025 | Table 3A | Hs.278428 | BG286817 | 13040034 | progesterin induced protein (DD5), mRNA /cds=(33,8432) | 1 | TCTCCTTTTCAGTTCCCTTTGTAGGATTT CTGGCCTTGAGGATAGCTCTTCA |
| 4026 | Table 3A | NA | BG288308 | 13043014 | cDNA clone IMAGE:4512706 5' | 1 | TCTCATCAACATTTGACTCTCAGAAG AGCCTCCATTTGCCCTTTCTCTCT |
| 4027 | Table 3A | Hs.115467 | BG288391 | 13043387 | 602388053F1 cDNA, 5' end /clone=IMAGE:4517076 /clone_end=5' | 1 | GCAGAGCAGACCTTATTACGCCACAAT TGCCGGTAACATGTAACACCAAGTT |
| 4028 | Table 3A | Hs.11637 | BG288429 | 13043463 | 602388093F1 cDNA, 5' end /clone=IMAGE:4517086 /clone_end=5' | 1 | ATTGGGCATGGTTGGTCCAATGCCTC ACATGGCCGGGATAACAGGACGCA |
| 4029 | Table 3A | Hs.79101 | BG288554 | 13043326 | cyclin G1 (CCNG1), mRNA /cds=(187,1074) | 1 | CAAAGGGTGTAATTCACATTGACAC TCCTGTCATGCGGTGGGCGGGAAC |
| 4030 | Table 3A | Hs.44577 | BG288837 | 13044076 | 602388170F1 cDNA, 5' end /clone=IMAGE:4517129 /clone_end=5' | 1 | CTAGCTCACTAGTTGTGCCTATATGC CACACCGGGGACCCAACAAGGGT |
| 4031 | Table 3A | Hs.173830 | BG289048 | 13044499 | 602383666F1 cDNA, 5' end /clone=IMAGE:4512712 /clone_end=5' | 1 | ATACTGTGTGATTTGCCCTTGCTGTC CAACCTGTCTTGCTGCCATTTA |
| 4032 | Table 3A | Hs.169363 | BG289347 | 13045100 | GLE1 (yeast homolog)-like, RNA export mediator (GLE1L), mRNA /cds=(87,2066) | 1 | GTGGCCTGAAGTGACCCATTCTATGA ATTGTTAATTAAGGTGCCAAAAAA |
| 4033 | Table 3A | Hs.79914 | BG290141 | 13046637 | lumican (LUM), mRNA /cds=(84,1100) | 1 | GGGTTTGAGACTTGGGTATGGAACA GAACCGGAAATGTGTGCTCTGGT |
| 4034 | Table 3A | Hs.129872 | BG290577 | 13047679 | sperm associated antigen 9 (SPAG9), mRNA /cds=(110,2410) | 1 | ATTTCTATTATGGAATCCCTGGGGTT CAGAATGTAACCTTTGTACATGAGA |
| 4035 | Table 3A | Hs.95835 | BG291649 | 13049586 | RST8356 cDNA | 1 | GACAGTACACCTCAGGGAAGGGACA AACAAACACGATAAATCGACACACG |
| 4036 | Table 3A | Hs.289088 | BG291970 | 13050316 | heat shock 90kD protein 1, alpha (HSPCA), mRNA /cds=(60,2258) | 1 | TCAGACCCAGTCTTGTTGGATGGAAT GTAGTGCTCGAGTCACATTCTGCT |
| 4037 | Table 3A | Hs.322804 | BG311130 | 13112931 | ia55a08.y1 cDNA, 5' end /clone_end=5' | 1 | TCCTGAGCCCCACACGCCCGAAGCA ATAAAGAGTCCACTGACTTCCAAAA |
| 4038 | Table 3A | Hs.190219 | BG326781 | 13133218 | 602425659F1 cDNA, 5' end /clone=IMAGE:4563471 /clone_end=5' | 1 | ACGAATATCGAATCTCCACGCGGG GGGTGAGACCCGAATCTGCGGCTGC |
| 4039 | Table 3A | Hs.292457 | BG339050 | 13145488 | Homo sapiens, clone MGC:16362 IMAGE:3927795, mRNA, complete cds /cds=(498,635) | 1 | AGACACACGAGCAAAACGACGCAGC AAGAATCAGATAGCATAGCAAAACAT |
| 4040 | Table 3A | Hs.170980 | BG387694 | 13281140 | cell cycle progression 2 protein (CPR2), mRNA /cds=(126,1691) | 1 | GCAGTGGGACGGAACGGGTGAAGCC TGATGGCTGATCGGCGACGATCTTG |
| 4041 | Table 3A | Hs.266175 | BG391695 | 13285143 | cDNA FLJ20673 fis, clone KIAA4464 /cds=(104,1402) | 1 | CTTTAAATCTTAGATTGCTCCGCACA GATAAAGAGAACCAGGATTGGGGC |
| 4042 | Table 3A | Hs.301226 | BG396292 | 13289740 | mRNA for KIAA1085 protein, partial cds /cds=(0,1755) | 1 | TTTATTTGGGTACTTTTCCCAACACA AGTCCTTTTATCCCACTCTGGG |
| 4043 | Table 3A | Hs.58643 | BG397564 | 13291012 | 602438603F1 cDNA, 5' end /clone=IMAGE:4564968 /clone_end=5' | 1 | AAAAGATCTCGGAAATAGCATTTTG TTAAACCTTGGGGGTAAACCC |
| 4044 | Table 3A | Hs.26670 | BG403635 | 13297083 | PAC clone RP3-515N1 from 22q11.2- q22 /cds=(0,791) | 1 | AACCTTCATGCAAGTGGAGACGGGTA GGGGGTTCTATGGGGCATTGGTTG |
| 4045 | Table 3A | Hs.292457 | BG424974 | 13331480 | Homo sapiens, clone MGC:16362 IMAGE:3927795, mRNA, complete cds /cds=(498,635) | 1 | TGTGAAAAGCTGATAAGAAAACCATC CAGAAAAAGCTCTTCGTTTACA |
| 4046 | Table 3A | NA | BG427404 | 13334006 | cDNA clone IMAGE:4612518 5' | 1 | TCATTATAATTCTGTCTAGGAAATCA AATTAGAACGCTCCACAAGCCGG |
| 4047 | Table 3A | NA | BG432194 | 13338700 | cDNA clone IMAGE:4610035 5' | 1 | CGCAGAGCTGGGCTTACAAATGGG TTCCAAATCGGGCTTCTCACTCAGG |
| 4048 | Table 3A | Hs.28491 | BG434865 | 13341371 | spermidine/spermine N1- acetyltransferase (SAT), mRNA /cds=(165,680) | 1 | TACAACTGTACCACCTGGGTACTC TAGAAGTCTCTGGTCGGATCCTTC |
| 4049 | Table 3A | Hs.281397 | BG438232 | 13344738 | hypothetical protein AD034 (AD034), mRNA /cds=(195,1880) | 1 | CATAGAGCACAGAGACACATGGAC CGGCACGCGACCCGACCAAGCGC |
| 4050 | Table 3A | Hs.301226 | BG468330 | 13400600 | mRNA for KIAA1085 protein, partial cds /cds=(0,1755) | 1 | TTTACCTCATTTATTTGGTACTTTCCC CACACAGTCCTTTATCCACCTGG |
| 4051 | Table 3A | Hs.334787 | BG473228 | 13405503 | Homo sapiens, clone MGC:19556 IMAGE:4304831, mRNA, complete cds /cds=(1505,1666) | 1 | CCATTTTTAGTGGGGGAGAAAAGTGT CACTGTGCTGGCGAAAAGAGGTCCA |
| 4052 | Table 3A | Hs.292457 | BG473813 | 13406090 | Homo sapiens, clone MGC:16362 IMAGE:3927795, mRNA, complete cds /cds=(498,635) | 1 | CCGCACCGATTAAACGGCCAGAGAAG CAACAAGCAAATAAAAGTGGGAAA |
| 4053 | Table 3A | Hs.173737 | BG482798 | 13415077 | ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) (RAC1), transcript variant Rac1b, mRNA /cds=(0,635) | 1 | AACCTTAACCTACTGGCGAGAATACAG CGTGGGACCCCTTCAGCCACTACAA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|--|
| 4054 | Table 3A | Hs.24054 | BG489375 | 13450885 | hypothetical protein GL009 (GL009), mRNA /cds=(77,628) | 1 | AGGACTTAACGGGAATACGGGAATAA CTCCAATTACTTCATCTCTAGGGC |
| 4055 | Table 3A | Hs.166254 | BG493253 | 13454765 | hypothetical protein DKFZp566l133 (DKFZP566l133), mRNA /cds=(133,1353) | 1 | AAGGAGGTTGCTCACCAGTATGCTT GTTACCAAAATGTCACCAGGAGTT |
| 4056 | Table 3A | Hs.29131 | BG497765 | 13459282 | nuclear receptor coactivator 2 (NCOA2), mRNA /cds=(162,4556) | 1 | TGAATTAAGTGCATTATCAATTAACCT TATGGTGGTTGGAATAGTGATCA |
| 4057 | Table 3A | Hs.172089 | BG501063 | 13462580 | mRNA; cDNA DKFZp586l2022 (from clone DKFZp586l2022) /cds=UNKNOWN | 1 | AAACACACAGGAAAAGGGCAAAGGG GGCACCAGGAGAACCGGGAGACAAA |
| 4058 | Table 3A | NA | BG501895 | 13463412 | cDNA clone IMAGE:4654344 5' | 1 | CGGAGAAACGGGGCCAAAAGGTTGC CGAGAGACCCGGCGAAAAGGACAGG |
| 4059 | Table 3A | Hs.279009 | BG503693 | 13465210 | matrix Gla protein (MGP), mRNA /cds=(46,357) | 1 | ACAAAGCATCAAACAGCAGGGAGCTA GTGGAGAGGTCTATTGTCCAGTG |
| 4060 | Table 3A | Hs.86437 | BG505271 | 13466788 | 602411368F1 cDNA, 5' end /clone=IMAGE:4540096 /clone_end=5' | 1 | GGGTGCATGCCAAGAAAGTATGGTT GGAATTCCTGGTACACTGAAGTGGA |
| 4061 | Table 3A | Hs.237868 | BG505379 | 13466896 | interleukin 7 receptor (IL7R), mRNA /cds=(22,1401) | 1 | ATGTTATCTTGGGAATTAGTGTCTTG AGCCTCTGTCTGTTACCGTAGTTT |
| 4062 | Table 3A | Hs.3280 | BG505961 | 13467478 | caspase 6, apoptosis-related cysteine protease (CASP6), transcript variant alpha, mRNA /cds=(78,959) | 1 | TGACCGAGTAAAAACATCTATCAAT TACACAAATGAACAAGATGTGAG |
| 4063 | Table 3A | Hs.293842 | BG506472 | 13467989 | 601571679F1 cDNA, 5' end /clone=IMAGE:3838675 /clone_end=5' | 1 | ACAAGAAATGGTTGAGGCGAATATTG GAAACACATGGGCTTAATGCTGAA |
| 4064 | Table 3A | Hs.111911 | BG527060 | 13518597 | 602540462F1 cDNA, 5' end /clone=IMAGE:4671519 /clone_end=5' | 1 | GGTATTGATGCTTGGTTTTCTGCC AGTCCGAAATTCCTGTATTTGTCA |
| 4065 | Table 3A | Hs.12396 | BG527658 | 13519195 | 602302446F1 cDNA, 5' end /clone=IMAGE:4403866 /clone_end=5' | 1 | TCATGCTACTTGTCTGGTTTTGTCA TGATACTCTCATAGCCCTTTTGA |
| 4066 | Table 3A | NA | BG531486 | 13523023 | cDNA clone IMAGE:4699409 5' | 1 | GCCTGGCGGACCGGCAGCCTATATG ACGGACTTCCTCATTACTTACCACG |
| 4067 | Table 3A | Hs.279009 | BG532345 | 13523883 | matrix Gla protein (MGP), mRNA /cds=(46,357) | 1 | AAACTGTTTGGAGAATTTAAGCACTC TCTGATGGGGGACAACCTATGGA |
| 4068 | Table 3A | Hs.129872 | BG532470 | 13524009 | sperm associated antigen 9 (SPAG9), mRNA /cds=(110,2410) | 1 | TCTTTGTGCAGATACGTTACCACAT AAGTGTGAGCCATTTAAACCTGGT |
| 4069 | Table 3A | Hs.343475 | BG533994 | 13525534 | 601556208T1 cDNA, 3' end /clone=IMAGE:3826392 /clone_end=3' | 1 | CACCAAAGTGGAGACAAATACATGAT CTCAAAGATACACAGTACCTACTT |
| 4070 | Table 3A | Hs.74647 | BG536394 | 13527940 | T-cell receptor active alpha-chain mRNA from JM cell line, complete cds /cds=(136,969) | 1 | AATAATTGGTCTTTTAAACAAACACG GAAGTTTGGTGAATCGGTCATGT |
| 4071 | Table 3A | Hs.343475 | BG536641 | 13528187 | 601556208T1 cDNA, 3' end /clone=IMAGE:3826392 /clone_end=3' | 1 | TGTTCTGCTCTCTCTCTGGGTTCCA CAAAGGTGGGACCTTACTTATCTA |
| 4072 | Table 3A | Hs.72988 | BG537502 | 13529734 | signal transducer and activator of transcription 2, 113kD (STAT2), mRNA /cds=(57,2612) | 1 | AGGGAAAAACGCAGGGGTTCAAAA ACTCTCTCACTCTATGCAGTGTATA |
| 4073 | Table 3A | NA | BG538731 | 13530964 | cDNA clone IMAGE:4691392 5' | 1 | AAGCAGCTCAATAGCAGCATAGAGGA TTAGATTAATGGAACAGCACTGCA |
| 4074 | Table 3A | Hs.124675 | BG541679 | 13533912 | 602571256F1 cDNA, 5' end /clone=IMAGE:4695805 /clone_end=5' | 1 | ACATATACAAGGACACAGGAAAGG CGGGAACAACGGGAAGAGGTTTTG |
| 4075 | Table 3A | NA | BG542394 | 13534627 | cDNA clone IMAGE:4696046 5' | 1 | TGTGGCGATTAAGAGAGGTGAAGCAT AACTGATTTGCAGGATATGGTTTG |
| 4076 | Table 3A | Hs.198427 | BG547561 | 13546239 | hexokinase 2 (HK2), mRNA /cds=(1490,4243) | 1 | AAAAGCCAAAAGGTTTCATGTAGATT TTAGTTCACTAAAGGGTGCCCA |
| 4077 | Table 3A | Hs.83077 | BG547627 | 13546292 | interleukin 18 (interferon-gamma-inducing factor) (IL18), mRNA /cds=(177,758) | 1 | GCAGAACTGTAATTGTACGGGGTCAC AGAGGCGTGATATGGTATCCCAA |
| 4078 | literature | Hs.227656 | XM_001289 | 14732543 | xenotropic and polytropic murine leukemia virus receptor (X3) mRNA, complete cds /cds=(165,2255) | 1 | CTTAACCATACAGAATGATATAACTC CTGTGCAATGAAGGTGATAACAGT |
| 4079 | literature | Hs.55468 | XM_001939 | 11426048 | H4 histone, family 2 | 1 | CTTCGGAGGCTAGGCCGCCGCTCCA GCTTTGCACGTTTCGATCCCAAAGG |
| 4080 | Table 3A | Hs.170171 | XM_002068 | 14732456 | mRNA; cDNA DKFZp434M0813 (from clone DKFZp434M0813); partial cds /cds=(430,768) | 1 | CAAAGTCAAATAACTCTATTGTAAA CAAAGTGTGTAAGTCCCAAAAGC |
| 4081 | literature | Hs.181097 | XM_002135 | 11428074 | tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kD) (TNFSF4), mRNA /cds=(36,587) | 1 | CCAATCCGATCCAATCATATTTG TTCTTAAGTATACTGGGCAGGTCC |
| 4082 | Table 3A | Hs.76913 | XM_002158 | 13639010 | proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA /cds=(21,746) | 1 | TCCAGCTCCTGTTCTTGGAAAATCT CCATTGTATGTGCATTTTTTAAAT |
| 4083 | Table 3A | Hs.10927 | XM_002269 | 13636009 | HSZ78330 cDNA /clone=2.49-(CEPH) | 1 | AACTGATGCCTGCTAGTCTTTCTGA TTACTCGCATCTGTTTCTTGCTT |
| 4084 | literature | Hs.81424 | XM_002513 | 13646509 | ubiquitin-like 1 (sentrin) (UBL1), mRNA /cds=(66,371) | 1 | TCAGGTTGAAGTCAAGATGACAGATA AGGTGAGAGTAATGACTACTCCAA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|---|
| 4085 | Table 3A | Hs.173912 | XM_003189 | 14735115 | eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA /cds=(15,1238) | 1 | TCCTAGGTAGGGTTTAAATCCCCAGTA AAATTGCCATATTGCACATGTCTT |
| 4086 | Table 3A | Hs.63668 | XM_003304 | 14720715 | tol-like receptor 2 (TLR2), mRNA /cds=(129,2483) | 1 | AGCGGGAAGGATTTTGGGTAAATCTG AGAGCTGCGATAAAGTCTAGGTT |
| 4087 | Table 3A | Hs.89714 | XM_003507 | 14731038 | small inducible cytokine subfamily B (Cys-X-Cys), member 5 (epithelial-derived neutrophil-activating peptide 78) (SCYB5), mRNA /cds=(106,450) | 1 | GAGGCCCTAGCATTTCTCCTTGGATA GGGGACCAGAGAGAGCTTGAATG |
| 4088 | Table 3A | Hs.66052 | XM_003593 | 13646753 | CD38 antigen (p45) (CD38), mRNA /cds=(69,971) | 1 | CTCCACAATAAGGTCAATGCCAGAGA CGGAAGCCTTTTCCCAAAGTCT |
| 4089 | Table 3A | Hs.251664 | XM_004020 | 11417288 | DNA for insulin-like growth factor II (IGF-2); exon 7 and additional ORF /cds=(0,233) | 1 | CCAATGTTTCTCTTTGGCCCTATACA AAGGCAAGAAGGAAAGACCAAGA |
| 4090 | Table 3A | Hs.79197 | XM_004500 | 13631147 | CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA /cds=(41,658) | 1 | TTTACCTCTGTCTTGGCTTTCATGTTA TTAAACGTATGCATGTGAAGAAG |
| 4091 | db mining | Hs.159651 | XM_004585 | 14758499 | tumor necrosis factor receptor superfamily, member 21 (TNFRSF21), mRNA /cds=(0,1967) | 1 | GGGAAGTTGGTTTATAAGCCTTTGCC AGGTGTAACGTGTGTGAATACCC |
| 4092 | Table 3A | Hs.279903 | XM_004611 | 14740071 | Ras homolog enriched in brain 2 (RHEB2), mRNA /cds=(23,577) | 1 | CCCTCCCTTCAGATTATGTTAACTCT GAGTCTGTCCAAATGAGTTCACCT |
| 4093 | Table 3A | Hs.302981 | XM_004720 | 14745195 | hypothetical protein FLJ11000 (FLJ11000), mRNA /cds=(223,780) | 1 | TTATTCATATATTCCTGTCCAAAGCCA CACTGAAAACAGAGGCAGAGACA |
| 4094 | Table 3A | Hs.239138 | XM_004839 | 13629023 | pre-B-cell colony-enhancing factor (PBEF), mRNA /cds=(27,1502) | 1 | TGCACCTCAAGATTTTAAGGAGATAA TGTTTTAGAGAGAAATTTCTGCTT |
| 4095 | Table 3A | Hs.79022 | XM_005162 | 14746130 | GTP-binding protein overexpressed in skeletal muscle (GEM), mRNA /cds=(213,1103) | 1 | TATGGCCTTCAAGCTCAAGTCCAAT CCTGCCATGCCTCTGTAGACTCT |
| 4096 | Table 3A | Hs.234642 | XM_005543 | 13641011 | aquaporin 3 (AQP3), mRNA /cds=(64,942) | 1 | TCCATCTGTGCATAAGGAGAGGAAAG TTCCAGGGTGTGTATGTTTTTCAGG |
| 4097 | Table 3A | Hs.124029 | XM_005693 | 14737168 | inositol polyphosphate-5-phosphatase, 40kD (INPP5A), mRNA /cds=(101,1192) | 1 | GGACCATTCCGGAGCAGCCCCACAT ACCTCACTGTCTCGTCTGTCTATGT |
| 4098 | Table 3A | Hs.326248 | XM_005698 | 13627052 | cDNA: FLJ22071 fls, clone HEP11691 /cds=UNKNOWN | 1 | TTTGTAAAGCGAAGGAGATGGAGGTC GTCTTAAACCAGAGAGCTACTGAAT |
| 4099 | Table 3A | Hs.287797 | XM_005799 | 13629831 | mRNA for FLJ00043 protein, partial cds /cds=(0,4248) | 1 | ACCACTGTATGTTTACTTCTCACCATT TGAGTTGCCCATCTTGTTCACA |
| 4100 | Table 3A | Hs.1395 | XM_005883 | 14740090 | early growth response 2 (Krox-20) (<i>Drosophila</i>) homolog) (EGR2), mRNA /cds=(338,1768) | 1 | AAATCTATTCTAACGCAAAACCACTAA CTGAAGTTCAGATAATGGATGGT |
| 4101 | Table 3A | Hs.1908 | XM_005980 | 14748566 | proteoglycan 1, secretory granule (PRG1), mRNA /cds=(24,500) | 1 | TGTTATAAAAGAGGATTTTCCACCTT GACACCAGGCAATGTAGTTAGCA |
| 4102 | db mining | Hs.73958 | XM_006283 | 14763523 | recombination activating gene 1 (RAG1), mRNA /cds=(124,3255) | 1 | ACCAGGATGCAATGGATTTATTTGAT TCAGGGGACCTGTATTTCCATGTC |
| 4103 | Table 3A | Hs.146589 | XM_006741 | 14783662 | mRNA for MOP-3, complete cds /cds=(0,4178) | 1 | AACAGAAACAGCTATGGCAACACGAT CACCTCAGAGCATCACCAACTTG |
| 4104 | db mining | Hs.99954 | XM_006840 | 14763859 | activin A receptor, type IB (ACVR1B), transcript variant 1, mRNA /cds=(39,1556) | 1 | TATTTAACCTGAGTATAGTATTTAACG AAGCCTAGAAGCAGGGCTGTGGG |
| 4105 | Table 3A | Hs.287369 | XM_006881 | 13650909 | interleukin 22 (IL22), mRNA /cds=(71,610) | 1 | AACTAACCCCTTTCCCTGCTAGAAA TAACAATTAGATGCCCAAAGCGA |
| 4106 | literature | Hs.159 | XM_006950 | 13652420 | tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A), mRNA /cds=(255,1622) | 1 | ATAGCAAGCTGAAGTGTCTTAAGGCA GGGGCGAGCAGGAACAATGGGGC |
| 4107 | Table 3A | Hs.159492 | XM_007156 | 12737945 | sacsin (SACS) gene, complete cds /cds=(76,11565) | 1 | TGACAGGTTCACTTCTGAGGTTGCTA TGAGGGTGATGGAATGTACTGCCT |
| 4108 | Table 3A | Hs.170133 | XM_007189 | 14755876 | forkhead box O1A (rhabdomyosarcoma) (FOXO1A), mRNA /cds=(385,2352) | 1 | TGTTTAAATGGCTTGGTGTCTTTCTTT TCTAATTATGCAGAATAAGCTCT |
| 4109 | Table 3A | Hs.87409 | XM_007606 | 14749307 | thrombospondin 1 (THBS1), mRNA /cds=(111,3623) | 1 | TTGAAATTGGTGGCTTCATTCTAGAT GTAGCTTGTGCAGATGTAGCAGGA |
| 4110 | Table 3A | Hs.75415 | XM_007650 | 14785206 | cDNA: FLJ22810 fls, clone KAIA2933, highly similar to AB021288 mRNA for beta 2-microglobulin /cds=UNKNOWN | 1 | ACTTCTTATACATTTGATAAAGTAAGG CATGGTTGTGGTTAATCTGGTTT |
| 4111 | Table 3A | Hs.17279 | XM_008062 | 13627121 | tyrosylprotein sulfotransferase 1 (TPST1), mRNA /cds=(81,1193) | 1 | CATGAAGAAGCAAGACGAAAACACAC AGGAGGGAAAATCCTGGGATTCTT |
| 4112 | Table 3A | Hs.5344 | XM_008082 | 14779810 | adaptor-related protein complex 1, gamma 1 subunit (AP1G1), mRNA /cds=(28,2505) | 1 | GCCTGGCTTGGACCTTGGCATTCCGT TTGAATTCCTTCTAACTGGAACAT |
| 4113 | Table 3A | Hs.75703 | XM_008449 | 13652724 | small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA /cds=(108,386) | 1 | GTCCACTGTCACTGTTTCTGTGCTGT TGCAAATACATGGATAACACATTT |
| 4114 | literature | Hs.79241 | XM_008738 | 13646672 | B-cell CLL/lymphoma 2 (BCL2), nuclear gene encoding mitochondrial protein, transcript variant alpha, mRNA /cds=(31,750) | 1 | TTGTGTTGTTGGAAAAAGTCACATTG CCATTAACTTTCCTGTCTGTCT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|---|
| 4115 | db mining | Hs.9731 | XM_008901 | 11432998 | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta (NFKBIB), mRNA /cds=(0,1016) | 1 | CAGTAGCGACAGCGACGGCGGAGAC GAGGGCGTGAGTCAGGAGGAGAGAC |
| 4116 | db mining | Hs.69747 | XM_009101 | 11425196 | fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included) (FUT1), mRNA /cds=(103,1200) | 1 | AGCTGCCACGGGTGAGAGAGCAGGA GGTATGAATTAAGTCTACAGCAC |
| 4117 | db mining | Hs.46328 | XM_009103 | 14760495 | mRNA for alpha(1,2)fucosyltransferase, complete cds /cds=(111,1142) | 1 | CTTTCCTCAAAATCTTTAAGCCAGAG GCAGCCTTCCTGCCGGAGTGGACA |
| 4118 | Table 3A | Hs.84038 | XM_009533 | 14771190 | CGI-06 protein (LOC51604), mRNA /cds=(6,1730) | 1 | TCTGCCTCACGTGCACTGTGGTGGC CGTGTGCTACGGCTCCTTCTACAAT |
| 4119 | Table 3A | Hs.296585 | XM_009574 | 14771391 | nucleolar protein (KKE/D repeat) (NOP56), mRNA /cds=(21,1829) | 1 | CCATAGCCCAAGGTGACATTTCACAC CCTGTGCCGTGTTCCCAATAAAA |
| 4120 | Table 3A | Hs.198298 | XM_009641 | 14770741 | cDNA FLJ14219 fis, clone NT2RP3003800, highly similar to Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA /cds=(501,1256) | 1 | GGGGTATCCAGAATTGGTTGTAATA CTTTCATATTGTCTGATTAAACA |
| 4121 | Table 3A | Hs.334691 | XM_009917 | 13648023 | hypothetical protein FLJ22427 (FLJ22427), mRNA /cds=(40,2631) | 1 | GAGGCTTTGCCCTTGCTGCATATTTG TTTCGCTCTTACTCAGTTTGGGAA |
| 4122 | Table 3A | Hs.278027 | XM_009929 | 11417988 | LIM domain kinase 2 (LIMK2), transcript variant 2b, mRNA /cds=(315,2168) | 1 | GCAAGTGTAGGAGTGGTGGCCTGA ACTGGGCCATTGATCAGACTAAATA |
| 4123 | Table 3A | Hs.32970 | XM_010593 | 14727775 | signaling lymphocytic activation molecule (SLAM), mRNA /cds=(133,1140) | 1 | TTGCAAAACCCAGAAGCTAAAAAGTC AATAAACAGAAAGATGATTTTGA |
| 4124 | Table 3A | Hs.155595 | XM_010897 | 13637965 | neural precursor cell expressed, developmentally down-regulated 5 (NEDD5), mRNA /cds=(258,1343) | 1 | CCCACTGCTACACTTCTGATCCCC TTTGGTTTTACTACCCAAATCTAA |
| 4125 | Table 3A | NA | XM_011080 | 14738482 | T cell activation, increased late expression | 1 | AAAAGAAGCCCTAATAAACACCCGG ATAATAACCCGTCTACCATCTTT |
| 4126 | Table 3A | Hs.302014 | XM_011082 | 13626304 | interleukin 21 (IL21), mRNA /cds=(46,534) | 1 | GTGAAGATTCCTGAGGATCTAACTTG CAGTTGGACACTATGTTACATACT |
| 4127 | Table 3A | Hs.78687 | XM_011714 | 14749491 | neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA /cds=(12,2765) | 1 | AGAAGGATAGCAGTTCTTAGTAAGT TTACTGTGTATAGGAACGGTTTGT |
| 4128 | literature | Hs.91390 | XM_011844 | 14739654 | poly (ADP-ribose) glycohydrolase (PARG), mRNA /cds=(166,3096) | 1 | CGGCTGCCTCTCTTGAGACCATCTGC CAATCACACAGTAACATTTCGGGT |
| 4129 | Table 3A | Hs.76038 | XM_011865 | 14737830 | isopentenyl-diphosphate delta isomerase (IDI1), mRNA /cds=(50,736) | 1 | CCCAACTGAGGACCACTGTCTACAGA GTCAGGAAATATTGTAGGGAGAA |
| 4130 | Table 3A | Hs.180450 | XM_011914 | 13628205 | ribosomal protein S24 (RPS24), transcript variant 1, mRNA /cds=(37,429) | 1 | CTGGCAAAAAGCCGAAGGAGTAAAG GTGCTGCAATGATGTTAGCTGTGGC |
| 4131 | Table 3A | Hs.154938 | XM_012059 | 14771044 | hypothetical protein MDS025 (MDS025), mRNA /cds=(5,769) | 1 | TGTTTGCTTGAACAGTTGTGTAATC ATACAGGATTTTGTGGGTATTGGT |
| 4132 | Table 3A | Hs.1051 | XM_012328 | 14750596 | granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), mRNA /cds=(33,776) | 1 | GGAGCCAAGTCCAGATTACACTGG GAGAGGTGCCAGCAACTGAATAAAT |
| 4133 | Table 3A | Hs.251526 | XM_012649 | 13633583 | gene for monocyte chemotactic protein-3 (MCP-3) /cds=(0,329) | 1 | GGATGCTCCTCCCTTCTACCTCAT GGGGGTATTGTATAAGTCCTTGCA |
| 4134 | db mining | Hs.278454 | AF285431 | 12741752 | killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2 (KIR2DL2), mRNA /cds=(14,1060) | 1 | TAACITCAATGTAGTTTTCCATCCTTC AAATAAACATGTCTGCCCCCATG |
| 4135 | Table 3A | Hs.334437 | XM_015180 | 14778515 | hypothetical protein MGC4248 (MGC4248), mRNA /cds=(70,720) | 1 | GAGTCCTTTTGATTTTTAACTTATTC CCATGTCCTTACTTTCGTGTGC |
| 4136 | Table 3A | Hs.137555 | XM_015921 | 14760439 | putative chemokine receptor; GTP-binding protein (HM74), mRNA /cds=(60,1223) | 1 | TGCACGTTCTCCTGGTTCTTCGCT TGTGTTTCTGTACTACCAAAAAT |
| 4137 | Table 3A | Hs.164371 | XM_016138 | 13638510 | cDNA FLJ13175 fis, clone NT2RP3003842 /cds=UNKNOWN | 1 | CAGCTTCAGCTAGGAGTTGTAAAGCA AGGACTTTGTGACACATTTGTCCC |
| 4138 | Table 3A | Hs.323463 | XM_016481 | 14721648 | mRNA for KIAA1693 protein, partial cds /cds=(0,2707) | 1 | AATTGAAAAGTACCAAGAAGTGAAG AAGACCAAGACCCATCATGCCCCA |
| 4139 | Table 3A | Hs.15220 | XM_016721 | 14784971 | zinc finger protein 106 (ZFP106), mRNA /cds=(335,5986) | 1 | ACTTCCTAGAGACTTGTTCGTGAGAC AGTTCCTTGCTTCACTTCCCTGC |
| 4140 | Table 3A | Hs.323463 | XM_016972 | 14726508 | mRNA for KIAA1693 protein, partial cds /cds=(0,2707) | 1 | ACAACCTGACCTGTCTCCTTCACATAG TCCATATCACCAACAATCACACAA |
| 4141 | Table 3A | Hs.180946 | XM_018498 | 14723691 | ribosomal protein L5 pseudogene mRNA, complete cds /cds=UNKNOWN | 1 | GCTCAGGAGCGGGCTGCTGAGAGCT AAACCCAGCAATTTTCTATGATTTT |
| 4142 | Literature | Hs.194382 | U67093 | 2072143 | ataxia telangiectasia (ATM) gene, complete cds /cds=(795,9965) | 1 | AAAGAAAGCCAGTATATTGGTTTGAA ATATAGAGATGTGTCCTCAATTTC |
| 4143 | Literature | Hs.184167 | NM_006276 | 6857827 | splicing factor, arginine/serine-rich 7 (35kD) (SFRS7) mRNA /cds=(105,490) | 1 | ACTGGCAGGCTTATTTATCTGTTGCA CTTGTTAGCTTAAATTGTTCTGT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|--|
| 4144 | Literature | Hs.79037 | NM_002156 | 4504520 | Homo sapiens, heat shock 60kD protein 1 (chaperonin), clone MGC:19755 IMAGE:3630225, mRNA, complete cds /cds=(1705,3396) | 1 | AGCAGCCTTTCTGTGGAGAGTGAGAA TAATTGTGTACAAAGTAGAGAAGT |
| 4145 | Literature | Hs.206984 | U15177 | 988207 | cosmid CRI-JC2015 at D10S289 in 10sp13 /cds=(0,1214) | 1 | CAACTGTGCTGGCCGGGAGGAGAGC AGAGACGCAGTCCTGCCAGTGTAG |
| 4146 | Literature | Hs.395 | XM_002923 | 13643499 | chemokine (C-C motif) receptor 2 (CCR2), mRNA /cds=(39,1163) | 1 | CACATGGCTAAAGAAGGTTTCAGAAA GAAGTGGGGACAGAGCAGAACTTT |
| 4147 | Literature | NA | NC_001807 | 13959823 | mitochondrion, complete genome | 1 | CCGACATCTGGTTCTCTACTTCAGGGT CATAAAGCCTAAATAGCCACACG |
| 4148 | Literature | Hs.32017 | NM_020645 | 11034818 | ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene /cds=(66,791) | 1 | CTCATTTGTATTCAAGCCTTTAACAG GAGGGCAAAGAGGTGAGAAATGTGT |
| 4149 | Literature | Hs.74621 | U29185 | 2865216 | prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia) (PRNP), mRNA /cds=(49,810) | 1 | GCACTGAATCGTTTCATGTAAGAATC CAAAGTGGACACCATTAACAGGTC |
| 4150 | Literature | NA | X04948 | 36891 | T-cell receptor alpha-chain HAP05 V(a)3.1J(a)P | 1 | GCAGACACTGCTTCTTACTTCTGTGC TACGGATGGGAACAGAGATGACAA |
| 4151 | Literature | NA | X92768 | 1054779 | mRNA for T-cell receptor alpha (clone XPBP53) | 1 | GGGGAAACTGGAGGCTTCAAACCTAT CTTTGGAGCAGGAACAAGACTATT |
| 4152 | Literature | Hs.75064 | NM_003192 | 4507372 | tubulin-specific chaperone c (TBCC), mRNA /cds=(23,1063) | 1 | GGGGAAGGAGGGTGATTATATTGCTT TGTAATGGTTTGTGATACCTTGAAA |
| 4153 | Literature | Hs.99093 | BG179517 | 12686220 | chromosome 19, cosmid R28379 /cds=(0,633) | 1 | GTACGAATGGGAGGTCCTCGACACC TGGGGAAGTGGCGACTATCGGGCAG |
| 4154 | Literature | Hs.77356 | NM_003234 | 4507456 | transferrin receptor (p90, CD71) (TFRC), mRNA /cds=(263,2545) | 1 | TATCAGACTAGTGACAAGCTCCTGGT CTTGAGATGTCTTCTCGTTAAGGA |
| 4155 | Literature | Hs.194638 | U89387 | 2253634 | polymerase (RNA) II (DNA directed) polypeptide D (POLR2D), mRNA /cds=(30,458) | 1 | TGACCTCCACCAAGCCATATAAGG AGCGGAGTTGTTAAGGACTGAAGA |
| 4156 | Literature | Hs.15220 | NM_022473 | 14784971 | zinc finger protein 106 (ZFP106), mRNA /cds=(335,5986) | 1 | TTTCTCCGACTCATCAGTAAACCTG TAGAAGTGTGCGTTTCCAGCCTTT |
| 4157 | Literature | Hs.326248 | NM_014456 | 7657448 | cDNA: FLJ22071 fis, clone HEP11691 /cds=UNKNOWN | 1 | TTTGTAAGCGAAGGAGATGGAGGTC GTCTTAAACCAAGAGCTACTGAAT |
| 4158 | Literature | Hs.182447 | BC003394 | 13097278 | heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC), transcript variant 1, mRNA /cds=(191,1102) | 1 | AAAGTTGATACTGTGGGTTATTTTTGT GAACAGCCTGATGTTTGGGACCT |
| 4159 | Literature | Hs.31314 | X72841 | 297903 | retinoblastoma-binding protein 7 (RBBP7), mRNA /cds=(287,1564) | 1 | AACTTTTACACTTTTTCCTTCCAACAC TTCTTGATTGGCTTTGCAGAAAT |
| 4160 | Literature | Hs.177592 | NM_001003 | 4506668 | ribosomal protein, large, P1 (RPLP1), | 1 | ACAGCCAAAGCTTACGGTTACAGGGCA ACGCACTACTGTTTCAGCTTTGAAT |
| 4161 | Literature | Hs.81361 | M65028 | 337450 | heterogeneous nuclear ribonucleoprotein A/B (HNRPA), transcript variant 1, mRNA /cds=(224,1219) | 1 | ACGTGTCCTGATTTTGCACACCTG GATATTGAAGCTATCCAAGCTTTT |
| 4162 | Literature | Hs.279939 | BC004560 | 13528728 | mitochondrial carrier homolog 1 (MTCH1), nuclear gene encoding mitochondrial protein, mRNA /cds=(0,1118) | 1 | AGCTGTTGATGCTGGTTGGACAGGTT TGAGTCAAATTGTACTTTGCTCCA |
| 4163 | Literature | Hs.241567 | NM_002897 | 8400725 | RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant MSSP-2, mRNA /cds=(265,1434) | 1 | ATAAGGTGCATAAAACCTTTAAATTC ATCTAGTAGCTGTTCCCCGAACA |
| 4164 | Literature | NA | BE874440 | 10323216 | NIH_MGC_69 cDNA clone IMAGE:3891187 5' | 1 | CCAATGACAGCCTACCTATTACCAAG GGCTCCCCTACAACCTGAACTTT |
| 4165 | Literature | Hs.1074 | BC005913 | 13543508 | surfactant, pulmonary-associated protein C (SFTPC), mRNA /cds=(27,620) | 1 | GACAAACCTGGAGAAATGGGAGCT TGGGGAGAGGATGGGAGTGGGCAGA |
| 4166 | Literature | Hs.56205 | BC001880 | 12804864 | insulin induced gene 1 (INSIG1), mRNA /cds=(414,1247) | 1 | GTGTCAGTGCCCAAAGGAGGGAGGT TGATGGTGCTTAACAAACATGAAGT |
| 4167 | Literature | Hs.77356 | BC001188 | 12654696 | transferrin receptor (p90, CD71) (TFRC), mRNA /cds=(263,2545) | 1 | TCATTGTATAAAAGCTGTTATGTGCAA CAGTGTGGAGATTCTTGTCTGA |
| 4168 | Literature | Hs.194638 | BC002958 | 12804200 | polymerase (RNA) II (DNA directed) polypeptide D (POLR2D), mRNA /cds=(30,458) | 1 | TGACCTCCACCAAGCCATATAAGG AGCGGAGTTGTTAAGGACTGAAGA |
| 4169 | Literature | Hs.35406 | AA057484 | 1550124 | 602675161F1 cDNA, 5' end /clone=IMAGE:4797783 /clone_end=5' | 1 | TTGGCTTCATTACGAGAGAGAAACAT AACAGAGGCAGTGATGGTTTCAGA |
| 4170 | Literature | Hs.74451 | X04106 | 35327 | calpain 4, small subunit (30K) (CAPN4), mRNA /cds=(158,964) | 1 | TTTGTCTATATTCTGCTCCAGCCTG CCAGGCCAGGAGGAAATAAACATG |
| 4171 | Literature | Hs.13231 | H17596 | 883836 | od15d12.s1 cDNA /clone=IMAGE:1368023 | 1 | AGCAGATTGGGAGATACATGATAAAT TTCTATCTGCAAGTTGCTATTGCA |
| 4172 | Literature | Hs.74002 | U40396 | 1117914 | mRNA for steroid receptor coactivator 1e /cds=(201,4400) | 1 | GGCCAGCAGAAGAGCCTCCTTCAG CAGCTACTGACTGAATAACCACTTT |
| 4173 | Literature | NA | X17403 | 59591 | CMV HCMVTRL2 = IRL2 | 1 | AATAATAGATTAGCAGAAGGAATAAT CCGTGCGACCGAGCTTGTGCTTCT |
| 4174 | Literature | NA | X17403 | 59591 | CMV HCMVUL27 | 1 | ACATTCAAAAGTTTGAGCGTCTTCAT GTACGCCGTTTTCGGCTCACGAG |

Table 8

| | | | | | | | |
|------|------------|-----------|----------|---------|--|----|--|
| 4175 | Literature | NA | X17403 | 59591 | CMV HCMVUL106 | 1 | ACGAACAGAAATCTCAAAGACGCTG ACCCGATAAGTACCGTCACGGAGA AGGAACCAGCAAGTCAACAAAAGACT AACAAAGAAAAACCATCTTTGGAAT CCAACGACACATCCACAAAATCCCC CATCGACTCTCACAATCGCATCAT CCTCTGGAGGCAAGAGCACCCACCC TATGGTGAAGTAGAAGCAAGGCTGAC GATGTCGGTCTACGCGCTATCGGCC ATCATCGGCATCTATCTGCTCTACC TTCGTGGGCACCAAGTTTCGCAAGAA CTACACTGTCTGCTGGCCGAGTTT GAGATCGACATCGTCATCGACCGAC CTCCGCGACCAACCCCTACCCATCC CTTTGAGCAGGTTCTCAAGGCTGTAA CTAACGTGCTGTGCGCCGTCTTTC TCTTCTGGGACGCCAACGACATCTAC CGCATCTTCGCCGAATTGGAAGGC AGAGAACAACAAAACCAACACGACGA TGAACAAAACGCTCAACCAACA |
| 4176 | Literature | NA | X17403 | 59591 | CMV HCMVTRL7 = IRL7 | 1 | |
| 4177 | Literature | NA | X17403 | 59591 | CMV HCMVUL33 | 1 | |
| 4178 | Literature | NA | X17403 | 59591 | CMV HCMVUL123 | 1 | |
| 4179 | Literature | NA | X17403 | 59591 | CMV HCMVUL75 Glycoprotein H | 1 | |
| 4180 | Literature | NA | X17403 | 59591 | CMV HCMVUS28 | 1 | |
| 4181 | Literature | NA | X17403 | 59591 | CMV HCMVUL21 | 1 | |
| 4182 | Literature | NA | X17403 | 59591 | CMV HCMVUL54 | 1 | |
| 4183 | Literature | NA | X17403 | 59591 | CMV HCMVUL83 | 1 | |
| 4184 | Literature | NA | X17403 | 59591 | CMV HCMVUL109 | 1 | |
| 4185 | Literature | NA | X17403 | 59591 | CMV HCMVUL113; spliced to HCMVUL112 | 1 | GAGAAAAGATTGTGCGATCTCCCCCT GGTTTCCAGCAGACTCTTGCCAGA CATCTTCTCCACCAACAGGGTGGGT TCATGCTGCCTATCTACGACGG TCCCATTGTTCCCTTTATTTGTCTTTTG GTTCTGCTTTTGGGAGATTTTT |
| 4186 | Literature | NA | X17403 | 59591 | CMV HCMVUL122 | 1 | |
| 4187 | db mining | Hs.164427 | AI307795 | 4002399 | fb28c03.x1 cDNA, 3' end /clone=IMAGE:2055652 /clone_end=3' | -1 | TGGTGCGCTTTTGTGTGCGGTGGAG GAGTTCCTAACCCCTCGGCTTGTTTT |
| 4188 | Table 3A | Hs.169168 | AA977148 | 3154594 | oq24g08.s1 cDNA, 3' end /clone=IMAGE:1587326 /clone_end=3' | -1 | GCCGTTGGTTGGCTTAACTTGGTTT CGTCACTTCGGGCACCTTGGTTTT CTGGCCCTCCCCTGGCTCTTTAAGCTC CCCTTTGGTTAAAACTGGGTTTT AAAAGGCCAAGGGTGTTGTGGGGC GTCTGTCTAATGTGGTGGGTCTTTT GCTGTAATCTCTGTCTCATCATCCTT CTCTTTTGTTCATAGCCTTTT GTGTGTGCTCGAGGTGAGAAAGCCACTG TGAATTGATTTCTTCTTGAAGTTT AATAAGGGTGTGCGCTTTGTTCCCT CACATAATCGTGAAGGCTGCTTT |
| 4189 | Table 3A | Hs.117333 | AI023714 | 3238758 | mRNA for KIAA1093 protein, partial cds /cds=(179,5362) | -1 | |
| 4190 | Table 3A | NA | AI380955 | 4190797 | tg18b08.x1 cDNA, 3' end /clone=IMAGE:2109111 | -1 | |
| 4191 | Table 3A | Hs.93670 | AA976045 | 3151837 | cDNA: FLJ22664 fis, clone HSI08202 /cds=UNKNOWN | -1 | |
| 4192 | Table 3A | Hs.332583 | AA788623 | 2874972 | yc77a06.s1 cDNA, 3' end /clone=IMAGE:21844 /clone_end=3' | -1 | |
| 4193 | Table 3A | Hs.71433 | AA131524 | 1693030 | zl31h02.s1 cDNA, 3' end /clone=IMAGE:503571 /clone_end=3' | -1 | |
| 4194 | Table 3A | Hs.309127 | AI380687 | 4190540 | tg03e04.x1 cDNA, 3' end /clone=IMAGE:2107710 /clone_end=3' | -1 | |
| 4195 | Table 3A | Hs.102630 | AA808085 | 2877491 | 602440867F1 cDNA, 5' end /clone=IMAGE:4556561 /clone_end=5' | -1 | TTCCTCAGTCCCTGTTTCATACCATCT CTGCACCACAATCACACTGATTT |
| 4196 | Table 3A | Hs.134473 | AI074016 | 3400660 | oy66g02.x1 cDNA, 3' end /clone=IMAGE:1670834 /clone_end=3' | -1 | GACCACAGATATGCACTCCTTACATT AACCTCAGCCTTGATGTATCATTT |
| 4197 | Table 3A | Hs.158653 | AI370965 | 4149718 | ta29b11.x1 cDNA, 3' end /clone=IMAGE:2045469 /clone_end=3' | -1 | CCCCCTGTTATGAAAAGGGTTAAACT TGAACCCACCCATTTTAAAAATTT |
| 4198 | Table 3A | Hs.243029 | AA424812 | 2106917 | UI-H-B14-aow-c-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3086226 /clone_end=3' | -1 | TTATAGCTACCAGAAGCCACCAGGGC CTTAGCCAGCAGTAGAAAACCTCT |
| 4199 | Table 3A | Hs.188777 | AA432364 | 2114747 | zw76a09.s1 cDNA, 3' end /clone=IMAGE:782104 /clone_end=3' | -1 | GATCAGTAGACACACCCCTCAATGCT GCGAAGAAAATGAAGGCCACTCTT AGCAGACAATGGACAACCTGTAGTTTT TGAATTGACTTCTATAGCCATCTT |
| 4200 | Table 3A | Hs.132237 | AI031656 | 3249868 | ow48e06.x1 cDNA, 3' end /clone=IMAGE:1650082 /clone_end=3' | -1 | |
| 4201 | db mining | Hs.123445 | AA813728 | 2882413 | 602623674F1 cDNA, 5' end /clone=IMAGE:4748515 /clone_end=5' | -1 | TCCACCACAGTGCATGATAATTCCGA CAGAACGCCCTTTATTTGTACCT |
| 4202 | Table 3A | Hs.143049 | AI126688 | 3595202 | Homo sapiens, Similar to DKFZP727C091 protein, clone MGC:10677 IMAGE:3948445, mRNA, complete cds /cds=(79,1530) | -1 | TGTTCTCTGAACTGTCTGGATGAACC GGTCAACGGCACTCATCATACCTT |
| 4203 | Table 3A | Hs.108327 | AA701667 | 2704832 | damage-specific DNA binding protein 1 (127kD) (DDB1), mRNA /cds=(109,3531) | -1 | GCTTCACTCTGCTTTCTGTATAAAGG GCAGTCTGTGGTCACGCAAGACTT |
| 4204 | Table 3A | Hs.270264 | AA613224 | 2484262 | no19d06.s1 cDNA, 3' end /clone=IMAGE:1101131 /clone_end=3' | -1 | AGCAAAGACCAAAATTCTCCTGGGAA GTGTGGGAGCAGGCTGACATTATT |
| 4205 | Table 3A | Hs.158976 | AI380390 | 4190243 | UI-H-B12-ahi-a-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2726692 /clone_end=3' | -1 | GTCCTTTGATAGCAGAAACAAGAGGCT CTGTGATCCTCTGGACCTCAGATT |
| 4206 | Table 3A | Hs.204214 | AA826926 | 2900923 | EST389900 cDNA | -1 | TCCACGACATGGTACAGCTCTTCACT TTTTCAGCTTTTAAATGTCCATT GACAAGGCAATGCTACTGATCACTG AGGATAATGGTGAAGGACTTTTGT |
| 4207 | Table 3A | Hs.326392 | AA974839 | 3150631 | son of sevenless (Drosophila) homolog 1 (SOS1), mRNA /cds=(0,3998) | -1 | |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|---|
| 4208 | Table 3A | Hs.53542 | AI084224 | 3422647 | chorea-acanthocytosis (CHAC) mRNA, complete cds /cds=(260,9784) | -1 | TCAATAGTTGTGAAATTCCTCTCAGGCTCCTTAAACCGCTCGCTTTGTGT |
| 4209 | Table 3A | Hs.173334 | AA284232 | 1928532 | ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA /cds=(0,1922) | -1 | AGGCTTACGTTTATCCAAAAGCATTT CACCTTGCACATTACTGTTGTTGT |
| 4210 | db mining | Hs.86437 | AI300700 | 3960046 | 602411368F1 cDNA, 5' end /clone=IMAGE:4540096 /clone_end=5' | -1 | ACAAGCATTTAGATCATAACATGGTA AAGCCTATTACCAGCCAATGTTGT |
| 4211 | db mining | Hs.61558 | AI220970 | 3803173 | hz63d07.x1 cDNA, 3' end /clone=IMAGE:3212653 /clone_end=3' | -1 | TGTTTTGGCATAGAGCTTTACTTAAAA TGCTGCTTCATTTTACACATTGT |
| 4212 | Table 3A | Hs.239489 | AA639796 | 2563575 | TIA1 cytotoxic granule-associated RNA-binding protein (TIA1), transcript variant 2, mRNA /cds=(185,1345) | -1 | TGGAGCTCAATTCATATGCAGTTGTGC TGATATTTTCATTAAGTCACTGTGT |
| 4213 | Table 3A | Hs.228795 | AI094726 | 3433702 | qa08f05.x1 cDNA, 3' end /clone=IMAGE:1686177 /clone_end=3' | -1 | TTTCCCTTGGCCTGAGTTTTTATAAAA ATTTCCATTAATTGGGGCAGTGT |
| 4214 | db mining | Hs.62699 | AA740964 | 2779556 | EST386140 cDNA | -1 | TGCAGCTAAATTCGAAGCTTTTGGTC TATATTGTTAATTGCCATTGCTGT |
| 4215 | Table 3A | Hs.124675 | AA858297 | 2946599 | ob13b08.s1 cDNA, 3' end /clone=IMAGE:1323543 /clone_end=3' | -1 | GGATTGGAAGATGCTTTCAGAAATA TGGCATAGGTTTTTGTGCAAAATG |
| 4216 | Table 3A | NA | AI281442 | 3919675 | cDNA clone IMAGE:1967452 3' | -1 | AAAGAAAAATTCAGCCTGAACCCCTAC CCTTATAAAACAGGTTAATTGGGT |
| 4217 | Table 3A | Hs.228817 | AI199388 | 3751994 | qs75e05.x1 cDNA, 3' end /clone=IMAGE:1943936 /clone_end=3' | -1 | TGTAAGTCCCATGCCGAAATTTGGAG ATTTGGGTTTTCTTTTCAGGGGT |
| 4218 | Table 3A | Hs.291003 | AA504269 | 2240429 | hypothetical protein MGC4707 (MGC4707), mRNA /cds=(72,1067) | -1 | CGGATTCCAAATTACTTAAAGCCTTTA TGGGAACACGGTAGATTGTAGGT |
| 4219 | Table 3A | Hs.299416 | AA132448 | 1694015 | zo20a03.s1 cDNA, 3' end /clone=IMAGE:587404 /clone_end=3' | -1 | GCCTTCTGGCCCTCTGAGGCAAAGGT CAGTGACTAGTGGGAGGGTAGGT |
| 4220 | Table 3A | Hs.6733 | AI057025 | 3330814 | phosphoinositide-specific phospholipase C PLC-epsilon mRNA, complete cds /cds=(235,7146) | -1 | GCTCAAGATCACCTCTTTGTCATCTT GAACAATGTTTTCTCTTAGGT |
| 4221 | db mining | Hs.177712 | AA251806 | 1886786 | zs09c03.s1 cDNA, 3' end /clone=IMAGE:884676 /clone_end=3' | -1 | TGTTTCCACTTCATGGGATATGACTC CATCACAATGAAAATGGGTCCAGT |
| 4222 | Table 3A | Hs.133175 | AI051673 | 3307207 | oy77g06.x1 cDNA, 3' end /clone=IMAGE:1671898 /clone_end=3' | -1 | TTGTGATTGTAAATCATGTATGTACAA ATGCCATGAAAATTAAGCCAGT |
| 4223 | Table 3A | Hs.203041 | AI271437 | 3890604 | 602417270F1 cDNA, 5' end /clone=IMAGE:4536737 /clone_end=5' | -1 | TTTCCTTATGCACCTTCCAGTCTTTG GCAGGACATGATTTATGGACAGT |
| 4224 | Table 3A | Hs.56205 | AA846378 | 2932518 | insulin induced gene 1 (INSIG1), mRNA /cds=(414,1247) | -1 | TGCACTCTACCAGATTTGAACATCTA GTGAGGTTACATTCATACTAAGT |
| 4225 | Table 3A | NA | AA873734 | 2969856 | Vanin 2 | -1 | TCAACTGCAGGGAATCTCCTAGGAAG CCGATAAATCTGGCAATTGGAAGT |
| 4226 | Table 3A | NA | AA482019 | 2209697 | cDNA clone IMAGE:746046 3' | -1 | ACCACCAGCTATTTGTAATTCCTTCTT CTAAGGCATAGTGAAAACCTTGCT |
| 4227 | db mining | Hs.182594 | AA806247 | 2875516 | oc21f01.s1 cDNA, 3' end /clone=IMAGE:1341529 | -1 | TGCTTTCTAACTGATTCCTATCCAC CATGTCAGATACTCCTGGGCTGCT |
| 4228 | Table 3A | Hs.210727 | AI075288 | 3401879 | oy69h10.x1 cDNA, 3' end /clone=IMAGE:1671139 /clone_end=3' | -1 | CAGCAATGAGGGGATATTTTGTATGA GCTGGAATATCCAATTGAACAGCT |
| 4229 | Table 3A | Hs.252300 | AI383340 | 4196121 | tc76g05.x1 cDNA, 3' end /clone=IMAGE:2070584 /clone_end=3' | -1 | CCCCCTAAGTTAAAAGCTCTGTCTTT TTGGGGTTTGCCCTATGTAAAGCT |
| 4230 | Table 3A | Hs.191958 | AI347054 | 4084260 | immunoglobulin superfamily receptor translocation associated 2 (IRTA2), mRNA /cds=(158,3091) | -1 | GAAGCCTCTACTCTTGAGTCTCTTTC ATTACTGGGGATGTAATGTTCCCT |
| 4231 | Table 3A | Hs.283410 | AI253134 | 3849663 | 602635144F1 cDNA, 5' end /clone=IMAGE:4780090 /clone_end=5' | -1 | ACACTTGATCTCTTCCTTATTTCTCTC AGAAAACCTGTAGGATTGTGCCT |
| 4232 | Table 3A | Hs.44189 | AI361839 | 4113460 | yz99f01.s1 cDNA, 3' end /clone=IMAGE:291193 /clone_end=3' | -1 | AGTAGATATTTTGCCGGTGTACTTGG AATACCTTTTCAAGCCAAACCCCT |
| 4233 | Table 3A | Hs.148288 | AA908367 | 3047772 | og76c11.s1 cDNA, 3' end /clone=IMAGE:1454228 /clone_end=3' | -1 | AATCCAATCCTGGTATATAGCACCT GGTATTATGGGTACCAAAAACCCCT |
| 4234 | Table 3A | Hs.143534 | AI095189 | 3434165 | 602466053F1 cDNA, 5' end /clone=IMAGE:4594260 /clone_end=5' | -1 | ACTGCTCCAAATATCAACCCCATGTA GGCAGGATGTTTGATCTTGGTACT |
| 4235 | Table 3A | Hs.23349 | AI357493 | 4109114 | nab70e03.x1 cDNA, 3' end /clone=IMAGE:3273292 /clone_end=3' | -1 | TGTTGTTGGATACGTACTTAACTGGT ATGCATCCCATGTCTTTGGGTACT |
| 4236 | db mining | Hs.292235 | AI057035 | 3330824 | oy75b11.x1 cDNA, 3' end /clone=IMAGE:1671645 | -1 | TTAGGATTGCTCAGTTTCATCAAGGT TTGAAGGATAGGCAGGCTCTCACT |
| 4237 | Table 3A | Hs.337986 | AA101212 | 1647866 | Homo sapiens, clone MGC:17431 IMAGE:2984883, mRNA, complete cds /cds=(1336,1494) | -1 | GGCCAGTCTCTGTGTGCTTAAATCCC TTGTCCTTCATTAAGCAAAACT |
| 4238 | Table 3A | Hs.60088 | AA004799 | 1448296 | hypothetical protein MGC11314 (MGC11314), mRNA /cds=(221,673) | -1 | GCATTCGCGGTCACTCCCTCCCTAAT CTGAGCATCACTCAAGCTCTTTAT |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|---|
| 4239 | db mining | Hs.177376 | AA744590 | 2783354 | zb85a06.s1 cDNA, 3' end /clone=IMAGE:310354 /clone_end=3' | -1 | CTGAATGCCAAGAGCTTCAAGAGTGT GTGTAATAAAGCCACACCTTTAT |
| 4240 | Table 3A | Hs.163787 | AA627122 | 2540166 | nq70g02.s1 cDNA, 3' end /clone=IMAGE:1157714 /clone_end=3' | -1 | CCCGAGGAGGAAGACGAATCGTTAA ACATCTGAAAGGGTCAGGTGAGTAT |
| 4241 | Table 3A | Hs.332992 | AA760848 | 2809778 | nz14f06.s1 cDNA, 3' end /clone=IMAGE:1287779 /clone_end=3' | -1 | CAAACCTTGTTCTGAAGACAATTTCCA AGGTTGTGAGCCATGTACCATAT |
| 4242 | Table 3A | Hs.129572 | AA746320 | 2786306 | ob08f01.s1 cDNA, 3' end /clone=IMAGE:1323097 /clone_end=3' | -1 | TCAGGTTTCGTGTTAAACGCTGTATGT TAACATGACTGGAATTCTGTGAT |
| 4243 | Table 3A | Hs.233383 | AA745714 | 2785700 | RC2-CT0434-310700-013-c08 cDNA | -1 | ATGGAGATCCAGAGACGTTGGTTTTC AAATGGAGCAAAACAGCACTGTGAT |
| 4244 | Table 3A | Hs.156601 | AI146787 | 3674469 | qb83f02.x1 cDNA, 3' end /clone=IMAGE:1706715 /clone_end=3' | -1 | AGCTTTAGGCTGAGGGCATGGAAACT GTTACGCTTTTCTTTTATGTGAT |
| 4245 | Table 3A | Hs.273775 | AA527312 | 2269381 | ng36a08.s1 cDNA, 3' end /clone=IMAGE:936854 /clone_end=3' | -1 | TCACTCCAGAATAGAAATTAGAGTAT AGGTAGGCAGTCCAACCTCTGCAT |
| 4246 | Table 3A | Hs.159316 | AI380278 | 4190131 | cDNA: FLJ21572 fis, clone COL06651 /cds=UNKNOWN | -1 | TCAGATGCCACACTTATGAGACCCCTC ATCCTTCTGCTCACTCTCTTCCAT |
| 4247 | Table 3A | Hs.159424 | AI380255 | 4190108 | 602589478F1 cDNA, 5' end /clone=IMAGE:4723722 /clone_end=5' | -1 | CCCTGCCCTTTACCTCTCTACTTGTAG TGTTCTTTCAGAGCCTGCTCCCAT |
| 4248 | Table 3A | Hs.114931 | AA702108 | 2705221 | zi85e01.s1 cDNA, 3' end /clone=IMAGE:447576 /clone_end=3' | -1 | CAAAACAAGATGTGCCAGGGCCTGG GGGATGGGATAATTTAGAGAGAAT |
| 4249 | Table 3A | Hs.179779 | AI004582 | 3214092 | ribosomal protein L37 (RPL37), mRNA /cds=(28,321) | -1 | ACCCAAGAGGGCAGCAGTTGTGTCA TCCAGTTCATCTTAAGAAATTTCAAT |
| 4250 | Table 3A | Hs.100555 | AI352690 | 4089896 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 18 (Myc-regulated) (DDX18), mRNA /cds=(71,2083) | -1 | GGGGTAGGAAGAGGATGGAATTGAG ATGTTTGAGCCTCATTTACATCAAT |
| 4251 | Table 3A | Hs.157213 | AI351144 | 4088350 | qt23f10.x1 cDNA, 3' end /clone=IMAGE:1948459 /clone_end=3' | -1 | GCTCTCTGATGCTGGTGGCTGTTCCT CCAGAATGGAAGCATTGATTAAAT |
| 4252 | Table 3A | Hs.77399 | AI337347 | 4074274 | caudal type homeo box transcription factor 2 (CDX2), mRNA /cds=(360,1301) | -1 | GGGGAGAAGTGATATGGTGAAGGGA AGTGGGGAGTATTTGAACACAGTTG |
| 4253 | Table 3A | Hs.128630 | AI222805 | 3805008 | qp39c07.x1 cDNA, 3' end /clone=IMAGE:1925388 /clone_end=3' | -1 | CACCATGCCTCACTTTAGCGCAGTG TGATCCTACACAAATTGCCCTGTG |
| 4254 | Table 3A | Hs.270341 | AI270476 | 3889643 | 602307338F1 cDNA, 5' end /clone=IMAGE:4398848 /clone_end=5' | -1 | TATGGTTTTTAGGCTATGCAGATATTC TGTTGGTTTTGAGACAGCTCTG |
| 4255 | Table 3A | Hs.190229 | AA582958 | 2360318 | nn80d08.s1 cDNA, 3' end /clone=IMAGE:1090191 /clone_end=3' | -1 | CCTTCCTTTCTAAGGCATAAGTGCGA CGTTCGCTGCTGTGCGTGGAACTG |
| 4256 | Table 3A | Hs.170333 | AI373163 | 4153029 | qz13a07.x1 cDNA, 3' end /clone=IMAGE:2021364 /clone_end=3' | -1 | GAGAGGAAGGCAGACAGGCAGCCAT TTTAAGAGAGAAGAGCCAGACAATG |
| 4257 | Table 3A | Hs.158289 | AI199223 | 3751829 | qi47c06.x1 cDNA, 3' end /clone=IMAGE:1859626 /clone_end=3' | -1 | GTTATCAAAGGTGGAATCGGAAACAC CAGGCTCCTAGTGCCACGGAATG |
| 4258 | Table 3A | Hs.29282 | AA748714 | 2788672 | mitogen-activated protein kinase kinase kinase 3 (MAP3K3), mRNA /cds=(83,1963) | -1 | AAATGTGCCTATTGCTAGAGCTCCTC CCTCTCAACACCCAGTTTCTTGG |
| 4259 | Table 3A | Hs.230752 | AI025427 | 3241040 | ow27g06.s1 cDNA, 3' end /clone=IMAGE:1648090 /clone_end=3' | -1 | CAATCGCTTATCTCTACAGAGAGAA GTGGAATAATCTTTTCAAGGGGG |
| 4260 | Table 3A | Hs.131580 | AI024984 | 3240597 | ov39d11.x1 cDNA, 3' end /clone=IMAGE:1639701 /clone_end=3' | -1 | CTATGGAAGGCAGTTGGTGGGCAAA AGTCCGGTTTTACGCTTTGAGGGG |
| 4261 | Table 3A | Hs.98306 | AA418743 | 2080544 | mRNA for KIAA1862 protein, partial cds /cds=(0,1874) | -1 | GTCTGATCCTTAGACCGTCTCATCAC AGCAACCTAACTGCAGAGCAGGG |
| 4262 | Table 3A | Hs.337307 | AA719537 | 2732636 | zh40g12.s1 cDNA, 3' end /clone=IMAGE:414598 /clone_end=3' | -1 | AATGGTAAGAAATGCCCTGTGTGGGT GGCCCTCAGTCCCACTGTCAGGG |
| 4263 | Table 3A | NA | AA136584 | 1697794 | fetal retina 937202 cDNA clone IMAGE:565899 3' | -1 | AACATATCCAGGGAGGACAACTCTG GGCTGGACAATGTATCCACAAGGG |
| 4264 | Table 3A | Hs.339990 | AI263141 | 3871344 | qw90c01.x1 cDNA, 3' end /clone=IMAGE:1998336 /clone_end=3' | -1 | GCCCATGGTCTCTAGAATTCTTCCCT TAAAAATTTTGAATAGGGGCGG |
| 4265 | Table 3A | Hs.309122 | AI380449 | 4190302 | tg02f12.x1 cDNA, 3' end /clone=IMAGE:2107631 /clone_end=3' | -1 | GCCAACTGCTTAGAAGCCCAACACAA CCCCTCTGGTCTCTTGAATAAAGG |
| 4266 | Table 3A | Hs.290535 | AA719103 | 2732202 | zh33d10.s1 cDNA, 3' end /clone=IMAGE:413875 /clone_end=3' | -1 | GAGCCCTTAAATTAATGTATCTCCT CTAAAGTGTGATTTAATGGCTGCG |
| 4267 | Table 3A | Hs.188886 | AA576947 | 2354421 | nm82b04.s1 cDNA, 3' end /clone=IMAGE:1074703 /clone_end=3' | -1 | CTTTTGCTGGAGACTCATCGCTTTGG GAAGTGCAATTGCTTCGTCGTCGG |
| 4268 | Table 3A | Hs.130232 | AI089359 | 3428418 | qb05h03.x1 cDNA, 3' end /clone=IMAGE:1695413 /clone_end=3' | -1 | CCCAGTTCACAGTAGAGAGGTGGAG CTTAGTACTTCTGCTGCCATTAG |
| 4269 | Table 3A | Hs.44628 | AI384128 | 4196909 | EST389740 cDNA | -1 | CTGGGCTGTAGTACTGCTGGGTCA CTGTTGCTATAAATGGTCACTGGAG |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|---|----|--|
| 4270 | db mining | Hs.164284 | AI434146 | 4294137 | ti36g07.x1 cDNA, 3' end /clone=IMAGE:2132604 /clone_end=3' | -1 | CTTTAGATGTCCACGTCCTTCAAG CACATGAAAGAGCTCACACTGGAG |
| 4271 | Table 3A | Hs.173720 | AA534537 | 2278790 | nf80h10.s1 cDNA, 3' end /clone=IMAGE:926275 /clone_end=3' | -1 | GACTCTGGAACCTCGAGCGTGTGGCT GCTGCGCCGACAGCTGAATCTAGAG |
| 4272 | Table 3A | Hs.120891 | AA677952 | 2658474 | zi14a06.s1 cDNA, 3' end /clone=IMAGE:430738 /clone_end=3' | -1 | CCTTAGAGATCGTGACCTTCTCTGCT TGCTTCCCTGGTGGGCTCTTTCAG |
| 4273 | Table 3A | Hs.142838 | AI299573 | 3959158 | nucleolar protein interacting with the FHA domain of pKi-67 (NIFK), mRNA /cds=(54,935) | -1 | AGAGTGAGAAGGCAGTTCAGTTTTA GCACAGATTTGTTTATGTGTTTCAG |
| 4274 | Table 3A | Hs.8724 | AI298509 | 3958245 | serine threonine protein kinase (NDR), mRNA /cds=(595,1992) | -1 | TCTCAAGAGAGAAGCCACAGCAGA GAGACCCAATCCGCCTAAGTTGCAG |
| 4275 | db mining | Hs.204873 | AI086035 | 3424458 | oy70h04.x1 cDNA, 3' end /clone=IMAGE:1671223 /clone_end=3' | -1 | AGGTTTGGGGAGGGGTCCCAGTCTG CGATCCTTTCTCCTCTTCGTGCAG |
| 4276 | Table 3A | Hs.323950 | AA916990 | 3056382 | zinc finger protein 6 (CMPX1) (ZNF6), mRNA /cds=(1265,3361) | -1 | CCTCAGCTTCCAACCTCTGATTCCAGG ACAGGATGGAAAACCTTTGGACAG |
| 4277 | Table 3A | Hs.144114 | AI074020 | 3400664 | oy66g06.x1 cDNA, 3' end /clone=IMAGE:1670842 /clone_end=3' | -1 | AATCCCTTGTTACCATGTATACAAATG AGACAAGTGAGCTTGACATTCAAG |
| 4278 | Table 3A | Hs.235042 | AI076222 | 3405400 | oy65b09.x1 cDNA, 3' end /clone=IMAGE:1670681 /clone_end=3' | -1 | GCTACAGCCCGGAACACAAAAGAAG ACACCCATGCAAATACCATTAAG |
| 4279 | Table 3A | Hs.158975 | AI380388 | 4190241 | tf96a03.x1 cDNA, 3' end /clone=IMAGE:2107084 /clone_end=3' | -1 | ATTAACCCCTTTATTGCCCTAGCCAGT GGGGTGGGAGGGAGGAGATTGTTTC |
| 4280 | Table 3A | NA | AI361642 | 4113263 | qy86d04.x1 cDNA, 3' end /clone=IMAGE:2018887 | -1 | GTTATCCTTAGGCCAGGTCTCCACCC TTTGAGCCGGACAAAACAGAGTCT |
| 4281 | Table 3A | Hs.34549 | AI123826 | 3539592 | 602620663F1 cDNA, 5' end /clone=IMAGE:4746422 /clone_end=5' | -1 | TGCTGCTACAGTTGCAAAACACTGGA GCTAGAGAAAATAAAGTACTGATC |
| 4282 | Table 3A | Hs.185062 | AI085568 | 3423991 | oy68b05.x1 cDNA, 3' end /clone=IMAGE:1670961 /clone_end=3' | -1 | CGAGAGTCTTGCTGAGCCAGGACTT GAGTGCCTCGAAGTTTCAATGATC |
| 4283 | Table 3A | Hs.180201 | AA516406 | 2253768 | hypothetical protein FLJ20671 (FLJ20671), mRNA /cds=(72,494) | -1 | ATCAGGAGAGGGAGATAATTAGTTGC TTCTCTCTCACACTGTTTGAATC |
| 4284 | Table 3A | Hs.54452 | AI041828 | 3281022 | zinc finger protein, subfamily 1A, 1 (Ikaros) (ZNFN1A1), mRNA /cds=(168,1727) | -1 | TTGCCCTTTCTCTCACTGCCTTTTAT AGCCAATATCAATGTCTCTTTGC |
| 4285 | db mining | Hs.206654 | AA705316 | 2715234 | EST368531 cDNA | -1 | ATCCCTATTGCCAGACACATCATTCT CTCCATCCAGAAAGCCAACTTTGC |
| 4286 | Table 3A | Hs.147040 | AI187423 | 3738061 | qf31d04.x1 cDNA, 3' end /clone=IMAGE:1751623 /clone_end=3' | -1 | CTCTCTTCATCTTCTGATTGGGATTGT GTCCAGTCTCTGCTTCTTCTGTC |
| 4287 | Table 3A | Hs.105230 | AA489227 | 2218829 | aa57f07.s1 cDNA, 3' end /clone=IMAGE:825061 /clone_end=3' | -1 | GAGGGTTCTAGCAACTTAATCCCAT AGCATGTTAGCTGAAGACTACTGC |
| 4288 | db mining | Hs.309108 | AI378046 | 4187899 | te67h12.x1 cDNA, 3' end /clone=IMAGE:2091815 /clone_end=3' | -1 | GTCCCAAGGGTCAGTATATTGGAGGA AAGTAAAGGAGTGAAATCAGACTGC |
| 4289 | Table 3A | Hs.209203 | AI343473 | 4080679 | tb97a08.x1 cDNA, 3' end /clone=IMAGE:2062262 /clone_end=3' | -1 | CTGGAATTACTAATGTGGAGGTGATC TGAGAACTGGGAACAAAGTAGGGC |
| 4290 | Table 3A | Hs.158966 | AI380236 | 4190089 | tf94b10.x1 cDNA, 3' end /clone=IMAGE:2106907 /clone_end=3' | -1 | TCCAGGGACTGACAAGAGTGAGTGG TGTC AACCTAAAGAGAACTCAGGC |
| 4291 | Table 3A | Hs.50477 | AA923567 | 3070876 | Rab27a mRNA, complete cds /cds=(245,910) | -1 | CAGAACTCCATAGACAGCCTCACTTT GTGCTCGGGGGCCTGTCCCAAGGC |
| 4292 | Table 3A | Hs.133230 | AA984890 | 3163415 | Homo sapiens, ribosomal protein S15, clone MGC:2295 IMAGE:3507983, mRNA, complete cds /cds=(14,451) | -1 | GCACTTCTCCCGGTTCACTCCCTCTCA AGTAATGGCTCAGCTAATAAAGGC |
| 4293 | Table 3A | Hs.165051 | AI248204 | 3843601 | qh64h11.x1 cDNA, 3' end /clone=IMAGE:1849509 /clone_end=3' | -1 | TCCATCTCCTTTCTACTGTAGCGGAG ACTACAAGTCCCAGGATGCCCGC |
| 4294 | Table 3A | NA | AA683244 | 2669135 | schizo brain S11 cDNA clone IMAGE:971252 3' | -1 | CCACATCTTGTGTGCCACATCCTGC TGGGTGAAATTTGTGTTGAAGTAGC |
| 4295 | Table 3A | NA | AA826572 | 2898398 | cDNA clone IMAGE:1416447 3' | -1 | TGACTGTCTTGGTAATTTTCTTCTTGT TTTTACTTCTGGAACTGGGAGC |
| 4296 | Table 3A | Hs.11637 | AI275205 | 3897479 | 602388093F1 cDNA, 5' end /clone=IMAGE:4517086 /clone_end=5' | -1 | TGACTTTCAGGAATGTCAGCATTGAC CTCTCCTTGCCACTGTTACTCAGC |
| 4297 | Table 3A | Hs.21812 | AI131018 | 3601034 | AL562895 cDNA /clone=CS0DC021YO20-(3-prime) | -1 | AAGTTTGTGCAGCACATTCTGAGTG TACGATATTGACCTGTAGCCCAAGC |
| 4298 | Table 3A | Hs.21812 | AI888714 | 5593878 | AL562895 cDNA /clone=CS0DC021YO20-(3-prime) | -1 | AAGTTTGTGCAGCACATTCTGAGTG TACGATATTGACCTGTAGCCCAAGC |
| 4299 | Table 3A | Hs.59459 | AA889552 | 3016431 | ak20d12.s1 cDNA, 3' end /clone=IMAGE:1406519 /clone_end=3' | -1 | ACCAGACTTCAGGAAGAATAAAGGTC GCCAACTCAATAAAACCAACAGC |
| 4300 | Table 3A | Hs.230805 | AI087055 | 3425478 | oy70c09.x1 cDNA, 3' end /clone=IMAGE:1671184 /clone_end=3' | -1 | ACTTGCCACATAAACAGTTCCATCAT AAAAACTCTTCCCTTCTTGTTC |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|---|----|--|
| 4301 | Table 3A | Hs.125608 | AI380443 | 4190296 | tg02f04.x1 cDNA, 3' end /clone=IMAGE:2107615 /clone_end=3' | -1 | GCTTCCTTGAACCCAGAAATCCA CTCAAATTTGGGGATTGTCAATTCC |
| 4302 | Table 3A | Hs.229385 | AI354231 | 4094384 | qv12c04.x1 cDNA, 3' end /clone=IMAGE:1981350 /clone_end=3' | -1 | GGGGGTGATGGGTTAATTAATAAGT CCATTCTGGGATTTGAGGGGGCC |
| 4303 | Table 3A | Hs.330928 | AI371227 | 4149980 | 601659234R1 cDNA, 3' end /clone=IMAGE:3895641 /clone_end=3' | -1 | ATGCCCTCGTCTAGAAATTAATTC CCTAAAAATCTTTGAAATAGGGCC |
| 4304 | db mining | Hs.141153 | AI139639 | 3645611 | tx43b11.x1 cDNA, 3' end /clone=IMAGE:2272317 /clone_end=3' | -1 | TCAAACCTAAGACCAGGGTTGAAAACT ATGGCCAGGGACCACTTCAGCC |
| 4305 | Table 3A | Hs.134342 | AI363001 | 4114622 | mRNA for LanC-like protein 2 (lancl2 gene) /cds=(186,1538) | -1 | GACGCGCACACACCTTGAGTGACAG CGACCTCTTCTCTACAGTTTTTCCC |
| 4306 | Table 3A | Hs.226755 | AA909983 | 3049273 | RC1-UT0033-250800-022-h02 cDNA | -1 | ATCCAAGCTTTAATTCTGCCATCTCA GAATGCTGATAAACCAATTTCTCCC |
| 4307 | Table 3A | Hs.158894 | AI378457 | 4188310 | tc79d10.x1 cDNA, 3' end /clone=IMAGE:2072371 /clone_end=3' | -1 | TACTTCATTGCTATTGTAACCAAAAA TAAATTTGAAGCCCTGCCCC |
| 4308 | Table 3A | Hs.127327 | AI084064 | 3422487 | EST390862 cDNA | -1 | CTTCATCACTCAGGAACAGAAAAGG CTTCAGAAGGAGCGCCATGCCCC |
| 4309 | Table 3A | Hs.295945 | AW081320 | 6036472 | xc30f12.x1 cDNA, 3' end /clone=IMAGE:2585807 /clone_end=3' | -1 | AGAACCCTGATTATATAAATTTAGAC CAAAAAGGAAGGAATCGAACCCCC |
| 4310 | Table 3A | Hs.143410 | AA825245 | 2898544 | oe59g09.s1 cDNA, 3' end /clone=IMAGE:1415968 /clone_end=3' | -1 | TTTTCTATTTTCATCTGCTATTTTAC TGCAGAGCGCACCTCCCGGACCC |
| 4311 | db mining | Hs.228874 | AI356505 | 4108126 | qz22b04.x1 cDNA, 3' end /clone=IMAGE:2027599 /clone_end=3' | -1 | AGACTGAAGGGGTTGAAGACCCGT AGACGCTCCTTTCTCTTTTAGACC |
| 4312 | Table 3A | NA | AI364936 | 4124625 | qz23c12.x1 cDNA, 3' end /clone=IMAGE:2027734 | -1 | CTCTGCGGCCCTAGAGTTAATCCCAT CAGCCGAGGTGAGGCACCTGTTAC |
| 4313 | Table 3A | Hs.125892 | AI378032 | 4187885 | te67g08.x1 cDNA, 3' end /clone=IMAGE:2091806 /clone_end=3' | -1 | CCAATTCGCGAGTACAGAGCATTACG CAGGTAGTGGTGACCTGGGTGAC |
| 4314 | Table 3A | Hs.158943 | AI379953 | 4189806 | tc81a07.x1 cDNA, 3' end /clone=IMAGE:2072532 /clone_end=3' | -1 | GGCTCCAGCCACCGGCAGCTCTGAA AGAGTTTGAAGAATTTATTGTTAC |
| 4315 | Table 3A | Hs.108124 | AI362793 | 4114414 | cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN | -1 | GCTCGCTACCAGAAATCCTACCGATA AGCCCATCGTGACTCAAACTCAC |
| 4316 | db mining | Hs.129332 | AA992299 | 3179055 | ot53b06.s1 cDNA, 3' end /clone=IMAGE:1620467 /clone_end=3' | -1 | CACTGGAACACAACCCAGCCATGAAA AGGAAGAAGCTCTGACTCAGGCAC |
| 4317 | Table 3A | NA | AI318342 | 4034222 | ta73c09.x1 3' end /clone=IMAGE:2049712 | -1 | CATCTCATGCGTAGCACTGATCAATG TGCCCCAGGGTGTGTATTGCGCCAC |
| 4318 | Table 3A | Hs.157447 | AI028478 | 3245787 | EST388739 cDNA | -1 | CAATCAGAGCGCGAGTTACAAGCGC GGTGAGTGGGGAAGCGAATGAAAC |
| 4319 | Table 3A | Hs.205175 | AA885473 | 2994550 | am10c12.s1 cDNA, 3' end /clone=IMAGE:1466422 /clone_end=3' | -1 | GACATTGCACATTTTTGAACCTGTCT ACAGCAGCCTGGGTGGTGCACAAC |
| 4320 | Table 3A | NA | AI370412 | 4149165 | cDNA clone IMAGE:1987587 3' | -1 | ACACTGGCAGAGTCCAGAAAAGCAG CAGAAGAAAAATTACAGCAAAAAAC |
| 4321 | Table 3A | Hs.132594 | AI346336 | 4083542 | qp50b04.x1 cDNA, 3' end /clone=IMAGE:1926415 /clone_end=3' | -1 | TTTAACGTGCTTCTGAGACGCCACC ACCGAAAGGCACCTTTAGCGGTTA |
| 4322 | Table 3A | Hs.50252 | AA984245 | 3162770 | mitochondrial ribosomal protein L32 (MRPL32), mRNA /cds=(46,612) | -1 | TCAGCCAACCTGAATCTGGTATCTTT ACTTAAACACAGCAGTTGTAGTTA |
| 4323 | Table 3A | NA | AA744774 | 2783538 | cDNA clone IMAGE:1283731 3' | -1 | AAAAGGAGACGATGTCAGGCAAAACA CTCCTTACCCTGCCATTTCTAGTTA |
| 4324 | db mining | Hs.15200 | AW190635 | 6465115 | EST379783 cDNA | -1 | TCACAATCAGTCTCAGATTCAGCA GCAGAGAGTGAATTGTATGTTGTA |
| 4325 | Table 3A | Hs.276766 | AI380791 | 4190644 | tg04b12.x1 cDNA, 3' end /clone=IMAGE:2107775 /clone_end=3' | -1 | TAAAGACAATGCTATTTAAGTGCACA GTTCAGGGGCGCTTGTGGCTCTA |
| 4326 | Table 3A | NA | AA573427 | 2347955 | cDNA clone IMAGE:1028913 3' | -1 | GAAGACCAAGTCTACGCGCTGCAAGCT CTCAGACCGGGGAACATCCACTCTA |
| 4327 | Table 3A | Hs.127557 | AA953396 | 3117543 | on63h10.s1 cDNA, 3' end /clone=IMAGE:1561411 /clone_end=3' | -1 | CTGAAGAGACAGAAAGGGAGACACC AAAACCTTAAATGGCAGTTATTCCTA |
| 4328 | Table 3A | Hs.124391 | AA831838 | 2904937 | oc85h06.s1 cDNA, 3' end /clone=IMAGE:1356539 /clone_end=3' | -1 | GCCGCCCCCATGAAGCCCTTTCTTAC TGTAAGTGCTCAAGAACAAAGATA |
| 4329 | Table 3A | Hs.210943 | AI823511 | 5444182 | wh54h10.x1 cDNA, 3' end /clone=IMAGE:2384611 /clone_end=3' | -1 | GCTAGCAGCACTCTGCCTTGTTCCTT TGGAGACAAATTGTTATCATCAATA |
| 4330 | Table 3A | NA | AA757952 | 2805815 | zg49e07.s1 3' end /clone=IMAGE:396708 / | -1 | ATTGGGAATATAGATCATCAACAGAC ACAGCCCTGGAGCGCATAAATTTGA |
| 4331 | Table 3A | Hs.10056 | AA576946 | 2354420 | hypothetical protein FLJ14621 (FLJ14621), mRNA /cds=(525,1307) | -1 | ACTAACGTATTTTCATCATGGAAGGTC CTGTGGTGATGGTTTCCCTGGGA |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|---|
| 4332 | Table 3A | Hs.132156 | AI042377 | 3281571 | ox62c03.x1 cDNA, 3' end /clone=IMAGE:1660900 /clone_end=3' | -1 | AAGTAATAGCTCCCTGTTTGTGCCTT GTAGGGCTAGGGATGTTTAAAGGA |
| 4333 | Table 3A | Hs.173125 | AI052431 | 3308422 | peptidylprolyl isomerase F (cyclophilin F) (PPIF), mRNA /cds=(83,706) | -1 | AGCTCCTCCCCTTAGTGACCCCAAGT CTGTTTCCCTCAGCTGCATAAGGA |
| 4334 | Table 3A | Hs.122983 | AI081246 | 3418038 | oy67b06.x1 cDNA, 3' end /clone=IMAGE:1670867 /clone_end=3' | -1 | CCCTCAAATCTCCCAATCTACTCCAG GGAAAAGACACTTCAAGTGAGAGA |
| 4335 | db mining | Hs.85923 | AA194310 | 1784006 | zq04g12.s1 cDNA, 3' end /clone=IMAGE:628774 /clone_end=3' | -1 | ACATGCAAAACAGTGACTTACTTAGTG CTTCTGAAAAATTTCTGAGTCAGA |
| 4336 | Table 3A | Hs.118659 | AI052447 | 3308438 | oz07g04.x1 cDNA, 3' end /clone=IMAGE:1674678 /clone_end=3' | -1 | AATGCCCATTTGGTAAGTCAACATTGT TTTCCCTGAAAGTCTGAGACAGA |
| 4337 | Table 3A | Hs.231154 | AA761571 | 2818898 | oa30h07.s1 cDNA, 3' end /clone=IMAGE:1306525 /clone_end=3' | -1 | CCATGTTTGCTGCTGCTGTTGAGTTT CTGTGCTTTGGGAGTATAATAAGA |
| 4338 | Table 3A | Hs.57787 | AW029440 | 5888196 | 602381381F1 cDNA, 5' end /clone=IMAGE:4498845 /clone_end=5' | -1 | TGTGTTTGGTTGGGTGTAATGAGGAA AATACCTGATAAAATGTCTGAAGA |
| 4339 | Table 3A | Hs.57787 | AA588755 | 2402486 | 602381381F1 cDNA, 5' end /clone=IMAGE:4498845 /clone_end=5' | -1 | TGGATAAGTGAAGACAGTAATAACAT TGAAGCAGTGAACCAAGTGGAAGA |
| 4340 | Table 3A | NA | AA974991 | 3150783 | Soares_NFL_T_GBC_S1 cDNA clone IMAGE:1560953 3' | -1 | AGCACAAAAATGTTGAAGTATTAGGC CCAAGCTCCATGTTTGGTTAGTCA |
| 4341 | Table 3A | Hs.127514 | AI028267 | 3245576 | ow01d06.x1 cDNA, 3' end /clone=IMAGE:1645547 /clone_end=3' | -1 | CGTTTAAACAATAATAAGGTGACTGC TTCATCTAAGGAATCCGAGCCGCA |
| 4342 | Table 3A | Hs.88130 | AI184553 | 3735191 | qd60a05.x1 cDNA, 3' end /clone=IMAGE:1733840 /clone_end=3' | -1 | GGGCATTCCACCGAAATTTCTGGGGA AATTTAGTAGCTTCATTTTAGCA |
| 4343 | Table 3A | Hs.158965 | AI380220 | 4190073 | tf94a04.x1 cDNA, 3' end /clone=IMAGE:2106894 /clone_end=3' | -1 | TCCATGTTCTGTGCAAGAAGGAGACA CATTTTCAGTTGAGGTTCCAGCA |
| 4344 | Table 3A | Hs.235823 | AI379474 | 4189327 | 602631538F1 cDNA, 5' end /clone=IMAGE:4776728 /clone_end=5' | -1 | AGCTCAACACTGTGGTAGGAAAATAG CCACTAGAAAGAAAATAAAAGCA |
| 4345 | db mining | Hs.229560 | AI373169 | 4153035 | qz13b11.x1 cDNA, 3' end /clone=IMAGE:2021373 /clone_end=3' | -1 | GCATCTCCAGGGTTTAGCATCAGGAC AGAGGATTAAGTAAATCTTTCCA |
| 4346 | Table 3A | Hs.146627 | AI141004 | 3648461 | oy68f02.x1 cDNA, 3' end /clone=IMAGE:1671003 /clone_end=3' | -1 | GAGACTACAGAGCCTTAGCCCCCTTA AAGCCCTTAAAGTTACTACTTCCA |
| 4347 | Table 3A | NA | AA431959 | 2115667 | cDNA clone IMAGE:782188 3' | -1 | AGAGCAAGTCTCAGAAATAATGCTGT ATCTACACTGTCATGTTTGGCA |
| 4348 | db mining | Hs.56156 | AA257976 | 1894471 | 601463367F1 cDNA, 5' end /clone=IMAGE:3866512 /clone_end=5' | -1 | TGTTTCTGTGTTTGTGAATGAGCACC TGGATATGTCAATTAATGCCCCA |
| 4349 | Table 3A | Hs.264298 | AI380111 | 4189964 | tf98a11.x1 cDNA, 3' end /clone=IMAGE:2107292 /clone_end=3' | -1 | GCAAGACTGTTTCAGTATTATGTTAGC ATTGATATAAAAAGAAGCAGACCA |
| 4350 | Table 3A | Hs.40411 | AI266255 | 3884413 | qx69f01.x1 cDNA, 3' end /clone=IMAGE:2006617 /clone_end=3' | -1 | AATGTTCCCAAAGGCCAAATTTGTTG CCAGGTTTTATACGCAGGTCACCA |
| 4351 | Table 3A | Hs.90753 | AI223400 | 3805603 | Tat-interacting protein (30kD) (TIP30), mRNA /cds=(98,826) | -1 | TGCCTATTGTGATTATCGCTATCACTA CATCCCCTGACTAAGGGAAACCA |
| 4352 | Table 3A | Hs.192427 | AI380016 | 4189869 | 602296277F1 cDNA, 5' end /clone=IMAGE:4390770 /clone_end=5' | -1 | ACAAAATTCAGTGCAGGTCGGTGAA TGATAGAATGCATTTTAAATCACA |
| 4353 | Table 3A | NA | AA524720 | 2265648 | cDNA clone IMAGE:937468 3' | -1 | GGACGGTTGGCTGAATGGCAACAGT GATGGAATATTTATATTTAGCCACA |
| 4354 | Table 3A | Hs.92909 | AA187234 | 1773460 | NREBP mRNA, complete cds /cds=(49,7209) | -1 | ACATTGCACATTTAATAGCTGCACCA GACACTAAGAGTTCTCTCACACA |
| 4355 | Table 3A | Hs.158877 | AI378113 | 4187966 | tc80c12.x1 cDNA, 3' end /clone=IMAGE:2072470 /clone_end=3' | -1 | CGCTTGCTCTGTGAGTAGCTCGTCAC CTGAGGCCTTGCTGTAATATTAA |
| 4356 | Table 3A | Hs.314941 | AI039890 | 3279084 | 602381893F1 cDNA, 5' end /clone=IMAGE:4499447 /clone_end=5' | -1 | TGGAGCAAACCACAGTTTCATGCCCA TCGTCTAGAAATTAATCCCTCAA |
| 4357 | Table 3A | Hs.157813 | AI361761 | 4113382 | qz19a07.x1 cDNA, 3' end /clone=IMAGE:2021940 /clone_end=3' | -1 | GGGACAACACAGTGGATTTGAAATCT GAAGGGCATTGGTGGTACTGGAA |
| 4358 | Table 3A | Hs.205079 | AA742400 | 2784400 | EST388750 cDNA | -1 | ACCTCCATATCTTCTCGTACTTGTTC TGCTGGTCTCTAGCTCTCCGAA |
| 4359 | Table 3A | Hs.87908 | AI381586 | 4194367 | Snf2-related CBP activator protein (SRCAP), mRNA /cds=(210,9125) | -1 | CGAGGATGGTTTCTGATAGCTTTTCA AACACCTTTGCCATCTCTCGCAA |
| 4360 | Table 3A | Hs.208854 | AI766620 | 5233129 | nab69e11.x1 cDNA, 3' end /clone=IMAGE:3272949 /clone_end=3' | -1 | ACTCCTGACAGCTCATCTGCAAAAT TAAAATCCAAAATTAAGTCGCAA |
| 4361 | Table 3A | Hs.157556 | AI356405 | 4108026 | qz26g04.x1 cDNA, 3' end /clone=IMAGE:2028054 /clone_end=3' | -1 | GCTGGATCTCTGCCTAAAGTCACGGT AGGATGAGAAGTAGAAACGAGCAA |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|----------|--|----|---|
| 4362 | Table 3A | Hs.182594 | AA806222 | 2874997 | wd43h11.x1 cDNA, 3' end /clone=IMAGE:2330949 /clone_end=3' | -1 | TCAGACCATAGGTGGGTGTTGTTTCT TTTAAGTGTGTGTACTGTGTCCAA |
| 4363 | Table 3A | Hs.164168 | AA806766 | 2880855 | ob58h11.s1 cDNA, 3' end /clone=IMAGE:1335621 /clone_end=3' | -1 | TCATCTATGTAGCTTAATCTCATCGAC GTTTCGGTTCATTTCTGCACAA |
| 4364 | Table 3A | Hs.291129 | AA581115 | 2358887 | oe10d02.s1 cDNA /clone=IMAGE:1385475 | -1 | TTCCTTTTCCGCTAATCAAGAGTCCA GGGAGGTGGGAACAGCCTCAACAA |
| 4365 | Table 3A | Hs.33757 | AI114652 | 6359997 | HA1247 cDNA | -1 | CCGGCAGCTGTGTTTAGCCCTCCA GATGGAAGTTTCACCTGAATGTAAA |
| 4366 | Table 3A | Hs.121709 | AA767883 | 2824475 | ai35b09.s1 cDNA, 3' end /clone=1358969 /clone_end=3' | -1 | ACAAAGGAATGAAGCTTTATGACAGG GCACGTGAAATGTTTATAGTGAAA |
| 4367 | Table 3A | NA | AI335004 | 4071931 | tb21e09.x1 cDNA, 3' end /clone=IMAGE:2055016 /clone_end=3' | -1 | ACTAAAGGTCACAACCCATTAAACAAC CATGAAATTGGTGTGGGAAGAAA |
| 4368 | Table 3A | Hs.157815 | AI361849 | 4113470 | qz19h11.x1 cDNA, 3' end /clone=IMAGE:2022021 /clone_end=3' | -1 | TGCTCAGGAAACAAAAAGGATGTCT GCATGGAGGACAAAAAGGCACAAA |
| 4369 | Table 3A | Hs.98903 | AA913840 | 3053232 | 602680377F1 cDNA, 5' end /clone=IMAGE:4813147 /clone_end=5' | -1 | TGAGAACC CGCAGCCCTACCCATCG GCCACGTGACCAGTCTTTTAAAA |
| 4370 | Table 3A | Hs.292276 | AI184710 | 3735348 | qd64a01.x1 cDNA, 3' end /clone=IMAGE:1734216 /clone_end=3' | -1 | GTCTTTGGGTGAGTGTATCATTCTC TTCAAGTCTGGGGCTTGGGAAAA |
| 4371 | Table 3A | Hs.143314 | AI357640 | 4109261 | qy15b06.x1 cDNA, 3' end /clone=IMAGE:2012051 /clone_end=3' | -1 | CTCCACACAGGAGAATCTCGGCGATT TACACCCACAGGCTACGCAGAAAA |
| 4372 | Table 3A | Hs.259084 | AI144328 | 3666137 | hg02g06.x1 cDNA, 3' end /clone=IMAGE:2944474 /clone_end=3' | -1 | GCGCTGCTCCCAAAATCTATCTGCTG TTTAATAGTTTTTACCTTTCAAAA |
| 4373 | db mining | Hs.327454 | AI378123 | 4187976 | tc80e02.x1 cDNA, 3' end /clone=IMAGE:2072474 /clone_end=3' | -1 | GGGTTACAGGGGGTTTTCCCTTTGCC GTTTGGCCCTGGGTTTAATAAAAA |
| 4374 | db mining | Hs.132775 | AI028477 | 3245786 | ti02c07.x1 cDNA, 3' end /clone=IMAGE:2129292 /clone_end=3' | -1 | CCAACTCCTCACAGGCGAGGCTAGC GGGCACACAGGTGCGCCGGGAAGTG G |
| 4375 | db mining | Hs.283392 | AI052781 | 3308772 | oy78h07.x1 cDNA, 3' end /clone=IMAGE:1671997 /clone_end=3' | -1 | CGGCTGAGAGCCCGGTAGGGCCAG GGCCAAGCGCAGGCAGAGGCCGC G |
| 4376 | db mining | Hs.270564 | AI361877 | 4113498 | qz25d07.x1 cDNA, 3' end /clone=IMAGE:2027917 /clone_end=3' | -1 | CTTGGGGTCCAGGGCAGCGGTGC CGGGGACACAGCAGTTCGAGGGTC |
| 4377 | db mining | Hs.110059 | AA82600 | 2898912 | 601763318F1 cDNA, 5' end /clone=IMAGE:4026173 /clone_end=5' | -1 | AGTATGGTAATTAGAAAGCATGTTAG AACATGTGAAAAAGGGGGAAAAA |
| 4378 | Table 3A | NA | AI027844 | 3246543 | cDNA clone IMAGE:1671612 3' | -1 | CATCAGTCTCATCAGCTGAAGTGGC TTCCCAAGGATTAAATAAATAGT |
| 4379 | Table 3A | Hs.229374 | AI380491 | 4190344 | 602851994F1 cDNA, 5' end /clone=IMAGE:4993678 /clone_end=5' | -1 | AGACATTGACTACAGGGAATTTCTA TGATTATATTATTAGAAGTATGA |
| 4380 | Table 3A | Hs.124344 | H12462 | 877282 | MR1-GN0173-071100-009-g10 cDNA | -1 | CCAGTGAAGTGTAGCAACAATGCAG AAGAATCTGCATGTAATAAACTGA |
| 4381 | Table 3A | Hs.144119 | AI090305 | 3429364 | oy81b01.s1 cDNA, 3' end /clone=IMAGE:1672201 /clone_end=3' | -1 | ACTTAAATGCCTTTTAAATTTTGTGCA TGTAATAGTTTAATACCAGTAAA |
| 4382 | Table 3A | Hs.333513 | AI379735 | 4189588 | small inducible cytokine subfamily E, member 1 (endothelial monocyte- activating) (SCYE1), mRNA /cds=(49,987) | -1 | TTTTTAATCTAGCTTCTTTTAAAGA TTATTTGGGTACCTAATAAAGGA |
| 4383 | Table 3A | Hs.135339 | AI051664 | 3307198 | oy77f06.x1 cDNA, 3' end /clone=IMAGE:1671875 /clone_end=3' | -1 | CAAAGCCTCCACAGGAGACCCACC CAGCAGCCAGCCCTACCCAGGAG |
| 4384 | db mining | Hs.2186 | AA182528 | 1766227 | Homo sapiens, eukaryotic translation elongation factor 1 gamma, clone MGC:4501 IMAGE:2964623, mRNA, complete cds /cds=(2278,3231) | 1 | CGAGTGACATTGGCTGACATCACAGT TGTCTGAACCTGTTGTGGCTCTAT |
| 4385 | db mining | Hs.101370 | AA287260 | 1932959 | AL583391 cDNA /clone=CS0DL012YA12-(3-prime) | 1 | TGAATTGCTTCAAAACCTCTTCCATCT CAGAAGACCGACAGCCTGGGAAC |
| 4386 | Table 3A | Hs.238514 | AA613460 | 2464498 | xy52e08.x1 cDNA, 3' end /clone=IMAGE:2856806 /clone_end=3' | 1 | GCTGAAGTGGCAATAGAGAGAGTCT GCTAGAAAGACGGAAGTACCATCT |
| 4387 | Table 3A | NA | AA665359 | 2880102 | nt89f05.s1 NCI_CGAP_Pr12 cDNA clone IMAGE:1205697 similar to SV:ATP6_HUMAN P00846 ATP SYNTHASE A CH | 1 | TCTACTGACTATCCTAGAAATCGCTG TCGCCTTAATCCAAGCCTACGTTT |
| 4388 | db mining | Hs.98507 | AB011115 | 3043609 | mRNA for KIAA0543 protein, partial cds /cds=(0,3336) | 1 | GTGTGTGCTTAGCCAAATACAGTAAC TGTGACTGGCCAGGGATGTTCTC |
| 4389 | db mining | Hs.129268 | AB037809 | 7243156 | mRNA for KIAA1388 protein, partial cds /cds=(572,2371) | 1 | GTGAGTCCAATGTATGCTTTAGAAGT AAAGACATTGACCGTCACAGACCA |
| 4390 | Table 3A | Hs.296317 | AB058692 | 14017794 | mRNA for KIAA1789 protein, partial cds /cds=(3466,4899) | 1 | CTCAAGAAAAGACAGAAGAGACAGTG ATTTGGGATGAGTCTACTCTAGGA |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|----------|--|---|--|
| 4391 | Table 3A | Hs.195175 | AF005775 | 2286146 | mRNA for CASH alpha protein /cds=(481,1923) | 1 | ACCCTATGCCCATTTGCTCTGATCTGA AAATTCTTGGAAATTTGTCATGT |
| 4392 | db mining | Hs.62187 | AF022913 | 2558890 | GPI transamidase mRNA, complete cds /cds=(17,1204) | 1 | TTCACAGTCTTCTATTGTTGGACCAC TTACATTGTACCAAAATGTTTTCCCT |
| 4393 | db mining | Hs.248077 | AF044592 | 2852420 | lymphocyte-predominant Hodgkin's disease case #4 immunoglobulin heavy chain gene, variable region | 1 | ATTAAGCCCCCGTAGCCCATCCCGCA AGTTAGATACAGCTATGGTTAAGG |
| 4394 | db mining | Hs.248078 | AF044595 | 2852426 | lymphocyte-predominant Hodgkin's disease case #7 immunoglobulin heavy chain gene, variable region | 1 | TTATATTGTAGTGGTGGTATTTGCTTT CCGCCTGTTGGCTACTTCGACCC |
| 4395 | Table 3A | Hs.25812 | AF058696 | 3098674 | Nijmegen breakage syndrome 1 (nibrin) (NBS1), mRNA /cds=(52,2316) | 1 | TTGTTCTCTGTCATGCCACAAATCCC TTTCTAAGGAAGACTGCCCTACTA |
| 4396 | db mining | Hs.300865 | AF063725 | 3142513 | clone BCSynL38 immunoglobulin lambda light chain variable region mRNA, partial cds /cds=(0,116) | 1 | ACTGAGGACGAGGCTGACTACTACT GTCAGTCTTATGATAGCACCTATCA |
| 4397 | db mining | Hs.249208 | AF063764 | 3135618 | clone LBLG9 immunoglobulin lambda light chain variable region gene, partial cds /cds=(0,289) | 1 | AGATGGAGGATGAAGCTGACTACTAC TGTTACTCAACAGACAGCAGTGGT |
| 4398 | db mining | Hs.293441 | AF067420 | 3201899 | SNC73 protein (SNC73) mRNA, complete cds /cds=(395,1549) | 1 | CATGTCAATGTGTCTGTTGTCATGGC GGAGGTGGACGGCACCTGCTACTG |
| 4399 | db mining | Hs.293441 | AF067420 | 3201899 | SNC73 protein (SNC73) mRNA, complete cds /cds=(395,1549) | 1 | GTCAATGTGTCTGTTGTCATGGCGGA GGTGGACGGCACCTGCTACTGAGC |
| 4400 | db mining | Hs.247721 | AF073705 | 3335589 | clone mcg53-54 immunoglobulin lambda light chain variable region 4a mRNA, partial cds /cds=(0,324) | 1 | TCCAACCTCCAGTTTGAGGATGAGGC TGATTATTACTGTGAGACCTGGGA |
| 4401 | Table 3A | Hs.22380 | AF086431 | 3483776 | AL557896 cDNA /clone=CS0DJ003YD10-(5-prime) | 1 | GACTACAACCTGGCAATCCCACTCCT GGGCTAGGGCTTTTTCTACCTTTT |
| 4402 | db mining | Hs.283882 | AF103295 | 4838126 | clone N97 immunoglobulin heavy chain variable region mRNA, partial cds /cds=(0,377) | 1 | TATTCTGTGCGAGAGTTCCCCCTAA ACATGGCGGAGGCTTCTTCTACAA |
| 4403 | Table 3A | Hs.167827 | AF116909 | 4768835 | clone HH419 unknown mRNA /cds=(189,593) | 1 | TGGCTAGGAGACCTTGGGCAGTACC TACAGTCTTGCTGTTTCTGTTTCAT |
| 4404 | db mining | Hs.149235 | AF119843 | 7770122 | PRO1085 mRNA, complete cds /cds=(539,1582) | 1 | GTGAGCTGAACAAATACATCATTTAA ATCATGTCTGCACCTTTGAGTTGCT |
| 4405 | db mining | Hs.193053 | AF121255 | 6468774 | protein translation initiation factor 2C2 (EIF2C2) mRNA, partial cds /cds=(0,1133) | 1 | CCCGTGTGTTTACAGCATTTCCAGGT CCAGAGAGGTTGGCAGACAAGTGC |
| 4406 | db mining | Hs.247909 | AF127125 | 4337068 | isolate 459 immunoglobulin lambda light chain variable region (IGL) gene, partial cds /cds=(0,265) | 1 | AGCTGTGGGATATAAGTAGTGGTCAT TATGTCTTCGGAGGTGGCACCACT |
| 4407 | db mining | Hs.204588 | AF150138 | 5133574 | AF150138 cDNA /clone=CBCBOG02 | 1 | GCCCTTTGAGAAAGACTTTTGTTCTG AACTGCTCCCTTCTCTTTTAGGGT |
| 4408 | db mining | Hs.205158 | AF150141 | 5133577 | AF150141 cDNA /clone=CBCBQD03 | 1 | GGTCTGGTTCTAGATCAGCCTTTTCA GTCTGCCCTGGCCTGGTCATTAAAT |
| 4409 | db mining | Hs.205438 | AF150373 | 5133809 | AF150373 cDNA /clone=CBMACE02 | 1 | GAAAAACCTGGCTAGAGCAGAGCAC AGGATGTAAGGGGTGGGGAGAGAAC |
| 4410 | db mining | Hs.283929 | AF161340 | 6841093 | HSPC077 mRNA, partial cds /cds=(0,396) | 1 | GGTTATCTGAGCATAACAGGGACAG GGTGGGCCACAGGATACCTCTGAGG |
| 4411 | db mining | Hs.283931 | AF161351 | 6841115 | HSPC088 mRNA, partial cds /cds=(0,305) | 1 | ACAAGCAGGAGCACATCGCTCTTTTA TGAAAGCCCTCAACATTTAACGT |
| 4412 | db mining | Hs.326257 | AF161360 | 6841133 | 602288541T1 cDNA, 3' end /clone=IMAGE:4374059 /clone_end=3' | 1 | CAGGAGACACCATATCTCTGCTTCCA CTATGATGAATCAGTCTCTCTCT |
| 4413 | db mining | Hs.283934 | AF161365 | 6841143 | HSPC102 mRNA, partial cds /cds=(0,285) | 1 | CATCGCACACGAATTTGAATCATCTG CTCTTTTGGAAATCGCCTACACCTG |
| 4414 | db mining | Hs.283935 | AF161370 | 6841153 | HSPC107 mRNA, partial cds /cds=(0,473) | 1 | TGTATGTAGGTGTCTGAGCTTCACAA GCCTTTTATAGTCCATTTCAGCACT |
| 4415 | db mining | Hs.283924 | AF168811 | 5833844 | clone case06H1 immunoglobulin heavy chain variable region gene, partial cds /cds=(0,322) | 1 | CGACGACAACGGTGATATTATTGTG CGAAAGATCGGGCAGATTGACTT |
| 4416 | db mining | Hs.177461 | AF174394 | 5802906 | apoptotic-related protein PCAR mRNA, partial cds /cds=(0,439) | 1 | CGGTGAGACTCAGTGAAAGCCATCA GCAAAACTACAGTAATGCGGCACTA |
| 4417 | Table 3A | Hs.160422 | AF218032 | 10441993 | clone PP902 unknown mRNA /cds=(693,1706) | 1 | AAGTTAAACAAGACTCTGAAAGCCCT AAATCAACTAGTCCGTCGGCTGCA |
| 4418 | db mining | Hs.169992 | AF308298 | 12060846 | serologically defined breast cancer antigen NY-BR-84 mRNA, partial cds /cds=(0,721) | 1 | CTTGAGTGGTCTCTTCTGCTGCTG CTCATTTGTCTTGGGCAACCATTT |
| 4419 | db mining | Hs.170580 | AI475577 | 4328622 | tc92e07.y1 cDNA, 5' end /clone=IMAGE:2073636 /clone_end=5' | 1 | CCCAGGAATATACAGTACTTCTGTAG TGTCAGCCATTACTTAGCAAGGG |
| 4420 | Table 3A | Hs.145668 | AI793342 | 5341058 | fmfc5 cDNA /clone=CR6-21 | 1 | TGCTCTGTCTGTGTTTGCATTGTT TCTGTCTGAGTTAAGAGACTGGCA |
| 4421 | Table 3A | Hs.194382 | AI904071 | 6494458 | ataxia telangiectasia (ATM) gene, complete cds /cds=(795,9965) | 1 | TTCTTTTCTCCGTTAGCCACGCACT ACCTACTCCCGCTTCCGGTTCAAA |
| 4422 | db mining | Hs.333140 | AJ225092 | 3090425 | mRNA for single-chain antibody, complete cds (scFv2) /cds=(0,806) | 1 | AAAACATCATCTCAGAAGAGGATCTGA ATGGGGCCGACACATCACCATTCTG |
| 4423 | db mining | Hs.272356 | AJ275371 | 7573002 | partial IGVH3 gene for immunoglobulin heavy chain V region, case 1, clone 16 /cds=(0,236) | 1 | GATGAACAGTCTGAGAGGCGGAGAC ACGGCCTGTTTAACTGTGCGAGTC |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|----------|--|---|--|
| 4424 | db mining | Hs.272357 | AJ275374 | 7573008 | >partial IGVH3 gene for immunoglobulin heavy chain V region, | 1 | TACTACTTGCCAGGTCCAAGAACGGG |
| 4425 | db mining | Hs.272358 | AJ275383 | 7573027 | partial IGVH3 gene for immunoglobulin heavy chain V region, case 1, | 1 | GCGGGTCCTGTTATCATTATTACA GCTGTGTTTTCTGTGGGTGAAGATA AGGTTTCGGAGCCCGTTTAGATA |
| 4426 | db mining | Hs.272359 | AJ275397 | 7573056 | partial IGVH1 gene for immunoglobulin heavy chain V region, | 1 | CATTTCTGTGCGAGAGTGAAGAGGG GACCCTAGAGGATTTCGTTGTGGGA |
| 4427 | db mining | Hs.272360 | AJ275399 | 7573060 | partial IGVH2 gene for immunoglobulin lambda light chain V region | 1 | GGACTCCAGGCTGAGGACGAGGCTG ATTATTAGTGATGCTCATAAACAAG |
| 4428 | db mining | Hs.272361 | AJ275401 | 7573064 | partial IGVH3 gene for immunoglobulin heavy chain V region | 1 | CTCTTATTGTGCGAGAGACCTCCCG AACTGCCACTGAAGGTGGAGGCTA |
| 4429 | db mining | Hs.272362 | AJ275405 | 7573073 | partial IGVH1 gene for immunoglobulin lambda light chain V region | 1 | CTCCCTGACTATCTCGGCGCTCTAGC CTGAGGACGAGGCTGATTATTATT |
| 4430 | db mining | Hs.272364 | AJ275413 | 7573089 | partial IGVH3 DP29 gene for immunoglobulin heavy chain V region, case 1, cell Mo VII 116 /cds=(0,257) | 1 | AAGAACTCACTGTATCTGCAATGAA CAGCCTGAAAACCGAGGACACGGC |
| 4431 | db mining | Hs.272365 | AJ275453 | 7573172 | partial IGVH4 gene for immunoglobulin heavy chain V region | 1 | CACGGCTGTGTTAACTCTGCGACAT GCGGGGGACTATGGTTCGGGGGAA |
| 4432 | db mining | Hs.50102 | AK002096 | 7023770 | mRNA for rapa-2 (rapa gene) /cds=(836,3742) | 1 | TCAGGGTGATTGAAGGACACATATTG AAGTACCTAGAATGCCAGAAAGTG |
| 4433 | db mining | Hs.270247 | AK022039 | 10433357 | cDNA: FLJ11977 fis, clone HEMBB1001254 /cds=UNKNOWN | 1 | AACAAAACCTGTGTTTATATCAATAA CAATGGCTTGGAGGGGGTATGGA |
| 4434 | db mining | Hs.156110 | AK024974 | 10437403 | cDNA: FLJ21321 fis, clone COL02335, highly similar to HSA010442 mRNA for immunoglobulin kappa light chain /cds=UNKNOWN | 1 | TTTTCCACAGGGGACCTACCCCTATT GCGGTCTCCAGCTCATCTTTCAC |
| 4435 | db mining | Hs.156110 | AK024974 | 10437403 | cDNA: FLJ21321 fis, clone COL02335, highly similar to HSA010442 mRNA for immunoglobulin kappa light chain /cds=UNKNOWN | 1 | TTTTCCACAGGGGACCTACCCCTATT GCGGTCTCCAGCTCATCTTTCAC |
| 4436 | db mining | Hs.156110 | AK024974 | 10437403 | cDNA: FLJ21321 fis, clone COL02335, highly similar to HSA010442 mRNA for immunoglobulin kappa light chain /cds=UNKNOWN | 1 | TTTTCCACAGGGGACCTACCCCTATT GCGGTCTCCAGCTCATCTTTCAC |
| 4437 | db mining | Hs.323884 | AK025398 | 10437905 | cDNA: FLJ21745 fis, clone COLF5038 /cds=UNKNOWN | 1 | TGTGGCTGTACTTAACTTCTCCAAC ATACATCCTGCATTACATGAATGG |
| 4438 | db mining | Hs.1501 | AK025488 | 10438019 | heparan sulfate proteoglycan (HSPG) core protein, 3' end /cds=(0,1193) | 1 | AAGCCTTTGAAGTGCCCTCTGATTCTA TGTAACCTTGTGCACTGGTGT |
| 4439 | db mining | Hs.287697 | AK026199 | 10438971 | cDNA: FLJ22546 fis, clone HSI00290 /cds=UNKNOWN | 1 | GCATTGACCTGGAAGGAGAGAAGAT AGAGAGTGGAGGCTCTGAAGGAGAC |
| 4440 | db mining | Hs.287728 | AK026793 | 10439729 | cDNA: FLJ23140 fis, clone LNG09065 /cds=UNKNOWN | 1 | CAGTACAGGGCTGGCAAGCAGTGAT CTCTCAGGTATATTTATCAATAATT |
| 4441 | db mining | Hs.104696 | AK026832 | 10439779 | mRNA for KIAA1324 protein, partial cds /cds=(0,1743) | 1 | CAAACCTCTCTTCTGCTTGCCCTCAA ACCTGCCAAATATACCCACACTTT |
| 4442 | db mining | Hs.24684 | AK026917 | 10439889 | mRNA for KIAA1376 protein, partial cds /cds=(143,1456) | 1 | GGTGCTGAATATGTCCTTGTAGGCTC TGTTTAAAGAAAACAATATGTGGG |
| 4443 | db mining | Hs.152925 | AK027260 | 10440394 | mRNA for KIAA1268 protein, partial cds /cds=(0,3071) | 1 | AGTGATTGATTAACCTCAGGGCAAGG CTGAATATCAGAGTGATTCGCACT |
| 4444 | Table 3A | Hs.301763 | AL049935 | 4884177 | mRNA; cDNA DKFZp564O1116 (from clone DKFZp564O1116) /cds=UNKNOWN | 1 | GCTTCCACTGGAGGCTGTGATTGACC TTGTAACATATATGTTAATCTCGTG |
| 4445 | db mining | Hs.18368 | AL080186 | 5262664 | mRNA; cDNA DKFZp564B0769 (from clone DKFZp564B0769); partial cds /cds=(0,900) | 1 | ATGCATGTTTACCAAAATGGCTGTTT ACAGTGCATTCACTCTGATATTT |
| 4446 | Table 3A | Hs.326292 | AL134898 | 6603085 | DNA sequence from clone RP5-1167H4 on chromosome 20. Contains ESTs, STSs, GSSs and CpG islands. Contains a novel gene, the STK15 gene for serine/threonine kinase 15, the CSTF1 gene for cleavage stimulation factor subunit 1 (50 kDa), a novel gene similar to NEDD9 for neural precursor cell expressed developmentally down-regulated protein 9 (enhancer of filamentation 1, HEF1) (CRK-associated substrate-related protein, CAS-L) and a 60S ribosomal protein L39 (RPL39) pseudogene /cds=(44,622) | 1 | ACATGACAGGTGTAATTAGTCTGCTG AGCCAGCTTTACCCAATGAAGGGC |
| 4447 | Table 3A | Hs.260024 | AL136842 | 6807668 | mRNA; cDNA DKFZp434A0530 (from clone DKFZp434A0530); complete cds /cds=(968,1732) | 1 | AACAGCAACCAATAACGGATTGTAAG GTGTAAGGACAGGTTACTCATG |
| 4448 | db mining | Hs.296356 | AL137406 | 6807955 | mRNA; cDNA DKFZp434M162 (from clone DKFZp434M162) /cds=UNKNOWN | 1 | CCATGCCAAGGAATGGAATTTCCATC CTGAGCCAGTTCAGTTAGGTGTCA |
| 4449 | db mining | Hs.56265 | AL137736 | 6808315 | mRNA; cDNA DKFZp586P2321 (from clone DKFZp586P2321) /cds=UNKNOWN | 1 | CTAGAGTTCACTCTGAGCTGTAAGG GTGACCAGGGGGCAGGGGGACGAT |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|----------|--|---|--|
| 4450 | Table 3A | Hs.66151 | AL157438 | 7018513 | mRNA; cDNA DKFZp434A115 (from clone DKFZp434A115) /cds=UNKNOWN | 1 | CAAGTAGACACCAGAGTCACTGTTTG GTTGGTGGGTGATAGTGGGGTCAC |
| 4451 | Table 3A | Hs.106875 | AL355722 | 7799110 | EST from clone 35214, full insert /cds=UNKNOWN | 1 | TGTCACCCCTTCCATGACGCCTCCTCT GTGCATTGAGTTCAGTCTTTATG |
| 4452 | db mining | Hs.283849 | AL359560 | 8655615 | mRNA; cDNA DKFZp762F0616 (from clone DKFZp762F0616) /cds=UNKNOWN | 1 | GGTAACATGAGCTATGGCAGTCGGTT GTGAAACCACAGGAAGTGATGGG |
| 4453 | Table 3A | Hs.23964 | AL360135 | 8919158 | sin3-associated polypeptide, 18kD (SAP18), mRNA /cds=(573,1034) | 1 | CAAATCGGGCACCACCTCCTTCAGG GCGCATGAGACCATATTAATTTCTA |
| 4454 | Table 3A | Hs.10927 | AL365373 | 9187358 | HSZ78330 cDNA /clone=2.49-(CEPH) | 1 | CAGAACTGCTTTCCATGTTTACCCA GGGGACCTCCTTTCAGATGAAGTGA |
| 4455 | db mining | Hs.171118 | AL583913 | 13093778 | DNA sequence from clone RP11-165F24 on chromosome 9. Contains the 3' end of the gene for a novel protein (similar to Drosophila CG6630 and CG11376, KIAA1058, rat TRG), an RPL12 (60S ribosomal protein L12) pseudogene, ESTs, STSs, GSSs and a CpG island /cds=(0,4617) | 1 | AGCAATAATATCTCTGTTTTTCATTTC GAACATTGTGCTGTCTGTACGCA |
| 4456 | Table 3A | Hs.11806 | AU124763 | 10949479 | 7-dehydrocholesterol reductase (DHCR7), mRNA /cds=(194,1621) | 1 | TTACAACTACATGATGGGCATCGAGT TTAACCCCTTGGATCGGGGAAGTGGG |
| 4457 | db mining | Hs.205435 | AV740518 | 10858099 | AV740518 cDNA, 5' end /clone=CBDAGC01 /clone_end=5' | 1 | AATGTTTGAGCTGACCAAGCTTCTGA GATTCTTAACAGAAAAAGCCATGT |
| 4458 | db mining | Hs.204751 | AV741208 | 10858789 | AF150335 cDNA /clone=CBLAQF05 | 1 | ACGTACGCTTAAACCTGGAAAGAAGT CTTCTGGTGTATACTGAGATTTGA |
| 4459 | db mining | Hs.204932 | AV743878 | 10861459 | AV743878 cDNA, 5' end /clone=CBLAOC04 /clone_end=5' | 1 | GCCCAAAGGAGTAGCTCTCTGTTGTT ACTGTTGTGCTCTTCATGGATAAA |
| 4460 | db mining | Hs.205159 | AV744351 | 10861932 | AF150295 cDNA /clone=CBLADB01 | 1 | GCAAAAAGCCCAAGAGCCTGAATTTA GACCAATCTATCATCTTCTCCTC |
| 4461 | db mining | Hs.205789 | AV756240 | 10914088 | AV756240 cDNA, 5' end /clone=BMFAUH12 /clone_end=5' | 1 | TGGAGATGTGATAACAACTCCTTATC TCTTTGTTGGCTCATCTGAAGTGT |
| 4462 | db mining | Hs.254948 | AW291284 | 6697920 | UI-H-BI2-agi-h-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2724714 /clone_end=3' | 1 | CTTGACAGTAAATGTAGCCCTTCTC CTGGTTGTGCAGGAGTGGCCCTCG |
| 4463 | db mining | Hs.250605 | AW327360 | 6797855 | dq02e11.x1 cDNA, 5' end /clone=IMAGE:2846685 /clone_end=5' | 1 | TTTCTTTAGCCCAAGAGTGGAGGCTA AGCTACTTACTTCCAAGCCTGGGT |
| 4464 | Table 3A | Hs.211194 | AW362304 | 6866954 | CM3-CT0275-031199-031-a08 cDNA | 1 | AGGCAAAGGGAAGTTGAAATTAGAAA ACCCAGAAACAGTCACAATGGCT |
| 4465 | Table 3A | Hs.342300 | AW389509 | 6894168 | xm47a06.x1 cDNA, 3' end /clone=IMAGE:2687314 /clone_end=3' | 1 | AGGGTCCCTTCCATAGTCTCCTGCA TCATTTCTCCTCAACTTGAATAAA |
| 4466 | Table 3A | Hs.202402 | AW390251 | 6894910 | CM4-ST0182-051099-021-b06 cDNA | 1 | GCCAACCAAGTTCAGAGTGTCCCAAG GAATTGCCACCTTACTCTTCAAA |
| 4467 | Table 3A | Hs.192123 | AW838827 | 7932801 | CM1-LT0059-280100-108-e02 cDNA | 1 | ATCCCACTCTCAAATTTCTTCAATTTG AACTGATATGTAGGCCCTCATCG |
| 4468 | Table 3A | Hs.194589 | AW945538 | 8123293 | AV703056 cDNA, 5' end /clone=ADBCMB06 /clone_end=5' | 1 | TCTCTCACTGTATCATTTTTGCACAG GTGGTTTCAGCAGCTTGATGCCA |
| 4469 | Table 3A | Hs.83724 | BC000957 | 13111830 | Homo sapiens, clone IMAGE:3451448, mRNA, partial cds /cds=(0,901) | 1 | ATTGTCATTAGACTTTGAACAGCTCT GGGAAATAGAAGACTAGGGTTGT |
| 4470 | db mining | Hs.267690 | BC001224 | 12654762 | mRNA for KIAA1228 protein, partial cds /cds=(0,2176) | 1 | TTTCCTTGTTCCTCCCATGCCTAGC TGGATTGCAGAGTTAAGTTTATGA |
| 4471 | db mining | Hs.76932 | BC002332 | 12803062 | Homo sapiens, Similar to hypothetical protein FLJ20419, clone MGC:15417 IMAGE:3942735, mRNA, complete cds /cds=(208,918) | 1 | GGATTACCGTGGCCGACTCTTTTCC CTGCTTGTGTTTGTGAAATCTA |
| 4472 | Table 3A | Hs.343272 | BC002770 | 12803854 | Homo sapiens, clone IMAGE:3616574, mRNA, partial cds /cds=(0,640) | 1 | CCCTCCACACCATCCTCCCGATTTA AATATAGTCACTGCTACAAGTAAC |
| 4473 | db mining | Hs.81221 | BC002792 | 12803890 | Homo sapiens, clone MGC:3963 IMAGE:3621362, mRNA, complete cds /cds=(40,402) | 1 | TTCATCATTTGCTTGTGCTTCCTC CCTTCTGTCCGCTCTTACTCCCTC |
| 4474 | db mining | Hs.302063 | BC002963 | 12804210 | rearranged immunoglobulin mRNA for mu heavy chain enhancer and constant region /cds=UNKNOWN | 1 | GCAAACCTAACCGTGTCAACGGGGTG AGATGTTGCATCTTATAAAATTAGA |
| 4475 | db mining | Hs.302063 | BC002963 | 12804210 | rearranged immunoglobulin mRNA for mu heavy chain enhancer and constant region /cds=UNKNOWN | 1 | GCAAACCTAACCGTGTCAACGGGGTG AGATGTTGCATCTTATAAAATTAGA |
| 4476 | db mining | Hs.302063 | BC002963 | 12804210 | rearranged immunoglobulin mRNA for mu heavy chain enhancer and constant region /cds=UNKNOWN | 1 | GCAAACCTAACCGTGTCAACGGGGTG AGATGTTGCATCTTATAAAATTAGA |
| 4477 | Table 3A | Hs.334787 | BC003063 | 13937660 | Homo sapiens, clone MGC:19556 IMAGE:4304831, mRNA, complete cds /cds=(1505,1666) | 1 | AGTATCTGCTTTCCAGGCTGAAGTGA TTCATTATTATCTAGTCCTGCT |
| 4478 | Table 3A | Hs.334573 | BC006008 | 13937718 | Homo sapiens, clone IMAGE:4285740, mRNA /cds=UNKNOWN | 1 | AAGCTGTCTTCTTTGTTGGACAATCA GCCAGAATGATAAGCAAACCTGCA |
| 4479 | db mining | Hs.300697 | BC006402 | 13623574 | mRNA for immunoglobulin lambda heavy chain /cds=(65,1498) | 1 | CTCTCGGGTGCACGAGGATGCTT GGCAGTACCCCTGTACATACTTC |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|-----------------------------|
| 4480 | db mining | Hs.300697 | BC006402 | 13623574 | mRNA for immunoglobulin lambda heavy chain /cds=(65,1498) | 1 | CTCTCGCGGTGCGACGAGGATGCTT |
| 4481 | db mining | Hs.300697 | BC006402 | 13623574 | mRNA for immunoglobulin lambda heavy chain /cds=(65,1498) | 1 | GGCACGTACCCCGTGTACATACTTC |
| 4482 | Table 3A | Hs.155101 | BC007299 | 13938338 | mRNA for KIAA1578 protein, partial cds /cds=(0,3608) | 1 | CTCTCGCGGTGCGACGAGGATGCTT |
| 4483 | db mining | Hs.184776 | BC007583 | 14043190 | ribosomal protein L23a (RPL23A), mRNA /cds=(23,493) | 1 | GGTCTCTGATTACGATGCTTTGGATG |
| 4484 | db mining | Hs.250528 | BC007747 | 14043522 | Homo sapiens, clone IMAGE:4098694, mRNA, partial cds /cds=(0,2501) | 1 | TTGCCAACAAAATTGGGATCATCT |
| 4485 | Table 3A | Hs.44155 | BC008629 | 14250392 | mRNA; cDNA DKFZp586G1517 (from clone DKFZp586G1517); partial cds /cds=(0,2755) | 1 | AACGCCAGCATTTTGTTAGAGGAGTT |
| 4486 | Table 3A | Hs.164280 | BC008737 | 14250566 | Homo sapiens, Similar to solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5, clone MGC:3042 IMAGE:3342722, mRNA, complete cds /cds=(88,984) | 1 | AGACTTGAAAGTTAAGGGAAGA |
| 4487 | Table 3A | Hs.336425 | BC009111 | 14318625 | Homo sapiens, clone MGC:17296 IMAGE:3460701, mRNA, complete cds /cds=(3250,3498) | 1 | ATGGGGACTAAGGGATTAAGAGTGT |
| 4488 | db mining | Hs.287797 | BC009469 | 14495714 | mRNA for FLJ00043 protein, partial cds /cds=(0,4248) | 1 | GAACTAAAGGTAACATTTTCCACT |
| 4489 | literature | Hs.287797 | BC009469 | 14495714 | mRNA for FLJ00043 protein, partial cds /cds=(0,4248) | 1 | ACTGGCGAGTATGTTCTATGTTGGGC |
| 4490 | db mining | Hs.293842 | BG506472 | 13467989 | 601571679F1 cDNA, 5' end /clone=IMAGE:3838675 /clone_end=5' | 1 | CTCCTGCTGCAAAACAATAACAG |
| 4491 | db mining | Hs.224344 | BG623174 | 13674545 | 602648078F1 cDNA, 5' end /clone=IMAGE:4769802 /clone_end=5' | 1 | GCTGATTAAGTGTATTTCCCTTTCCC |
| 4492 | db mining | Hs.127128 | BI091076 | 14509406 | ok13e12.s1 cDNA, 3' end /clone=IMAGE:1507726 /clone_end=3' | 1 | CTATGGCTGCTGGTGTAAATAAAC |
| 4493 | db mining | Hs.330212 | D20259 | 501356 | HUMGS01233 cDNA, 3' end /clone=pm1527 /clone_end=3' | 1 | CCCAGGGTTTCATGCTGAGGCCCTC |
| 4494 | db mining | Hs.330467 | D20413 | 501509 | HUMGS01387 cDNA, 3' end /clone=pm1535 /clone_end=3' | 1 | ACCAAGTGTGAGTGACAGTATAAA |
| 4495 | db mining | Hs.330223 | D20542 | 501638 | HUMGS01517 cDNA, 3' end /clone=pm1520 /clone_end=3' | 1 | CCCAGGGTTTCATGCTGAGGCCCTC |
| 4496 | db mining | Hs.330255 | D20847 | 504667 | HUMGS01828 cDNA, 3' end /clone=mp1214 /clone_end=3' | 1 | ACCAAGTGTGAGTGACAGTATAAA |
| 4497 | db mining | Hs.141296 | D86979 | 6634000 | mRNA for KIAA0226 protein, partial cds /cds=(0,3033) | 1 | ACAAGAAATGGTTGAGGCCAATATTG |
| 4498 | db mining | Hs.303450 | H13491 | 878311 | yj15f02.r1 cDNA, 5' end /clone=IMAGE:148827 /clone_end=5' | 1 | GAAACACATGGGGCTTAATGTGAA |
| 4499 | db mining | Hs.138563 | H65914 | 1024654 | 601819705F1 cDNA, 5' end /clone=IMAGE:4051657 /clone_end=5' | 1 | ACACCTCTCTATTTTGAAGTCCCTAT |
| 4500 | db mining | Hs.73858 | J05158 | 179935 | carboxypeptidase N mRNA, 3' end /cds=(0,1610) | 1 | GTGCCCTGTAATGTCTCGTTTTAA |
| 4501 | db mining | Hs.69771 | K01566 | 187721 | B-factor, properdin | 1 | GGGAGAGCTCATGTCAAGTAAATAG |
| 4502 | literature | Hs.278625 | K02403 | 187768 | complement component 4B (C4B), mRNA /cds=(51,5285) | 1 | ATCATTTCTGTTGATACCCCTCTTT |
| 4503 | db mining | Hs.132807 | L29376 | 561725 | (clone 3.8-1) MHC class I mRNA fragment /cds=UNKNOWN | 1 | TTGAAACTTGTAAGTGAAGTCTGTA |
| 4504 | db mining | Hs.274509 | M16768 | 339399 | T-cell receptor aberrantly rearranged gamma-chain mRNA from cell line HPB-MLT /cds=UNKNOWN | 1 | GTTTTTGCCATCTGTAGTGAATGT |
| 4505 | db mining | Hs.247956 | M22005 | 186300 | interleukin 2 gene, clone pATtacIL-2C/2TT, complete cds, clone pATtacIL-2C/2TT /cds=(0,404) | 1 | AAAGGGTTTTATCCACTGTCAATTCAA |
| 4506 | db mining | Hs.247923 | M31949 | 185254 | Ig rearranged mu-chain V-region gene, subgroup VH-III, exon 1 and 2 | 1 | TTGGATAACATTTTGCAGAGTTT |
| 4507 | db mining | Hs.247930 | M55420 | 185346 | IgE chain, last 2 exons | 1 | TCGGAAAGAAAGAGTGGGAGGATGT |
| 4508 | literature | NA | M73276 | 177970 | Human angiotensin I-converting enzyme (ACE) gene, 5' flank | 1 | GAATTTTAGTTCTGAGTTTACCAAA |
| 4509 | Table 3A | Hs.154365 | M82882 | 180551 | cis-acting sequence /cds=UNKNOWN | 1 | GATCGGGAACCTGGCTCCGTTGTGCT |
| 4510 | Table 3A | Hs.171699 | N31778 | 1152177 | yx70d02.r1 cDNA, 5' end /clone=IMAGE:267075 /clone_end=5' | 1 | TTGCTATCTTTAATAAACTAAGGA |
| 4511 | db mining | Hs.269035 | N39815 | 1163360 | yx93c06.r1 cDNA, 5' end /clone=IMAGE:269290 /clone_end=5' | 1 | AGAACTACAAGATTTCTGCTTCTCT |
| 4512 | db mining | Hs.169401 | NM_000041 | 4557324 | apolipoprotein E (APOE), mRNA /cds=(60,1013) | 1 | CCATTAAGTACAATCTCCCTGGG |
| | | | | | | 1 | TACAAGTGAAAGCTAAGATGAACACA |
| | | | | | | 1 | TTTAAGTTAAATGGCAGCCTTGTT |
| | | | | | | 1 | AAAAGGATGTGACAGAAGCAGAGAT |
| | | | | | | 1 | GACCAGAAAGCACAGGGGCAGGGTT |
| | | | | | | 1 | GGGTTTTCTATAAGGGGTTTCCTGCT |
| | | | | | | 1 | GAACAGGGGGCGTGGGATTGAATTA |
| | | | | | | 1 | CCTGGGACCAGGGCATATTAAAGGC |
| | | | | | | 1 | TTTTGGCAGCAAAGTGTCAAGTGTG |
| | | | | | | 1 | TTTGTGGCTTGGGGCTGCCACTATA |
| | | | | | | 1 | AACATTGGGGGTTTCGTCCATTTT |
| | | | | | | 1 | TTTACACGCCCTGAAGCAGTCTTCTT |
| | | | | | | 1 | TGCTAGTTGAATTATGTGGTGTGT |
| | | | | | | 1 | AATTCCTGAACCGTTGGATCACCTTC |
| | | | | | | 1 | TGTCAGTCCATCATCTCCACCCTG |
| | | | | | | 1 | CTTACGTTGGGACACCTAAATTCGCC |
| | | | | | | 1 | CGGTCTGTAGAAGGCAGATTTCGAG |
| | | | | | | 1 | AAAACCGTGTCTGTCCCTTCAACAGA |
| | | | | | | 1 | GTTCATCGAGGAGGGGTGGCTGCTA |
| | | | | | | 1 | AAACTGCCGGGTCCCATCTTCAAAA |
| | | | | | | 1 | GAGAGGAGGCCCTTTCTCCAGCTT |
| | | | | | | 1 | CAAGAAAGCAACTTGAGCCTTGGGCT |
| | | | | | | 1 | AATCTGGCTGAGTAGTCAGTTATA |
| | | | | | | 1 | TGTGTTCTTTGAGTTCCCTTTTACC |
| | | | | | | 1 | CAAAAGTAATTTGGGGACCAAAGT |
| | | | | | | 1 | GGGAAGGCATCTGATGGGGAAGTT |
| | | | | | | 1 | GGCAATTTCTGGTTTGGGTGATTTA |
| | | | | | | 1 | CCAAGCGTCTCCTGGGGTGACCC |
| | | | | | | 1 | TAGTTTAATAAAGATTACCAAGTT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|--|
| 4513 | literature | Hs.38069 | NM_000066 | 4557390 | complement component 8, beta polypeptide (C8B), mRNA /cds=(27,1802) | 1 | CATGCAAGGGCAAAAGGCAGTGCCA TGCAAGCTGTTTAAATAAAGATGT |
| 4514 | literature | Hs.317585 | NM_000088 | 14719826 | cDNA: FLJ21026 fis, clone CAE06812 /cds=(27,677) | 1 | AGGGGTGGGAGGAAGCAAAAGACTC TGTACCTATTTTGTATGTGTATAAT |
| 4515 | db mining | Hs.1472 | NM_000173 | 4504070 | glycoprotein Ib (platelet), alpha polypeptide (GP1BA), mRNA /cds=(42,1922) | 1 | TCAGGATGTGAGCACTCGTTGTGTCT GGATGTTACAAATATGGGTGGTTT |
| 4516 | literature | Hs.180532 | NM_000175 | 4504086 | Homo sapiens, clone IMAGE:4098234, mRNA, partial cds /cds=(0,904) | 1 | TGTTACGCTTGTTCACATCCCATGTA GAAAAACAAAGATGCCACGGAGGA |
| 4517 | db mining | Hs.290070 | NM_000177 | 4504164 | gelsolin (amyloidosis, Finnish type) (GSN), mRNA /cds=(14,2362) | 1 | AGCCCTGCAAAAATTCAGAGTCCTTG CAAAATTGTCTAAATGTGAGTGT |
| 4518 | literature | Hs.227730 | NM_000210 | 1111111 | integrin, alpha 6 (ITGA6), mRNA /cds=(146,3367) | 1 | TGTCATCTCAAGTCAAGTCACTGGTC TGTTCGATTTGATACATTTTGT |
| 4519 | db mining | Hs.90598 | NM_000247 | 4557750 | MHC class I polypeptide-related sequence A (MICA), mRNA /cds=(39,1190) | 1 | GAGTGACCACAGGGATGCCACACAG CTCGGATTTCAGCCTCTGATGTCAG |
| 4520 | db mining | Hs.1817 | NM_000250 | 4557758 | myeloperoxidase (MPO), nuclear gene encoding mitochondrial protein, mRNA /cds=(177,2414) | 1 | GCCTGTGGCCCTTTCTGTACCATTTA TTTGCTCCCAATGTTTATGATAAT |
| 4521 | db mining | Hs.1817 | NM_000250 | 4557758 | myeloperoxidase (MPO), nuclear gene encoding mitochondrial protein, mRNA /cds=(177,2414) | 1 | GCCTGTGGCCCTTTCTGTACCATTTA TTTGCTCCCAATGTTTATGATAAT |
| 4522 | db mining | Hs.75093 | NM_000302 | 4557836 | procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD), mRNA /cds=(200,2383) | 1 | TCCTGGATGCCTCTGAAGAGAGGGA CAGACCGTCAGAAACTGGAGAGTTT |
| 4523 | db mining | Hs.10712 | NM_000314 | 4506248 | phosphatase and tensin homolog (mutated in multiple advanced cancers 1) (PTEN), mRNA /cds=(1034,2245) | 1 | ACTTAACCATATAAATGTGGAGGCTA TCAACAAAGAAATGGGCTTGAACA |
| 4524 | Table 3A | Hs.83848 | NM_000365 | 4507644 | triosephosphate isomerase 1 (TPI1), mRNA /cds=(34,783) | 1 | GTGCCTCTGTGCTGTGTATGTGAACC ACCCATGTGAGGGAATAAACCTAG |
| 4525 | Table 3A | Hs.78943 | NM_000386 | 4557366 | bleomycin hydrolase (BLMH), mRNA /cds=(78,1445) | 1 | AAACAGACCTAATGCTCCTTGTTCCT AGAGTAGAGTGGAGGGAGGTTGGC |
| 4526 | literature | Hs.285401 | NM_000395 | 4559407 | colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), mRNA /cds=(28,2721) | 1 | GAGATAGCCTTGCTCCGGCCCCCTT GACCTTCAGCAAATCACTTCTCTCC |
| 4527 | db mining | Hs.283743 | NM_000407 | 9945387 | glycoprotein Ib beta mRNA, complete cds /cds=(636,1871) | 1 | CTGCTGCGTCTCCCTTCCAAACTCTG GTGCTGAATAAACCTTCTGATCT |
| 4528 | db mining | Hs.20019 | NM_000410 | 4504376 | hemochromatosis (HFE), mRNA /cds=(221,1267) | 1 | CACCTTGGCTGCATAAATGTGGTACAA CCATTCTGTCTTGAAGGCGAGGTG |
| 4529 | literature | Hs.8986 | NM_000491 | 11038661 | complement component 1, q subcomponent, beta polypeptide (C1QB), mRNA /cds=(63,824) | 1 | CAGCCAAATGGACACAGTAGGGCTTG GTGAATGCTGCTGAGTGAATGAGTA |
| 4530 | db mining | Hs.278430 | NM_000500 | 14550408 | cytochrome P450, subfamily XXIA (steroid 21-hydroxylase, congenital adrenal hyperplasia), polypeptide 2 (CYP21A2), mRNA /cds=(118,1605) | 1 | TGCAGAGGATTGAGGCTTAATTCTGA GCTGGCCCTTTCCAGCCAATAAAT |
| 4531 | db mining | Hs.502 | NM_000544 | 9961245 | transporter 2, ATP-binding cassette, sub-family B (MDR/TAP) (TAP2), transcript variant 1, mRNA /cds=(96,2207) | 1 | TTGACCTTCCACTAGACCATGAGCAC CTGGCGGAAAGCCATATATCTTA |
| 4532 | literature | Hs.93210 | NM_000562 | 4557388 | complement component 8, alpha polypeptide (C8A), mRNA /cds=(137,1891) | 1 | ACAAGCAGACACCTGAAACAATCAAC GCCCAATAAAAACAAAGTAGGATGA |
| 4533 | db mining | Hs.68876 | NM_000564 | 10835130 | interleukin 5 receptor, alpha (IL5RA), mRNA /cds=(249,1511) | 1 | TGAGGAAGAAAGCATTTCATGCAGC CTGGAGTGAACCATGAACCTGGAT |
| 4534 | literature | Hs.241053 | NM_000573 | 10834973 | AL572804 cDNA /clone=CS0D1034YD15-(3-prime) | 1 | GGAATAAGGTGTTGCCTGGAATTTCT GGTTCGTAAGGTGGTCACTGTTCT |
| 4535 | Table 3A | Hs.89679 | NM_000586 | 10835148 | interleukin 2 (IL2), mRNA /cds=(47,517) | 1 | TGAACAGATGGATTACCTTTTGTCAA AGCATCATCTCAACACTAAGCTTGA |
| 4536 | literature | Hs.78065 | NM_000587 | 4557386 | complement component 7 (C7), mRNA /cds=(0,2531) | 1 | CCCAGAGTTTTCAGGGAGTACACAG GTAGATTAGTTTGAAGCATTGACCT |
| 4537 | literature | Hs.960 | NM_000590 | 10834979 | interleukin 9 (IL9), mRNA /cds=(11,445) | 1 | TTCCAGAAAGAAAGATGAGAGGGAT GAGAGGCAAGATATGAAGATGAAA |
| 4538 | literature | Hs.1285 | NM_000606 | 4557392 | complement component 8, gamma polypeptide (C8G), mRNA /cds=(61,669) | 1 | GGCTGCCCCAGAGGACAGTGGGTGG AGTGGTACCTACTTATTAATGTCT |
| 4539 | literature | Hs.167988 | NM_000615 | 10834989 | neural cell adhesion molecule 1 (NCAM1), mRNA /cds=(201,2747) | 1 | CCGAGCAAAGATCAAAATAAAAGTG ACACAGCAGCTTCACAGAGCATT |
| 4540 | Table 3A | Hs.17483 | NM_000616 | 10835166 | chromosome 12p13 sequence /cds=(194,1570) | 1 | TTTCCTTCAAGCCTAGCCCTTCTCTC ATTATTTCTCTCGACCTCTCCC |
| 4541 | db mining | Hs.100007 | NM_000635 | 10835184 | regulatory factor X, 2 (influences HLA class II expression) (RFX2), mRNA /cds=(159,2330) | 1 | GGGTCAAGTGTTCAGAAAGGAAAGCA GTTGTGAAGCTACAGAAGCCCAGG |
| 4542 | db mining | Hs.25954 | NM_000640 | 10834991 | interleukin 13 receptor, alpha 2 (IL13RA2), mRNA /cds=(93,1235) | 1 | TGAAGACTTTCCATATCAAGAGACAT GGTATTGACTCAACAGTTTCCAGT |
| 4543 | db mining | Hs.1721 | NM_000641 | 10834993 | interleukin 11 (IL11), mRNA /cds=(63,662) | 1 | GGACTGTCATTCAAGGAGGCTAAGG AGAGAGGCTTGCTTGGGATATAGAA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|---|
| 4544 | db mining | Hs.78712 | NM_000688 | 4502024 | aminolevulinate, delta-, synthase 1 (ALAS1), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,1998) | 1 | TCACTTAACCCAGGCCATTATCATATCCAGATGGTCTTCAGAGTTGTCT |
| 4545 | db mining | Hs.3003 | NM_000733 | 4502670 | CD3E antigen, epsilon polypeptide (TIT3 complex) (CD3E), mRNA /cds=(54,677) | 1 | CCACTGGATGGTCATTTGGCATCTCCGTATATGTGTCTCTGGCTCCTCAGC |
| 4546 | Table 3A | Hs.1349 | NM_000758 | 4503076 | colony stimulating factor 2 (granulocyte-macrophage) (CSF2), mRNA /cds=(8,442) | 1 | CTGGGCCCACTGACCCTGATACAGGCATGGCAGAAGATGGGAATATTT |
| 4547 | db mining | Hs.1349 | NM_000758 | 4503076 | colony stimulating factor 2 (granulocyte-macrophage) (CSF2), mRNA /cds=(8,442) | 1 | CTGGGCCCACTGACCCTGATACAGGCATGGCAGAAGATGGGAATATTT |
| 4548 | literature | Hs.86958 | NM_000874 | 4504600 | interferon receptor ifnar2-1 (splice variant IFNAR2-1) mRNA, complete cds /cds=(326,1321) | 1 | TGATAGCATTGGTCTTGACAAGCACCATAGTGACACTGAAATGGATTGGT |
| 4549 | literature | Hs.88474 | NM_000962 | 11386140 | prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1), mRNA /cds=(5,1804) | 1 | CTGAGGATGTAGAGAGAACAGGTGGGCTGTATTACGCCATTGGTTGGAA |
| 4550 | Table 3A | Hs.180450 | NM_001026 | 14916502 | ribosomal protein S24 (RPS24), transcript variant 1, mRNA /cds=(37,429) | 1 | CTGGCAAAAAGCCGAAGGAGTAAAGGTGCTGCAATGATGTTAGCTGTGGC |
| 4551 | Table 3A | Hs.113029 | NM_001028 | 14591916 | ribosomal protein S25 (RPS25), mRNA /cds=(63,440) | 1 | TGGTCCAAAGGCAAAGTTCGGGACAAGCTCAATAACTTAGCTCTTGTTGA |
| 4552 | literature | Hs.161305 | NM_001057 | 4507344 | tachykinin receptor 2 (TACR2), mRNA /cds=(0,1196) | 1 | CAACAGGTGTACACTAAGGAGACTTTGTTCATGGCTGGGGACACAGCCC |
| 4553 | literature | Hs.1080 | NM_001058 | 7669544 | tachykinin receptor 1 (TACR1), transcript variant long, mRNA /cds=(210,1433) | 1 | GCATGGAAATCCCTTCATCTGGAACCATCAGAAACCCCTCACACTGGG |
| 4554 | literature | Hs.942 | NM_001059 | 7669547 | tachykinin receptor 3 (TACR3), mRNA /cds=(143,1540) | 1 | GGCAGCTATGGTCAAATTGAGAAAGGTAGTGTATAATGTGACAAAGACA |
| 4555 | db mining | Hs.86947 | NM_001109 | 4557252 | a disintegrin and metalloproteinase domain 8 (ADAM8), mRNA /cds=(9,2483) | 1 | GCTATCTTGTCTGGTTTTCTTGAGACCTCAGATGTGTGTTCCAGCAGGGCT |
| 4556 | literature | Hs.1239 | NM_001150 | 4502094 | alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150) (ANPEP), mRNA /cds=(120,3023) | 1 | CCGCCCTGTACCCTCTTTACCTTTTCCTAAAGACCCTAAATCTGAGGAA |
| 4557 | db mining | Hs.507 | NM_001264 | 4502758 | corneodesmosin (CDSN), mRNA /cds=(14,1603) | 1 | CATATGGGAGAAGGCCAGTGCCCCAGGCATAGGGTTAGCTCAGTTTCCCTC |
| 4558 | Table 3A | Hs.74441 | NM_001273 | 4557452 | chromodomain helicase DNA binding protein 4 (CHD4), mRNA /cds=(89,5827) | 1 | TTAATACCAGGAACCCAGCGGCTCTAGCCACTGAGCGGCTAAATGAAATA |
| 4559 | db mining | Hs.5057 | NM_001304 | 8051580 | carboxypeptidase D (CPD), mRNA /cds=(15,4148) | 1 | GTGGAGGGGTTTACCACCTTCCTAGGTCGTTCAACCAGGTTTTGTGAGGA |
| 4560 | db mining | Hs.2246 | NM_001308 | 4503010 | carboxypeptidase N, polypeptide 1, 50kD (CPN1), mRNA /cds=(213,1589) | 1 | GCAACCCCTCAGAAAGGCTTTGCTCCGTCTCTCAGATCAGATCAAGCATT |
| 4561 | db mining | Hs.336916 | NM_001350 | 4503256 | death-associated protein 6 (DAXX), mRNA /cds=(147,2369) | 1 | AACATTTGGAGGAAGGTGGGAAGCAGATGACTGAGGAAGGGATGGACTAA |
| 4562 | Table 3A | Hs.288036 | NM_001402 | 4503470 | tRNA isopentenylpyrophosphate transferase (IPT), mRNA /cds=(60,1040) | 1 | TGCCCAGAAAGCTCAGAAAGGCTAAATGAATATTATCCCTAATACCTGCCA |
| 4563 | Table 3A | Hs.129673 | NM_001416 | 4503528 | eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1), mRNA /cds=(16,1236) | 1 | AGAGGACTCTTCGAGACATTGAGACCTTCTACAACACCTCCATTGAGGAA |
| 4564 | Table 3A | Hs.99855 | NM_001462 | 4503780 | formyl peptide receptor-like 1 (FPRL1), mRNA /cds=(772,1827) | 1 | TGGGGTAAGTGGAGTTGGGAAATAC AAGAAGAGAAAGACCACTGGGGATT |
| 4565 | literature | Hs.198252 | NM_001504 | 4504098 | G protein-coupled receptor 9 (GPR9), mRNA /cds=(68,1174) | 1 | AAACTAAAATTCTCTTCCCAAGTGCAGGGAGTACAAGGCATGGCGTA |
| 4566 | db mining | Hs.113207 | NM_001505 | 4504090 | G protein-coupled receptor 30 (GPR30), mRNA /cds=(691,1818) | 1 | AAAACCTTCCATAAAATGTAAGAAAAGCTGATGAGGCTGGTGACGTTCA |
| 4567 | db mining | Hs.278589 | NM_001518 | 14670355 | general transcription factor II, i (GTF2I), transcript variant 1, mRNA /cds=(370,3366) | 1 | TGACATGGTAGCAGAAATAGGCCCTTTATGTGTTGCTCTATTTTACCT |
| 4568 | db mining | Hs.101840 | NM_001531 | 4504416 | major histocompatibility complex, class I-like sequence (HLALS), mRNA /cds=(5,1030) | 1 | GCCACAAAATGTTCTTTGTTCTTTGGCTCCAAAAGACTGTGAGCTTTCA |
| 4569 | db mining | Hs.81234 | NM_001542 | 4504626 | mRNA for KIAA0466 protein, partial cds /cds=(40,3684) | 1 | CTGAGGCTCTCCCTTTCTCTGTGATTGGACAGTTGACAGACCCAACTC |
| 4570 | db mining | Hs.22111 | NM_001555 | 4504624 | mRNA for KIAA0364 gene, complete cds /cds=(1144,5127) | 1 | CCCTGTAACTCTCTACTGTACTGATTACTGGCGCATGAAATCTATTAA |
| 4571 | Table 3A | Hs.285115 | NM_001560 | 4504646 | interleukin 13 receptor, alpha 1 (IL13RA1), mRNA /cds=(43,1326) | 1 | CTTGAGTAAATAATATTTGCTTTTTGTATGGCAAGCGGGCCGCCACCG |
| 4572 | literature | Hs.1211 | NM_001611 | 6138970 | acid phosphatase 5, tartrate resistant (ACP5), mRNA /cds=(89,1066) | 1 | GGGAGGGAGGGAGGGAAAGCTTCCTCCTAAATCAAGCATCTTTCTGTTC |
| 4573 | literature | Hs.10247 | NM_001627 | 4502028 | mRNA for MEMD protein /cds=(0,1748) | 1 | TCACAGATGCATATAGACACACATACATAATGGTACTCCAAACTGACAA |
| 4574 | db mining | Hs.268571 | NM_001645 | 5174774 | intergenic region between apoE and apoC1 genes /cds=UNKNOWN | 1 | GCTGAGGACTCCCGCATGTGGCCCAGGTGCCACCAATAAAATCTCTAC |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|-----------------------------|
| 4575 | db mining | Hs.69771 | NM_001710 | 14550403 | B-factor, properdin (BF), mRNA /cds=(129,2423) | 1 | CAAGATGAGGATTGGGTTTCTATA |
| 4576 | literature | Hs.1281 | NM_001735 | 4502506 | complement component 5 (C5), mRNA /cds=(12,5042) | 1 | AGGGGTTTCTGCTGGACAGGGGC |
| 4577 | literature | Hs.171763 | NM_001771 | 4502650 | CD22 antigen (CD22), mRNA /cds=(56,2599) | 1 | AAACATAGGCCTTTGCTTGAAAGAAA |
| 4578 | literature | Hs.83731 | NM_001772 | 4502654 | CD33 antigen (gp67) (CD33), mRNA /cds=(12,1106) | 1 | TACCAAGGAACAGGAACTGATCA |
| 4579 | Table 3A | Hs.340325 | NM_001774 | 4502662 | yf59e04.s1 cDNA, 3' end /clone=IMAGE:26202 /clone_end=3' | 1 | GTTTGAGATGGACACACTGGTGTGGA |
| 4580 | literature | Hs.82685 | NM_001777 | 4502672 | CD47 antigen (Rh-related antigen, integrin-associated signal transducer) (CD47), mRNA /cds=(106,1077) | 1 | TTAACCTGCCAGGGAGACAGACT |
| 4581 | literature | Hs.264190 | NM_001780 | 4502678 | cDNA: FLJ22121 fis, clone HEP18876, highly similar to AF191298 vacuolar sorting protein 35 (VPS35) mRNA /cds=UNKNOWN | 1 | GSACCAAGGCTGATTCTTGGAGATT |
| 4582 | literature | Hs.3107 | NM_001784 | 4502690 | CD97 antigen (CD97), mRNA /cds=(70,2298) | 1 | TAACCTCCACAGGCAATGGGTTT |
| 4583 | Table 3A | Hs.10029 | NM_001814 | 4503140 | cathepsin C (CTSC), mRNA /cds=(33,1424) | 1 | AATATTTGTTTAATCCCCAGTTCGCCT |
| 4584 | db mining | Hs.11 | NM_001815 | 4502792 | carcinoembryonic antigen-related cell adhesion molecule 3 (CEACAM3), mRNA /cds=(54,692) | 1 | GGAGCCCTCCGCTTCACATTC |
| 4585 | db mining | Hs.119140 | NM_001970 | 4503544 | eukaryotic translation initiation factor 5A (EIF5A), mRNA /cds=(43,507) | 1 | CCCTTACGTGATTGTAGTTAAGT |
| 4586 | db mining | Hs.99863 | NM_001972 | 4503548 | elastase 2, neutrophil (ELA2), mRNA /cds=(38,841) | 1 | CTCAGCCTCCTCATCTGGGGAGTG |
| 4587 | db mining | Hs.99863 | NM_001972 | 4503548 | elastase 2, neutrophil (ELA2), mRNA /cds=(38,841) | 1 | GAATAGTATCCTCCAGGTTTTTCAA |
| 4588 | literature | Hs.193122 | NM_002000 | 4503672 | Fc fragment of IgA, receptor for (FCAR), mRNA /cds=(39,902) | 1 | GGCAGGAGTTCTCACTGTTGTGAA |
| 4589 | db mining | Hs.897 | NM_002001 | 4503674 | Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A), mRNA /cds=(106,879) | 1 | GGTTGTAGACGTTGTGTAATGTGTT |
| 4590 | db mining | Hs.77252 | NM_002012 | 4503718 | fragile histidine triad gene (FHIT), mRNA /cds=(362,805) | 1 | AAGCTAGAGTAATAGAGTTTGCT |
| 4591 | db mining | Hs.108694 | NM_002099 | 8051602 | glycophorin A (includes MN blood group) (GYPA), mRNA /cds=(55,507) | 1 | GCCTGTGGCCACCTGGGGTCACTT |
| 4592 | literature | Hs.342656 | NM_002119 | 4504400 | major histocompatibility complex, class II, DN alpha (HLA-DNA), mRNA /cds=(76,828) | 1 | GGAAAGGATCTGAATAAAGGGGACC |
| 4593 | literature | Hs.342656 | NM_002119 | 4504400 | major histocompatibility complex, class II, DN alpha (HLA-DNA), mRNA /cds=(76,828) | 1 | AAATACTGGCTCCAGGGTGGCGG |
| 4594 | db mining | Hs.1802 | NM_002120 | 4504402 | major histocompatibility complex, class II, DO beta (HLA-DOB), mRNA /cds=(56,877) | 1 | TGTTGGCAGCAGTGATCCTCTGAAC |
| 4595 | db mining | Hs.279930 | NM_002124 | 4504410 | major histocompatibility complex, class II, DR beta 3 (HLA-DRB3), mRNA /cds=(35,835) | 1 | TGCCCACACCCACACTCTCCAGCATC |
| 4596 | db mining | Hs.73885 | NM_002127 | 4504414 | HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA /cds=(5,1021) | 1 | TGGCACAATAAACATTTCTGTTT |
| 4597 | db mining | Hs.1521 | NM_002180 | 4504622 | immunoglobulin mu binding protein 2 (IGHMBP2), mRNA /cds=(49,3030) | 1 | TGCCACAATAAACATTTCTGTTT |
| 4598 | db mining | Hs.173880 | NM_002182 | 4504660 | interleukin 1 receptor accessory protein (IL1RAP), mRNA /cds=(206,1918) | 1 | GCACCCACCTTTCTGCACATAAGTTA |
| 4599 | literature | Hs.172689 | NM_002183 | 13324709 | interleukin 3 receptor, alpha (low affinity) (IL3RA), mRNA /cds=(146,1282) | 1 | TGGTTTTTCTCATCTTATCTGCTTC |
| 4600 | literature | Hs.12503 | NM_002189 | 4504648 | interleukin 15 receptor, alpha (IL15RA), mRNA /cds=(82,885) | 1 | AATTGTCAAACACAGCTTGAATATA |
| 4601 | literature | Hs.149609 | NM_002205 | 4504750 | integrin, alpha 5 (fibronectin receptor, alpha polypeptide) (ITGA5), mRNA /cds=(23,3172) | 1 | CATAGAAACGTCTGTGCTCAAGGA |
| 4602 | Table 3A | Hs.149846 | NM_002213 | 4504772 | integrin, beta 5 (ITGB5), mRNA /cds=(29,2419) | 1 | TCCAGAAACATGACAAGGAGGACTTT |
| 4603 | db mining | Hs.78465 | NM_002228 | 7710122 | v-jun avian sarcoma virus 17 oncogene homolog (JUN), mRNA /cds=(974,1969) | 1 | CCTGCTCTTGGAGATCAGAGGAG |
| 4604 | db mining | Hs.169824 | NM_002258 | 4504878 | killer cell lectin-like receptor subfamily B, member 1 (KLRB1), mRNA /cds=(60,737) | 1 | TCATAGTTAAATTTGGTATTCTGTTG |
| 4605 | db mining | Hs.172195 | NM_002408 | 6031183 | mannosyl (alpha-1,6)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT2), mRNA /cds=(489,1832) | 1 | GGAAGAAATGACCATTTCCCTTGT |
| 4606 | literature | Hs.77367 | NM_002416 | 4505186 | monokine induced by gamma interferon (MIG), mRNA /cds=(39,416) | 1 | ACACACATTCTTGCTCTACCCAAAGC |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|---|
| 4607 | Table 3A | Hs.926 | NM_002463 | 11342663 | myxovirus (influenza) resistance 2, homolog of murine (MX2), mRNA /cds=(104,2251) | 1 | TTTCCTGATTATGATGAGCTTCCATT GTTCTGTAAAGTCTTGAAGAGGA |
| 4608 | db mining | Hs.173084 | NM_002470 | 11342671 | myosin, heavy polypeptide 3, skeletal muscle, embryonic (MYH3), mRNA /cds=(84,5906) | 1 | CACGAGAGTGAAGAGTGAGCCAGCC CTTCTGGAGCAGGAGCAGGACAGAA |
| 4609 | db mining | Hs.113973 | NM_002472 | 4505300 | myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA /cds=(73,5886) | 1 | AAGAAAGGCACAAAATGTGCTATTTT TGGTCACTTGCTTTATGACGTTTA |
| 4610 | db mining | Hs.275163 | NM_002512 | 4505408 | non-metastatic cells 2, protein (NM23B) expressed in (NME2), nuclear gene encoding mitochondrial protein, mRNA /cds=(72,530) | 1 | GTCCCTGGACACAGCTCTTCATTCCA TTGACTTAGAGGCAACAGGATTGA |
| 4611 | Table 3A | Hs.85844 | NM_002529 | 4585711 | neurotrophic tyrosine kinase, receptor, type 1 (NTRK1), mRNA /cds=(0,2390) | 1 | GTACCAGCTCTCCAACACGGAGGCA ATCGACTGCATCAGCGAGGGACGTG |
| 4612 | db mining | Hs.93728 | NM_002586 | 4505624 | pre-B-cell leukemia transcription factor 2 (PBX2), mRNA /cds=(0,1292) | 1 | GGGGGCTAGTCTCTCCTCACTTGTA AACTTGTGTAGTTTCACAGAAAAA |
| 4613 | db mining | Hs.41639 | NM_002598 | 4505654 | programmed cell death 2 (PDCD2), mRNA /cds=(29,1063) | 1 | ACAGAAGAAATTTGTGTGGAAGCAGGA TGTAACAGATACACCGTAAAGGCA |
| 4614 | Table 3A | Hs.181013 | NM_002629 | 4505752 | phosphoglycerate mutase 1 (brain) (PGAM1), mRNA /cds=(31,795) | 1 | CCCTGCCACATGGGTCCAGTGTTCAT CTGAGCATACTGTACTAAATCCT |
| 4615 | db mining | Hs.288579 | NM_002644 | 11342673 | polymeric immunoglobulin receptor (PIGR), mRNA /cds=(156,2450) | 1 | CTTGAAGGAAGAGGGACCAGGGTGG GAGAGCTGATTGCAGAAAGGAGAGA |
| 4616 | db mining | Hs.261285 | NM_002669 | 4505894 | pleiotropic regulator 1 (PRL1, Arabidopsis homolog) (PLRG1), mRNA /cds=(0,1544) | 1 | AAACCATTAAAGTATACAGAGAGGAT GACACAGCCACAGAAGAACTCAT |
| 4617 | Table 3A | Hs.79402 | NM_002694 | 14702172 | polymerase (RNA) II (DNA directed) polypeptide C (33kD) (POLR2C), transcript variant gamma, mRNA /cds=(57,884) | 1 | AACATGCACAAAGCAGTTAATTAGGC AGCCTGGAGAAAACCAGAGATCCA |
| 4618 | Table 3A | Hs.77202 | NM_002738 | 4506068 | protein kinase C, beta 1 (PRKCB1), mRNA /cds=(136,2151) | 1 | ACTTCCAGAACTCATCAATGAACA GACAAATGTCAAACTACTGTGTCT |
| 4619 | literature | Hs.180533 | NM_002756 | 4506098 | mitogen-activated protein kinase kinase 3 (MAP2K3), mRNA /cds=(337,1293) | 1 | GCTTTATGGGTTTGGCTTGTTTTCTT GCATGGTTTGGAGCTGATCGCTT |
| 4620 | literature | Hs.118825 | NM_002758 | 14589899 | mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA /cds=(340,1344) | 1 | TTCTTCTTGGCCTCAAGTTCAATATG GAGAGGATTGCTTCCCTGAATCC |
| 4621 | db mining | Hs.241561 | NM_002770 | 4506146 | protease, serine, 2 (trypsin 2) (PRSS2), mRNA /cds=(6,749) | 1 | AACTATGTGGACTGGATTAAGGACAC CATAGCTGCCAACAGCTAAAGCCC |
| 4622 | db mining | Hs.928 | NM_002777 | 7382457 | proteinase 3 (serine proteinase, neutrophil, Wegener granulomatosis autoantigen) (PRTN3), mRNA /cds=(48,818) | 1 | CCTGACTTCTTCACGCGGGTAGCCCT CTACGTGGACTGGATCCGTTCTAC |
| 4623 | db mining | Hs.78575 | NM_002778 | 11386146 | prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), mRNA /cds=(38,1612) | 1 | AGCCAGCAGGACATGAAGTTGCTATT AAATGGACTTCGTGATTTTTGTTT |
| 4624 | db mining | Hs.250655 | NM_002823 | 4506276 | prothymosin, alpha (gene sequence 28) (PTMA), mRNA /cds=(155,487) | 1 | TTTGCCCTGTTTTGATGTATGTGTGA AACAATGTTGTCCAACAATAAACA |
| 4625 | db mining | Hs.82547 | NM_002888 | 4506424 | retinoic acid receptor responder (tazarotene induced) 1 (RARRES1), mRNA /cds=(36,722) | 1 | AACCTGTGCCACAAGAGTTACAATCA AAGTGGTCTCCTTAGACTGAATTC |
| 4626 | db mining | Hs.106061 | NM_002904 | 14670267 | RD RNA-binding protein (RDBP), mRNA /cds=(108,1250) | 1 | AAAGCCTTTAAAAACGGCTGTCAGGT TTGATCTCAGTGTAACAACATGGC |
| 4627 | db mining | Hs.139226 | NM_002914 | 4506486 | replication factor C (activator 1) 2 (40kD) (RFC2), mRNA /cds=(207,1271) | 1 | GAAAATGCGCCTTAGGCTGAGCCAA CATGACTGTCCCCCAAACCTCCAGTG |
| 4628 | db mining | Hs.123638 | NM_002918 | 4506492 | regulatory factor X, 1 (influences HLA class II expression) (RFX1), mRNA /cds=(93,3032) | 1 | CCAGCTTCGGTTCCTCCACCTCATC CGGCTGTCTACGACGAGTACATG |
| 4629 | db mining | Hs.166019 | NM_002919 | 4506494 | regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA /cds=(8,2131) | 1 | AAGATTGGTGCTCCTGATAAAGCAAA GGGCTAGGAATACAATGAAAGGA |
| 4630 | db mining | Hs.21273 | NM_002920 | 15011897 | transcription factor NYD-sp10 mRNA, complete cds /cds=(109,2034) | 1 | TCATTGGTACACATTCTGTATGCTGC TGTTTTCAAGTTGGCAAATTAAGC |
| 4631 | literature | Hs.73839 | NM_002935 | 4506550 | ribonuclease, RNase A family, 3 (eosinophil cationic protein) (RNASE3), mRNA /cds=(63,545) | 1 | TATCAGCAACTGTCCCTCATAGTCTC CATACCCCTTCAGCTTCTCTGAGC |
| 4632 | Table 3A | Hs.74267 | NM_002948 | 4506602 | 60S ribosomal protein L15 (EC45) mRNA, complete cds /cds=(34,648) | 1 | GCAGCTTGGAGAAGGCGCAATACTC CAGCTCCACCGTTACCGCTAATATA |
| 4633 | Table 3A | Hs.74267 | NM_002948 | 4506602 | 60S ribosomal protein L15 (EC45) mRNA, complete cds /cds=(34,648) | 1 | GCAGCTTGGAGAAGGCGCAATACTC CAGCTCCACCGTTACCGCTAATATA |
| 4634 | db mining | Hs.74592 | NM_002971 | 4506790 | special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's) (SATB1), mRNA /cds=(214,2505) | 1 | CGGAGCCTCAAACAAGCATTATACCT TCTGTGATTATGATTTCTCTCCT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|---|
| 4635 | Table 3A | Hs.89714 | NM_002994 | 4506848 | small inducible cytokine subfamily B (Cys-X-Cys), member 5 (epithelial-derived neutrophil-activating peptide 78) (SCYB5), mRNA /cds=(106,450) | 1 | ATGTTTCTTGGGGAATATGTTAGAGA ATTCCCTTACTCTTGATTGTGGGA |
| 4636 | db mining | Hs.82109 | NM_002997 | 4506858 | syndecan 1 (SDC1), mRNA /cds=(205,1137) | 1 | AGAGTGATAGTCTTTTGCTTTTGCCA AAACTCTACTTAATCCAATGGGTT |
| 4637 | db mining | Hs.301698 | NM_003033 | 4506950 | BAC 180i23 chromosome 8 map 8q24.3 beta-galactoside alpha-2,3-sialyltransferase (SIAT4A) gene, complete sequence /cds=(12296,13318) | 1 | GCCTCTTGCTTGGCGTGATAACCTCG TCATCTTCCCAAAGCTCATTATG |
| 4638 | db mining | Hs.78403 | NM_003083 | 4507102 | small nuclear RNA activating complex, polypeptide 2, 45kD (SNAPC2), mRNA /cds=(24,1028) | 1 | TTCAACTGACCAGTCGTGGTTACTCC CTGCTGCCAGGTCCTCCCTTCC |
| 4639 | literature | Hs.80738 | NM_003123 | 4507180 | gene for sialophorin (CD43) /cds=(159,1361) | 1 | GGCTGGCACCTCTCAACGTCTGTGG ACTGAATGAATAAACCTCCTCATC |
| 4640 | db mining | Hs.81884 | NM_003167 | 4507306 | sulfotransferase family, cytosolic, 2A, dehydroepiandrosterone (DHEA) - preferring, member 1 (SULT2A1), mRNA /cds=(52,909) | 1 | TGGGAATAACGTCCAAAACACTCTGG ATCTTATATGGAGAATGACATTGA |
| 4641 | literature | Hs.7510 | NM_003188 | 4507360 | DNA sequence from clone RP1-154G14 on chromosome 6q15-16.3. Contains the 3' end of the MAP3K7 gene for mitogen-activated protein kinase kinase kinase 7 (TGF-beta activated kinase 1, TAK1), ESTs, STSs and GSSs /cds=(0,1700) | 1 | AGTACTGAACTCAGTTCATCCGTAA AATATGTAAAGGTAAGTGGCAGCT |
| 4642 | db mining | Hs.250641 | NM_003290 | 4507650 | tropomyosin 4 (TPM4), mRNA /cds=(50,796) | 1 | GCCCAACTTCATTTCCATACTTCAGG GAACAGCAAATTGAGGATTTACTT |
| 4643 | Table 3A | Hs.178551 | NM_003316 | 10835036 | ribosomal protein L8 (RPL8), mRNA /cds=(43,816) | 1 | CCGTTGAATGAGTGTGTTTTGTACAT AATCTCAGATACTTGTGAACATGC |
| 4644 | Table 3A | Hs.4248 | NM_003371 | 4507870 | vav 2 oncogene (VAV2), mRNA /cds=(5,2641) | 1 | TTTCTTGGGAGAGTCACTCCAGCCCT GAAGTCTGTCTCTAGCTCCTCTGT |
| 4645 | Table 3A | Hs.89414 | NM_003467 | 4503174 | chemokine (C-X-C motif), receptor 4 (fusin) (CXCR4), mRNA /cds=(88,1146) | 1 | TCAGGAGTGGGTTGATTTCAGACCT ACAGTGACAGCTCTGTATTAAGT |
| 4646 | Table 3A | Hs.100293 | NM_003605 | 6006036 | O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) (OGT), mRNA /cds=(2039,4801) | 1 | TTAGGAGTGATTACTAATTATCAAGG GCACAGTTGTGGTACTGTCATTGA |
| 4647 | db mining | Hs.24640 | NM_003612 | 4504236 | sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A (SEMA7A), mRNA /cds=(17,2017) | 1 | CGGACGGAAGGACGGAAAAAGCTCT ATTTTTATGTTAGGCTTATTTTCATG |
| 4648 | db mining | Hs.131814 | NM_003747 | 4507612 | TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, partial cds /cds=(0,3284) | 1 | AGTCCCTGACAGCCTAGAAATAAGCT GTTTGTCTTCTATAAAGCATTGCT |
| 4649 | db mining | Hs.321231 | NM_003779 | 13929468 | UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3 (B4GALT3), mRNA /cds=(262,1443) | 1 | GCATTTTCTGCCTATGCTGGAATAGC TCCCTCTTCTGGTCCTGGCTCAGG |
| 4650 | Table 3A | Hs.151461 | NM_003797 | 14523051 | embryonic ectoderm development (EED), mRNA /cds=(34,1317) | 1 | AGTAAGGGCACGTAGAGCATTTAGAG TTGTCTTTCAGCATTCATCAGGC |
| 4651 | Table 3A | Hs.103755 | NM_003821 | 4506536 | receptor-interacting serine-threonine kinase 2 (RIPK2), mRNA /cds=(0,1622) | 1 | TGGGTCTTCAGCCTTACCCGGAATA CTTGTGGTTTCTAGATCACCATCT |
| 4652 | db mining | Hs.184376 | NM_003825 | 4507096 | Homo sapiens, synaptosomal-associated protein, 23kD, clone MGC:5155 IMAGE:3461227, mRNA, complete cds /cds=(73,708) | 1 | ACAAGGCTGACACCAACAGAGATCGT ATTGATATTGCCAATGCCAGAGCA |
| 4653 | db mining | Hs.158315 | NM_003853 | 4504656 | interleukin 18 receptor accessory protein (IL18RAP), mRNA /cds=(483,2282) | 1 | AGCTACTTCTGCCTTATGGCTAGGGA ACTGTCTATGTCTACCATGTATTGT |
| 4654 | db mining | Hs.102865 | NM_003854 | 4504662 | interleukin 1 receptor-like 2 (IL1RL2), mRNA /cds=(134,1822) | 1 | TGACTTGTTTTGTCTCATGTCTCCTC ATTCCTACACCTATTTTCTGCTGC |
| 4655 | db mining | Hs.159301 | NM_003855 | 4504654 | interleukin 18 receptor 1 (IL18R1), mRNA /cds=(24,1649) | 1 | CTGTGAAACCGTCAGTTCGGAAGGCT GGTAGAACATGTGGAGCAACAT |
| 4656 | db mining | Hs.35947 | NM_003925 | 4505120 | methyl-CpG binding domain protein 4 (MBD4), mRNA /cds=(176,1918) | 1 | GCCTAGTGTGTGTGCTTTCTTAATGT GTGTGCCAATGGTGGATCTTTGCT |
| 4657 | db mining | Hs.287832 | NM_003953 | 4506356 | myelin protein zero-like 1 (MPZL1), mRNA /cds=(132,941) | 1 | ACCAAACGGAAGTCTCGTGCAGAAAA TGTAGCCCATGACCATGTAGCC |
| 4658 | Table 3A | Hs.108371 | NM_003973 | 4506600 | E2F transcription factor 4, p107/p130-binding (E2F4), mRNA /cds=(62,1303) | 1 | GCACCTGCTCCAAAGGCATCTGGCA AGAAAGCATAAGTGGCAATCATAAA |
| 4659 | Table 3A | Hs.155101 | NM_004046 | 4757809 | mRNA for KIAA1578 protein, partial cds /cds=(0,3608) | 1 | CTCCTGTGGATTACATCAAATACCA GTTTCAGTTTGTCTTGTCTAGT |
| 4660 | Table 3A | Hs.238990 | NM_004064 | 4757961 | Homo sapiens, Similar to cyclin-dependent kinase inhibitor 1B (p27, Kip1), clone MGC:5304 IMAGE:3458141, mRNA, complete cds /cds=(377,973) | 1 | GCCAACAGAACAGAGAAAATGTTTC AGACGGTTCCCCAAATGCCGGTTC |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|--|
| 4661 | Table 3A | Hs.239760 | NM_004077 | 4758075 | Homo sapiens, clone MGC:19593 IMAGE:3542491, mRNA, complete cds /cds=(118,1518) | 1 | CTCTAGAAAGGCCCAAGTCCATGAGC ACAGAGGGTCTGATGAAGTTTGTG |
| 4662 | db mining | Hs.272537 | NM_004088 | 4758185 | deoxynucleotidyltransferase, terminal (DNTT), mRNA /cds=(0,1532) | 1 | AGACCAAGAGGATATTCCTCAAAGCA GAAAGTGAAGAGAAATTTTTCG |
| 4663 | db mining | Hs.75450 | NM_004089 | 4758197 | mRNA for GILZ, complete cds /cds=(233,637) | 1 | TGGAGAAGTTCAGTCTGTCTGAGC CCTGAAGAGCCAGCTCCCGAATCC |
| 4664 | db mining | Hs.32981 | NM_004186 | 4759089 | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F (SEMA3F), mRNA /cds=(78,2435) | 1 | GAAGTAGACTTTCTGTCTCACACCG AAGAACCCGAGTGAGCAGGAGGGA |
| 4665 | db mining | Hs.444 | NM_004197 | 4759179 | serine/threonine kinase 19 (STK19), transcript variant 2, mRNA /cds=(128,1234) | 1 | GTGGGATTTCTGGGGAGGCTGGTGA AGGAGGGCAGGGTTCTTTCTCTAC |
| 4666 | db mining | Hs.74115 | NM_004258 | 4758589 | immunoglobulin superfamily, member 2 (IGSF2), mRNA /cds=(21,3086) | 1 | CTATAGCTTCATGACCGTAACATGTG ACCTGTGTGCTGGCAGGACGACTC |
| 4667 | db mining | Hs.25887 | NM_004263 | 4759093 | mRNA; cDNA DKFZp761O15121 (from clone DKFZp761O15121); complete cds /cds=(111,2423) | 1 | ATGATCCCCATGTTGCAATATGGAGT CTCTGCCTGAGATCTTCCCCATC |
| 4668 | Table 3A | Hs.184211 | NM_004279 | 4758733 | peptidase (mitochondrial processing) beta (PMPCB), mRNA /cds=(13,1482) | 1 | TGGTCAGTCTTTGTTCTCTGAGAAAT TATGTTGGAAGCAGCATACCTTCA |
| 4669 | db mining | Hs.18142 | NM_004313 | 4757779 | arrestin, beta 2 (ARRB2), mRNA /cds=(53,1282) | 1 | CCCCAAGATACACACTGGACCCCTCTC TTGCTGAATGTGGGCATTAAATTTT |
| 4670 | literature | Hs.54457 | NM_004356 | 4757943 | CD81 antigen (target of antiproliferative antibody 1) (CD81), mRNA /cds=(238,948) | 1 | TTCTAACACGTCTGCCTTCAACTGTAA TCACAACATCCTGACTCCGTCATT |
| 4671 | db mining | Hs.42853 | NM_004381 | 14577922 | cAMP responsive element binding protein-like 1 (CREBL1), mRNA /cds=(33,2144) | 1 | TTTTTCATTTTGAGCTAGTTACTGG GAGTAAGGGAGGGTGGGGTGGGGG |
| 4672 | db mining | Hs.318546 | NM_004390 | 4758095 | cDNA: FLJ22499 fis, clone HRC11250, highly similar to HSCATHH mRNA for cathepsin H (EC 3.4.22.16) /cds=UNKNOWN | 1 | GGGACTGTCTTTTCTGTATTCGCTGT TCAATAAACATTGAGTGAGCACCT |
| 4673 | literature | Hs.318546 | NM_004390 | 4758095 | cDNA: FLJ22499 fis, clone HRC11250, highly similar to HSCATHH mRNA for cathepsin H (EC 3.4.22.16) /cds=UNKNOWN | 1 | GGGACTGTCTTTTCTGTATTCGCTGT TCAATAAACATTGAGTGAGCACCT |
| 4674 | Table 3A | Hs.124024 | NM_004416 | 4758201 | deltex (Drosophila) homolog 1 (DTX1), mRNA /cds=(503,2365) | 1 | AGAGAAGACTCATCTTCACTATCGGC ACGTCCAACACCACGGCGAGTCG |
| 4675 | Table 3A | Hs.74088 | NM_004430 | 4758251 | early growth response 3 (EGR3), mRNA /cds=(357,1520) | 1 | AAACCGAAATATTGAAATGGTGTAAT GTTGTACCATTTGCAGTGTGAGCA |
| 4676 | db mining | Hs.278611 | NM_004482 | 9945386 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 3 (GalNAc-T3) (GALNT3), mRNA /cds=(0,1901) | 1 | AGGTGGGGGAGAAATGAAATTTTGATG CTGAATTTCTAAGCGCCTATTGTT |
| 4677 | db mining | Hs.73734 | NM_004488 | 4758459 | glycoprotein V (platelet) (GP5), mRNA /cds=(270,1952) | 1 | GTGGATGTGGAGCAGGAGAGCTGGA TCGTGGCATTGTTTCTGGGTTCTG |
| 4678 | db mining | Hs.182447 | NM_004500 | 14110430 | heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC), transcript variant 1, mRNA /cds=(191,1102) | 1 | AAAGTTGATACTGTGGGATTTTGTG AACAGCCTGATGTTTGGGACCTTT |
| 4679 | db mining | Hs.111065 | NM_004505 | 4758563 | ubiquitin specific protease 6 (Tre-2 oncogene) (USP6), mRNA /cds=(1696,4056) | 1 | TGTGGTTGCCTCTATGTGCTGTTTTT CCTCATACAAGTAAACACAGAAAG |
| 4680 | Table 3A | Hs.76038 | NM_004508 | 4758583 | isopentenyl-diphosphate delta isomerase (IDI1), mRNA /cds=(50,736) | 1 | CCCAACTGAGGACCACTGTCTACAGA GTCAGGAAATATTGTAGGGAGAAA |
| 4681 | db mining | Hs.296281 | NM_004514 | 4758599 | interleukin enhancer binding factor 1 (ILF1), mRNA /cds=(197,2164) | 1 | TGTTTTGTTTCTTTGTGTTGACTTTGTC CCTGGCAAAATTTTCACTCTGA |
| 4682 | db mining | Hs.172674 | NM_004555 | 4758803 | nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 (NFATC3), mRNA /cds=(210,3416) | 1 | AGGTGACCTGGTTACTTAGCTAGGAT TGGTGATTTGTAAGTCTTTATGGT |
| 4683 | Table 3A | Hs.78920 | NM_004581 | 4759015 | Rab geranylgeranyltransferase, alpha subunit (RABGGTA), mRNA /cds=(274,1977) | 1 | CCCTACCCTTGCCCTTTAACTTATTG GGACTGAATAAAGATGGAGAGGC |
| 4684 | db mining | Hs.90957 | NM_004620 | 4759253 | TNF receptor-associated factor 6 (TRAF6), mRNA /cds=(221,1789) | 1 | GGGCTTTTGCTCTGGTGATTTTATT GTCAGAAAGTCCAGACTCAAGAGT |
| 4685 | db mining | Hs.25333 | NM_004633 | 4758597 | interleukin 1 receptor, type II (IL1R2), mRNA /cds=(61,1257) | 1 | TGGTCTGACTGTGCTATGGCCTCATC ATCAAGACTTTCAATCCTATCCCA |
| 4686 | db mining | Hs.82222 | NM_004636 | 4759091 | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B (SEMA3B), mRNA /cds=(235,2484) | 1 | GGGCGAGGCGAGGCCGACTGTACTAA AGTAACGCAATAAAGCATTATCAG |
| 4687 | db mining | Hs.332229 | NM_004669 | 4758005 | zh68e05.s1 cDNA, 3' end /clone=IMAGE:417248 /clone_end=3' | 1 | GTACGCCGCTACCTGGACAGCGCGA TGCAGGAGAAAGAGTTCAAATACAC |
| 4688 | Table 3A | Hs.77324 | NM_004730 | 4759033 | eukaryotic translation termination factor 1 (ETF1), mRNA /cds=(135,1448) | 1 | TGCAGAGAGATACTAAGCAGCAAAAT CTTGTTGTTGTGATGTACAGAAAT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|--|
| 4689 | Table 3A | Hs.326159 | NM_004735 | 4758689 | leucine rich repeat (in FLII) interacting protein 1 (LRRFIP1), mRNA /cds=(178,2532) | 1 | GGATAACAAGTAAATGTCTGAAAGCA TGAGGGGCTTTATTTGCCTTTACC |
| 4690 | db mining | Hs.107526 | NM_004776 | 13929470 | UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5 (B4GALT5), mRNA /cds=(112,1278) | 1 | TGAGCTTGCTCTTACGTTTTAAGAGG TGCCAGGGGTACATTTTGCACGTG |
| 4691 | Table 3A | Hs.49587 | NM_004811 | 4758669 | leupaxin (LPXN), mRNA /cds=(93,1253) | 1 | ACTGGACAACCTTTGAGTACTGACATC ATTGATAAAATAAACTGGCTTGTGG |
| 4692 | db mining | Hs.24395 | NM_004887 | 4757869 | NJAC protein (NJAC) mRNA, complete cds /cds=(7,306) | 1 | CGCAGGGGTCTACGAAGAATAGGGTG AAAAACCTCAGAAAGGAAAACTCCA |
| 4693 | Table 3A | Hs.145696 | NM_004902 | 4757925 | splicing factor (CC1.3) (CC1.3), mRNA /cds=(149,1723) | 1 | AGGTTTTGTCTGGTTGCATATAATCTT TGCTCTTTTTAAGCTCTGTGAGC |
| 4694 | db mining | Hs.129738 | NM_004977 | 4826787 | potassium voltage-gated channel, Shaw-related subfamily, member 3 (KCNC3), mRNA /cds=(295,2568) | 1 | CCTTGCAGACCCACCCCTGCCTG CTCTCTTCCCTACAACCTAGGTCAG |
| 4695 | db mining | Hs.279946 | NM_004990 | 14043021 | methionine-tRNA synthetase (MARS), mRNA /cds=(23,2725) | 1 | GCCCCCTAAAGGCAAGAAGAAAAAGTA AAAGACCTTGGCTCATAGAAAGTC |
| 4696 | db mining | Hs.927 | NM_004997 | 4826841 | myosin-binding protein H (MYBPH), mRNA /cds=(28,1458) | 1 | GGAGTTGCACCTCGGGTGGGAAGCA CTCAAATAAAGATGCGTGGTGTAA |
| 4697 | Table 3A | Hs.180610 | NM_005066 | 4826997 | splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-associated) (SFPQ), mRNA /cds=(85,2208) | 1 | AGCTTTTGAAAGTGGAAGGTCATT TTGTTGCATTCCCCATTCTTGT |
| 4698 | literature | Hs.100001 | NM_005074 | 4827009 | solute carrier family 17 (sodium phosphate), member 1 (SLC17A1), mRNA /cds=(12,1415) | 1 | ACCTCCTTATTGAAGGGAAGAGGGAC CAGCACATGAGGCTGAGGCTGAGG |
| 4699 | db mining | Hs.81737 | NM_005155 | 6325470 | inactive palmitoyl-protein thioesterase-2i (PPT2) mRNA, complete cds /cds=(568,1473) | 1 | GGTATCTCCACACAGCCTGGCACTC CAACCGTACCCTTTATGAGACCTG |
| 4700 | db mining | Hs.179735 | NM_005167 | 4885066 | ras homolog gene family, member C (ARHC), mRNA /cds=(76,657) | 1 | AAGGATGGTCACACACCAGCACTTTA TACACTTCTGGCTCAGAGGAAAGT |
| 4701 | literature | Hs.113222 | NM_005201 | 13929430 | chemokine (C-C motif) receptor 8 (CCR8), mRNA /cds=(120,1187) | 1 | ATCATCTGCGCAGCAGCACTCCTCCC GTTCTCCAGCGGTAGACTACATTT |
| 4702 | db mining | Hs.181128 | NM_005229 | 11496880 | DNA sequence from PAC 212G6 on chromosome Xp11.3-p11.4. Contains synapsin 1, brain protein 4.1, properdin, tyrosine kinase (ELK1) oncogene, ESTs, STS, GSS /cds=(9150,10436) | 1 | AGTGCTACACTCGTCTCCACTGTTTG TTTTACTTCCCCAAAATGGACCTT |
| 4703 | Table 3A | Hs.248109 | NM_005238 | 4885218 | v-ets avian erythroblastosis virus E26 oncogene homolog 1 (ETS1), mRNA /cds=(278,1603) | 1 | ACGCTACTATTACGACAAAAACATCA TCCACAAGACAGCGGGGAAACGCT |
| 4704 | Table 3A | Hs.85146 | NM_005239 | 4885220 | chromosome 21 derived BAC containing erythroblastosis virus oncogene homolog 2 protein (ets-2) gene, complete cds /cds=(290,1699) | 1 | TTTGAGAGGGTAGGAGGGTGGGAAG GAAACAACCATGTCAATTCAGAAGT |
| 4705 | db mining | Hs.129953 | NM_005243 | 4885224 | Ewing sarcoma breakpoint region 1 (EWSR1), transcript variant EWS, mRNA /cds=(43,2013) | 1 | CATGCTCAGTATCATTTGTGGAGAACC AAGAGGGCTCTTAAGTGAACAA |
| 4706 | db mining | Hs.289098 | NM_005265 | 4885270 | kidney gamma-glutamyl transpeptidase type II mRNA, 3' end /cds=(0,596) | 1 | GACCGGCTTCCCTGTGAGCAGCAG AGCAGCACATAAATGAGGCCACTG |
| 4707 | Table 3A | Hs.181307 | NM_005324 | 4885384 | H3 histone, family 3A (H3F3A), mRNA /cds=(374,784) | 1 | GAAGATACCAACCTGTGTGCCATCCA CGCTAAGAGAGTCAACCATCATGCC |
| 4708 | Table 3A | Hs.79334 | NM_005384 | 4885516 | nuclear factor, interleukin 3 regulated (NFIL3), mRNA /cds=(213,1601) | 1 | GTTATCACTCTGCCTGTGTATAGTCA GATAGTCCATGCGAAGGCTGTATA |
| 4709 | db mining | Hs.297939 | NM_005385 | 6631099 | cathepsin B (CTSB), mRNA /cds=(177,1196) | 1 | ACTGACAGAGTGAAGTACAGAAATAG CTTTTCTTCTAAAGGGGATTGTT |
| 4710 | db mining | Hs.78824 | NM_005424 | 4885630 | tyrosine kinase with immunoglobulin and epidermal growth factor homology domains (TIE), mRNA /cds=(36,3452) | 1 | TAAGCCAGCACTCACACCCTAACAT GCCCTGTTCACTACTCCCACTCC |
| 4711 | Table 3A | Hs.181195 | NM_005494 | 4885494 | Homo sapiens, MRJ gene for a member of the DNAJ protein family, clone MGC:1152 IMAGE:3346070, mRNA, complete cds /cds=(163,1143) | 1 | GGATGTTTTCTAGTTGTGCATGAATG CTGGCAACTAGTAAGTTTTGACA |
| 4712 | db mining | Hs.153299 | NM_005510 | 5031670 | DOM-3 (C. elegans) homolog Z (DOM3Z), transcript variant 2, mRNA /cds=(129,1319) | 1 | CCCAAATAGTAATGCTTTAGAGGGAG GCAGTCATATCTCTGTGTGCAGAT |
| 4713 | db mining | Hs.77961 | NM_005514 | 5031742 | major histocompatibility complex, class I, B (HLA-B), mRNA /cds=(0,1088) | 1 | ATGTGTAGGAGGAAGAGTTCAGGTG GAAAAGGAGGGAGCTACTCTCAGGC |
| 4714 | literature | Hs.279853 | NM_005516 | 5031744 | HSPC018 protein (HSPC018), mRNA /cds=(148,651) | 1 | CCCCTTCTCAGACTGACCTGTGTTT CTTCCCTGTTCTCTTTCTATTAA |
| 4715 | db mining | Hs.80288 | NM_005527 | 5031768 | heat shock 70kD protein-like 1 (HSPA1L), mRNA /cds=(0,1925) | 1 | AAACTCTACCAAGGAGGATGCACTGG GCCTGCCTGCGGAACAGGGTATGT |
| 4716 | db mining | Hs.171776 | NM_005536 | 8393607 | inositol(myo)-1(or 4)-monophosphatase 1 (IMPA1), mRNA /cds=(98,931) | 1 | CCCTTGGCACGTAAACAGACTACTAG ACTTATTGTAGGTTCTGTTGAGCT |
| 4717 | db mining | Hs.102171 | NM_005545 | 5031808 | immunoglobulin superfamily containing leucine-rich repeat (ISLR), mRNA /cds=(98,1384) | 1 | CAAAGGCCAGCCAGCTTGGGAGCAG CAGAGAAATAAACAGCATTTCTGAT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|---|
| 4718 | literature | Hs.150101 | NM_005561 | 7669500 | lysosomal-associated membrane protein 1 (LAMP1), mRNA /cds=(190,1440) | 1 | GTGAGATCGGTGCGTTCTCCTGATGT TTTGCCGTGGCTTGGGGATTGTAC |
| 4719 | db mining | Hs.154970 | NM_005653 | 5032174 | transcription factor CP2 (TFCP2), mRNA /cds=(508,1860) | 1 | GAACCTTCAGGAAGAAGCATGTTTTA TTCTGGACACAATGAAAGAAACCA |
| 4720 | Table 3A | Hs.82173 | NM_005655 | 5032176 | TGFB inducible early growth response (TIEG), mRNA /cds=(123,1565) | 1 | TTGGGTGTAGATTTCTGACATCAAAA CTTGGACCCCTTGAAACAAAGT |
| 4721 | db mining | Hs.200600 | NM_005698 | 5032076 | secretory carrier membrane protein 3 (SCAMP3), mRNA /cds=(96,1139) | 1 | CAACCCAGCTTCCCTCTGCTGTGCCA CGGCTGTTGCTTCGGTTATTTAAA |
| 4722 | db mining | Hs.157144 | NM_005819 | 5032130 | syntaxin 6 (STX6), mRNA /cds=(0,767) | 1 | ATAGCCATCCCTCTTTGCAGTCCTGTT GGTTGTGCTCATCCTCTTCTAGT |
| 4723 | db mining | Hs.17704 | NM_005844 | 5031730 | PERB11 family member in MHC class I region (HCGIX), mRNA /cds=(37,270) | 1 | ACATGAGCTTCTACCTCCAGATGTGC CAGGGTGCATCTCAATAAACCTTGG |
| 4724 | db mining | Hs.135194 | NM_005849 | 5031672 | immunoglobulin superfamily, member 6 (IGSF6), mRNA /cds=(44,769) | 1 | ACTGAAAAGACAACCTGGCTACAAAGA AGGATGTCAGAATGTAAGGAAACT |
| 4725 | db mining | Hs.4953 | NM_005895 | 5174440 | golgi autoantigen, golgin subfamily a, 3 (GOLGA3), mRNA /cds=(269,4861) | 1 | AAGTTGTGGCTGTTCTTGGGAAAGGG GTCACCGTGTCTGACAAAGTGTA |
| 4726 | db mining | Hs.211580 | NM_005931 | 5174564 | MHC class I polypeptide-related sequence B (MICB), mRNA /cds=(5,1156) | 1 | CCCCTCGCCCCGTACACCGTTATG CATTACTCTGTGTCTACTATTATGT |
| 4727 | Table 3A | Hs.68583 | NM_005932 | 5174566 | mitochondrial intermediate peptidase (MIPEP), nuclear gene encoding mitochondrial protein, mRNA /cds=(74,2215) | 1 | GCTGTGAGAGCTTGTCTGATTGTT TCATTGTTGCTTCTGTAATTCTG |
| 4728 | Table 3A | Hs.54452 | NM_006060 | 5174500 | zinc finger protein, subfamily 1A, 1 (Ikaros) (ZNFN1A1), mRNA /cds=(168,1727) | 1 | ACCAACACTGTCCCAAGGTGAAATGA AGCAACAGAGAGGAAATTGTACAT |
| 4729 | db mining | Hs.292276 | NM_006068 | 5174720 | qd64a01.x1 cDNA, 3' end /clone=IMAGE:1734216 /clone_end=3' | 1 | TGCTCAGTTTTTCAGCTCCTCTCCAC TCTGCTTTCCCAATGGATTCTGT |
| 4730 | db mining | Hs.131342 | NM_006072 | 5174670 | small inducible cytokine subfamily A (Cys-Cys), member 26 (SCYA26), mRNA /cds=(0,284) | 1 | ATATTCACCTACCAAAAGAGGCAAGAA AGTCTGTACCCATCCAAGGAAAAA |
| 4731 | db mining | Hs.2414 | NM_006080 | 5174672 | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (SEMA3A), mRNA /cds=(15,2330) | 1 | GCTGCATTACCTCTAGAAACCTCAAA CAAGTAGAACTTGCTAGACAAT |
| 4732 | db mining | Hs.2654 | NM_006081 | 5174562 | MHC binding factor, beta (MHCBBF), mRNA /cds=(90,1286) | 1 | TCCAAGTCGAAATCGCTGCTGAGGCT GAGATGAAGAAAGAAAGTCCAAA |
| 4733 | literature | Hs.125359 | NM_006288 | 5454117 | Homo sapiens, clone MGC:846 IMAGE:3507917, mRNA, complete cds /cds=(60,545) | 1 | CATCTCCTCCAGAACGTCACAGTGC TCAGAGACAACCTGGTCAAGGTG |
| 4734 | db mining | Hs.23168 | NM_006313 | 14149626 | ubiquitin specific protease 15 (USP15), mRNA /cds=(9,2867) | 1 | TTTGTCTGCACTTGAGTTCACTTGAG TTTACATTGAAATGTGCATGTTT |
| 4735 | db mining | Hs.171921 | NM_006379 | 5454047 | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA /cds=(562,2817) | 1 | AGTTCCTTTATTTACATAAGCCCAA ACTGATAGACAGTAACGGGTGTTT |
| 4736 | db mining | Hs.240534 | NM_006411 | 5453717 | 1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) | 1 | GGAGAGGGTGGGACCCAGTTTTCGG TGGTTGGTTTTTATTAATTATCTGG |
| 4737 | db mining | Hs.181368 | NM_006445 | 5453983 | U5 snRNP-specific protein (220 kD), ortholog of S. cerevisiae Prp8p (PRP8), mRNA /cds=(41,7048) | 1 | CCTCTTCCCTCTGTCTGTGCTTGTG TTGTTGACCTCCTGATGGCTTGTG |
| 4738 | db mining | Hs.239506 | NM_006561 | 5729815 | mab-21 (C. elegans)-like 1 (MAB21L1), mRNA /cds=(818,1897) | 1 | CTGATTCTCTGTCTCATTGTGAAC ATAACCGTGTAGTTGAAACAGTCA |
| 4739 | db mining | Hs.34526 | NM_006564 | 5730105 | G protein-coupled receptor (TYMSTR), mRNA /cds=(81,1109) | 1 | TTTCCAATGTCTGCCACACAAACGTA TGAAATGTATATACCCACACACA |
| 4740 | db mining | Hs.86998 | NM_006599 | 5729944 | nuclear factor of activated T-cells 5, tonicity-responsive (NFAT5), mRNA /cds=(318,4913) | 1 | TCCTGAGAAACAACACATTTTCCCC ATGAACGGTGCTGTTCTGAAGTCT |
| 4741 | db mining | Hs.167751 | NM_006604 | 5730012 | ret finger protein-like 3 (RFPL3), mRNA /cds=(292,1158) | 1 | TATTGCCACCATCCAACCTATTGAGT CTTATGGTTCACATCTTGTTCCT |
| 4742 | db mining | Hs.157427 | NM_006605 | 5730010 | ret finger protein-like 2 (RFPL2), mRNA /cds=(292,1158) | 1 | AGTCCTATGGTTCACATCTTGTTCCT ATAGAAATGTCCTGTATTTCTGGG |
| 4743 | db mining | Hs.74861 | NM_006713 | 5729967 | activated RNA polymerase II transcription cofactor 4 (PC4), mRNA /cds=(0,383) | 1 | AAACCAAGAAAGAAAGGTATTCTTT AAATCCAGAACAAATGGAGCCAGCT |
| 4744 | db mining | Hs.75063 | NM_006734 | 5803032 | DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAAT repeat polymorphism /cds=(545,7885) | 1 | AAGCAGTTGGACTTTTACAGCAGCAA GGAATTATCTTCAAGCACAGAGGA |
| 4745 | db mining | Hs.56328 | NM_006737 | 5803051 | killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2 (KIR3DL2), mRNA /cds=(2,1369) | 1 | CTTCAGTGTAGCTCTCTCCTCTTCAA ATAACATGTCTGCCCTCATGGTT |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|-----------------------------|
| 4746 | db mining | Hs.82210 | NM_006766 | 5803097 | zinc finger protein 220 (ZNF220), mRNA /cds=(393,6407) | 1 | TTCTCTCGTGCAACCAGTTTGCCCAT |
| 4747 | db mining | Hs.57692 | NM_006781 | 11321623 | chromosome 6 open reading frame 10 (C6orf10), mRNA /cds=(236,1942) | 1 | TCTCTTCCTATTACTTGTCTCCAGG |
| 4748 | db mining | Hs.84665 | NM_006790 | 5803105 | titin immunoglobulin domain protein (myotilin) (TTID), mRNA /cds=(280,1776) | 1 | TGCTCTTCAGAAAGTTTACCCTTTTTA |
| 4749 | db mining | Hs.170027 | NM_006880 | 6031173 | mouse double minute 2, homolog of; p53-binding protein (MDM2), transcript variant MDM2, mRNA /cds=(311,1786) | 1 | ATCTCTCAGCCACAAACCTCAGT |
| 4750 | literature | Hs.27954 | NM_006889 | 5901919 | CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (CD86), mRNA /cds=(147,1118) | 1 | ACGTTTACTGGTACTGCTTTCTAAATA |
| 4751 | Table 3A | Hs.173737 | NM_006908 | 9845510 | ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) (RAC1), transcript variant Rac1b, mRNA /cds=(0,635) | 1 | CTGTTTTACCGCTTTTCTCTTGT |
| 4752 | db mining | Hs.216354 | NM_006913 | 5902053 | ring finger protein 5 (RNF5), mRNA /cds=(0,542) | 1 | GACAACCAATTCAAATGATTGTGCTA |
| 4753 | db mining | Hs.153299 | NM_006929 | 13787218 | DOM-3 (C. elegans) homolog Z (DOM3Z), transcript variant 2, mRNA /cds=(129,1319) | 1 | ACTTATTTCCCTAGTTGACCTGT |
| 4754 | literature | Hs.278721 | NM_006979 | 5901935 | HLA class II region expressed gene KE4 (HKE4), mRNA /cds=(326,1615) | 1 | GGCCAAGCCCAGCTTAATGGCTCAT |
| 4755 | Table 3A | Hs.97437 | NM_007018 | 5901923 | centrosomal protein 1 (CEP1), mRNA /cds=(472,3456) | 1 | GACCTGGAATAAAATTTAGGACCA |
| 4756 | db mining | Hs.41716 | NM_007036 | 13259505 | endothelial cell-specific molecule 1 (ESM1), mRNA /cds=(68,622) | 1 | CTCAAGACAGTGTGTGACGAAGCGAT |
| 4757 | db mining | Hs.155150 | NM_007042 | 5902065 | ribonuclease P (14kD) (RPP14), mRNA /cds=(169,543) | 1 | CCGAGCAGTCCTCTGCCCGCCTCC |
| 4758 | db mining | Hs.81743 | NM_007053 | 5901909 | natural killer cell receptor, immunoglobulin superfamily member (BY55), mRNA /cds=(215,760) | 1 | CTTTTTCAACCACCGTCTTCAATGCC |
| 4759 | db mining | Hs.43543 | NM_007056 | 5902129 | suppressor of white apricot homolog 2 (SWAP2), mRNA /cds=(143,2122) | 1 | ATGAGCCTTTCCGCCGGGGTACAG |
| 4760 | db mining | Hs.247979 | NM_007128 | 9507238 | pre-B lymphocyte gene 1 (VPREB1), mRNA /cds=(0,437) | 1 | ACATCGTATTTGCGGCCAGCCTCTAC |
| 4761 | literature | Hs.41682 | NM_007334 | 7669498 | killer cell lectin-like receptor subfamily D, member 1 (KLRD1), transcript variant 1, mRNA /cds=(260,799) | 1 | ACCCAGTGAATGCCCATGTAAAA |
| 4762 | Table 3A | Hs.173334 | NM_012081 | 6912353 | ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA /cds=(0,1922) | 1 | TATTCCTTTTATATCACTGTGTTTGAA |
| 4763 | db mining | Hs.268555 | NM_012255 | 6912743 | 5'-3' exoribonuclease 2 (XRN2), mRNA /cds=(68,2920) | 1 | TCGAGGGGGAGGGGTGGTAACCG |
| 4764 | db mining | Hs.258612 | NM_012312 | 6912471 | killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 4 (KIR2DS4), mRNA /cds=(46,960) | 1 | ATGGGAATAGTTGCATATGGGAATTT |
| 4765 | db mining | Hs.212414 | NM_012431 | 6912649 | sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3E (SEMA3E), mRNA /cds=(466,2793) | 1 | AAACCAACATGTGGCTGAGCCTTT |
| 4766 | Table 3A | Hs.144519 | NM_012468 | 10947106 | T-cell leukemia/lymphoma 6 (TCL6), transcript variant TCL6a2, mRNA /cds=(1767,2192) | 1 | GGCCTTTGAATGTAAAGCTGCATAAG |
| 4767 | db mining | Hs.334729 | NM_013230 | 7019342 | cDNA FLJ20161 fis, clone COL09252, highly similar to L33930 CD24 signal transducer mRNA /cds=UNKNOWN | 1 | CTGTTAGGTTTTGTTTTAAAGGA |
| 4768 | db mining | Hs.278911 | NM_013278 | 7019434 | interleukin 17C (IL17C), mRNA /cds=(0,593) | 1 | CAGTTTGGCCTTATGCCTTATGCAGA |
| 4769 | db mining | Hs.71979 | NM_013371 | 7019574 | interleukin 19 (IL19), mRNA /cds=(47,580) | 1 | CTTGAGTGTATGCAGGATTTTCAAT |
| 4770 | db mining | Hs.247362 | NM_013974 | 7524353 | dimethylarginine dimethylaminohydrolase 2 (DDAH2), mRNA /cds=(276,1133) | 1 | CAGACCAAGAGGCGAGAGTAAAGA |
| 4771 | Table 3A | Hs.8360 | NM_014039 | 7662640 | PTD012 protein (PTD012), mRNA /cds=(473,1087) | 1 | CTGCCCAGCTTCATCTAAATACTT |
| 4772 | Table 3A | Hs.6975 | NM_014086 | 7662589 | AF001542 cDNA /clone=alpha_est218/52C1 | 1 | GAGTTTCTCTATCGCATTGGTCAACC |
| 4773 | db mining | Hs.278944 | NM_014148 | 7661751 | HSPC048 protein (HSPC048), mRNA /cds=(87,419) | 1 | AAAAGAGACGCATTCCATTGGCG |
| 4774 | db mining | Hs.278946 | NM_014152 | 7661759 | HSPC054 protein (HSPC054), mRNA /cds=(107,397) | 1 | TTCTCTGCATCTAGGCCATCACTG |
| 4775 | db mining | Hs.278948 | NM_014163 | 7661781 | HSPC073 protein (HSPC073), mRNA /cds=(278,649) | 1 | CCAGGCTGGTTATGACTCAGAAGA |
| | | | | | | | TGCCAAATGTGGGACTGTGGACTGT |
| | | | | | | | GATTCTAAGTGGGGGAAATAGGCT |
| | | | | | | | GAACCTTTCTGAAACCGATGGCAGCC |
| | | | | | | | CAAGTTAGAGCCCAGCATTAAGTC |
| | | | | | | | CCAGAATCTTCTATTCCCACTCCCA |
| | | | | | | | TTTCTCAAATCATTTGACCTGTCCG |

Table 8

| | | | | | | | |
|------|-----------|-----------|-----------|----------|--|---|---|
| 4776 | db mining | Hs.130101 | NM_014227 | 14140235 | solute carrier family 5 (neutral amino acid transporters, system A), member 4 (SLC5A4), mRNA /cds=(16,1995) | 1 | CCTCCTGGCTGTGGTGGTCTTTATTC ACGGCTACTATGCCTGAACCTCTAT |
| 4777 | db mining | Hs.205736 | NM_014260 | 7657161 | HLA class II region expressed gene KE2 (HKE2), mRNA /cds=(0,389) | 1 | GAAATTAAGCGATACGAATCCCAGCT TCGGGATCTTGAGCGGCAGTCAGA |
| 4778 | db mining | Hs.241385 | NM_014271 | 7657231 | interleukin 1 receptor accessory protein-like 1 (IL1RAPL1), mRNA /cds=(510,2600) | 1 | TCACAGTGACCACTACAGAGTACTAA GAAGAGAAGATCAAGGGGCATGAAA |
| 4779 | Table 3A | Hs.211973 | NM_014285 | 7657527 | Homo sapiens, Similar to homolog of Yeast RRP4 (ribosomal RNA processing 4), 3'-5'-exoribonuclease, clone MGC:2403 IMAGE:2821702, mRNA, complete cds /cds=(11,892) | 1 | TCTTAAAGCCAGAAATAATGGAGGAG ATTGTGATGGAAACACGCCAGAGG |
| 4780 | db mining | Hs.129751 | NM_014339 | 7657229 | interleukin 17 receptor (IL17R), mRNA /cds=(32,2632) | 1 | CTTTTCTTTGTGCAGCGGTCTGGTTA TCGTCTATCCCCAGGGGAATCCAC |
| 4781 | db mining | Hs.296429 | NM_014348 | 7657468 | similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA /cds=(0,1286) | 1 | CCACGTTGGGGTCACTACTGGAGTG GATGGAGGCCCTTCACATTTCTGGG |
| 4782 | db mining | Hs.21814 | NM_014432 | 7657690 | interleukin 20 receptor, alpha (IL20RA), mRNA /cds=(236,1897) | 1 | TGACCTTTCGTGATTATCCGCAAAATG CAAACAGTTTCAGATCTAATGGTT |
| 4783 | db mining | Hs.110040 | NM_014443 | 7657227 | interleukin 17B (IL17B), mRNA /cds=(41,583) | 1 | CAGTCATGGAGACCATCGCTGTGGG CTGCACCTGCATCTTCTGAATCACC |
| 4784 | db mining | Hs.76698 | NM_014445 | 7657551 | mRNA; cDNA DKFZp434L1621 (from clone DKFZp434L1621); complete cds /cds=(315,515) | 1 | AGGTTTCTTCATGAGTCATTCCAAGT TTTCTAGTCCATACCACAGTGCCT |
| 4785 | db mining | Hs.326248 | NM_014456 | 7657448 | cDNA: FLJ22071 fis, clone HEP11691 /cds=UNKNOWN | 1 | GAGGTCGCTTAAACCAGAGAGCTAC TGAATATAAGAACTCTTGCACTCT |
| 4786 | db mining | Hs.278441 | NM_014634 | 7661861 | KIAA0015 gene product (KIAA0015), mRNA /cds=(106,1470) | 1 | GCAGTCTCCCAAGGACCCACCATGC AGAAGTGTCAATTAACCAACAAGTTC |
| 4787 | db mining | Hs.19056 | NM_014824 | 7662295 | KIAA0769 gene product (KIAA0769), mRNA /cds=(239,2293) | 1 | GGAGGGAGCCTCTGTGCAGATGTGC TTTCTTTACAGTGGCTGTAAAAAGT |
| 4788 | db mining | Hs.11711 | NM_014844 | 7662057 | mRNA for KIAA0297 gene, partial cds /cds=(0,3815) | 1 | GATGCTTTTAAAGTTGTAGCTTCGTG CTTTGTACAGTTTCTTTCTGGTT |
| 4789 | db mining | Hs.7724 | NM_014963 | 7662409 | KIAA0963 protein (KIAA0963), mRNA /cds=(215,4315) | 1 | AATATATGCAATTCTCCCTCCCCCAG CCCTTCCCTGACCCCTAAGTTATT |
| 4790 | Table 3A | Hs.31989 | NM_015449 | 14149687 | DKFZP586G1722 protein (DKFZP586G1722), mRNA /cds=(210,869) | 1 | AATCTGCCAGGCTATGTGACAGTAGG AAGGAATGGTTTCCCTAACAAGC |
| 4791 | db mining | Hs.30488 | NM_015453 | 14149689 | DKFZP434F091 protein (DKFZP434F091), mRNA /cds=(334,1857) | 1 | AGCACATACATTGATAGATGGGGTGT GGGACCAACAAACCAAAATTAAG |
| 4792 | Table 3A | Hs.104640 | NM_015898 | 7705374 | HIV-1 inducer of short transcripts binding protein (FBI1), mRNA /cds=(0,1754) | 1 | CAACGGCCAGGAGAAGCACTTTAAG GACGAGGACGAGGACGAGGACGTGG |
| 4793 | db mining | Hs.278428 | NM_015902 | 13435357 | progesterone induced protein (DD5), mRNA /cds=(33,8432) | 1 | TTGTGGAACCTGTTTCAGCAAAGGTT CTTGATAGAGGGAATAGGGAATT |
| 4794 | db mining | Hs.279583 | NM_016025 | 7705788 | Homo sapiens, Similar to CGI-81 protein, clone MGC:705 IMAGE:3350598, mRNA, complete cds /cds=(248,1099) | 1 | GGGGGAAGGAAGGCTTCAGACTTGG GGGAAGGGGAGATTATTGCAAATTG |
| 4795 | db mining | Hs.179817 | NM_016026 | 7705790 | CGI-82 protein (LOC51109), mRNA /cds=(40,996) | 1 | CTATGGAGGAATTGAGGGCAAGCAC CCAGGACTGATGAGGTCTTAACAAA |
| 4796 | db mining | Hs.236494 | NM_016131 | 7705848 | RAB10, member RAS oncogene family (RAB10), mRNA /cds=(90,692) | 1 | ACACCAAACAGTTAAGTCCATTCTCT GGTACTAGCTACAAATTCGGTTTC |
| 4797 | db mining | Hs.115515 | NM_016184 | 7705337 | C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 6 (CLECSF6), mRNA /cds=(241,954) | 1 | TGCACACAGGGAGAGAATCATGAGTC TCTCTTAATTTTATCTGGTTGCTA |
| 4798 | Table 3A | Hs.7905 | NM_016224 | 7706705 | SH3 and PX domain-containing protein SH3PX1 (SH3PX1), mRNA /cds=(43,1830) | 1 | TTCAATGGAAAATGAGGGGTTTCTCC CCACTGATATTTTACATAGAGTCA |
| 4799 | db mining | Hs.66 | NM_016232 | 11136631 | interleukin 1 receptor-like 1 (IL1RL1), mRNA /cds=(0,1670) | 1 | GACCACATTGCCAATAAAGGTCCCT GAATTCCAAATCTGGAAGCACGT |
| 4800 | db mining | Hs.180403 | NM_016271 | 7706722 | STRIN protein (STRIN), mRNA /cds=(221,958) | 1 | AGGCCCAAATCACAGAATAAAGGACT AAGAGTGGATTGCTGACATTCCA |
| 4801 | Table 3A | Hs.3059 | NM_016451 | 7705368 | coatamer protein complex, subunit beta (COPB), mRNA /cds=(178,3039) | 1 | GCTGTCCTCAAAGTATATAATGTTTCA TGTACCAAGACCCTTTTACAGT |
| 4802 | Table 3A | Hs.321245 | NM_016530 | 7706562 | cDNA FLJ10249 fis, clone HEMBB1000725, highly similar to Rattus norvegicus GTPase Rab8b mRNA /cds=UNKNOWN | 1 | AAGGGTATTTGGTCTGGTTCATATGG TCAAATATTACTGCCTTGGTAGCA |
| 4803 | db mining | Hs.115897 | NM_016580 | 14589925 | protocadherin 12 (PCDH12), mRNA /cds=(1211,4765) | 1 | GGGGTGCCAGGAAATGCTCTCTGAC CTATCAATAAAGGAAAGCAGTGAT |
| 4804 | db mining | Hs.98309 | NM_016584 | 7706701 | SGRF protein, Interleukin 23 p19 subunit (SGRF), mRNA /cds=(143,712) | 1 | TGGGAAGGGAAATTTGGGGATTATTT ATCCTCCTGGGGACAGTTTGGGGA |
| 4805 | Table 3A | Hs.273385 | NM_016592 | 7706588 | guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1 (GNAS1), mRNA /cds=(68,1252) | 1 | GCCACAAAGTTCCTCTCACTTTCA GTAAAAATAAATAAACAGCAGCA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|--|
| 4806 | db mining | Hs.241567 | NM_016838 | 1111111 | RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant MSSP-2, mRNA /cds=(265,1434) | 1 | ATAAGGTGCATAAAACCCTTAAATTC ATCTAGTAGCTGTTCCCCGAACA |
| 4807 | db mining | Hs.272354 | NM_017416 | 11225606 | interleukin 1 receptor accessory protein-like 2 (IL1RAPL2), mRNA /cds=(756,2816) | 1 | GATACCCAGGAATTTACAGGAACAG TTCTTGTGTCCTTTATCCTCCAA |
| 4808 | db mining | Hs.105956 | NM_017436 | 8392829 | globotriaosylceramide/CD77 synthase; Gb3/CD77 synthase; alpha1,4-galactosyltransferase; 4-N-acetylglucosaminyltransferase (A14GALT), mRNA /cds=(133,1194) | 1 | CCCACCTGCGCCCGCATTATAAAC ACAGGAGAATAATCAATAGATAA |
| 4809 | db mining | Hs.283690 | NM_017548 | 8923709 | clone H41 unknown mRNA /cds=(323,1099) | 1 | AAACCAGGCCCTTAACTTCAGCTAG ACAACCAATATGCTGTGCTTGAAG |
| 4810 | db mining | Hs.14512 | NM_017583 | 8923748 | DIPB protein (HSA249128), mRNA /cds=(177,1211) | 1 | CCAGATCCACAGCAGGCACATATCTC TCCAAGGGATGACCAGTTTTATGC |
| 4811 | Table 3A | Hs.288036 | NM_017646 | 8923064 | tRNA isopentenylpyrophosphate transferase (IPT), mRNA /cds=(60,1040) | 1 | GGACTTGAAGACCAAGACTTTGAAA TTTGCGAGCTGCTCATGTGTGAGT |
| 4812 | Table 3A | Hs.106650 | NM_017866 | 8923499 | Homo sapiens, Similar to hypothetical protein FLJ20533, clone MGC:3448 IMAGE:3631570, mRNA, complete cds /cds=(380,865) | 1 | GAAACGGCATAAAGATGAGAAATGAG CCTATTTGTTAGTGTTCTGCTTA |
| 4813 | Table 3A | Hs.272134 | NM_018067 | 8922367 | AL544307 cDNA /clone=CS0DI019YG13-5-prime) | 1 | CCTGCCCTCGCCTGGAATCAGTGTTA CTGCATCTGATTAATGTCTCCAG |
| 4814 | Table 3A | Hs.7187 | NM_018187 | 8922606 | mRNA for KIAA1757 protein, partial cds /cds=(347,4576) | 1 | AATGAGTTGTGTTGAAGCCTCCGTCT CCCATCCTTGCTGTAGCCCGTAG |
| 4815 | db mining | Hs.85752 | NM_018461 | 8923923 | mRNA for KIAA1541 protein, partial cds /cds=(908,2341) | 1 | CAGAGTTGACGGACACTGCTCCCAAA AGGTCATTACTCAGATAAATGTA |
| 4816 | db mining | Hs.272373 | NM_018724 | 11036633 | interleukin 20 (IL20), mRNA /cds=(0,530) | 1 | GAACCTCAGGCAGCAGTTGTGAAGG CTTTGGGGGAAGTACATCTTCT |
| 4817 | db mining | Hs.110309 | NM_018950 | 9665231 | major histocompatibility complex, class I, F (HLA-F), mRNA /cds=(0,1088) | 1 | GGACTGAGAAGCAAGATATCAATGTA GCAGAATTGCACTGTGCTCACG |
| 4818 | Table 3A | Hs.225674 | NM_018963 | 11321643 | mRNA for WDR9 protein (WDR9 gene), form B /cds=(79,6888) | 1 | CAATGGTTGCACCTTATGACCTTGAG GGAAAGCCAGTTCATTTAAGAGGA |
| 4819 | db mining | Hs.278430 | NM_019105 | 14719824 | cytochrome P450, subfamily XXIA (steroid 21-hydroxylase, congenital adrenal hyperplasia), polypeptide 2 (CYP21A2), mRNA /cds=(118,1605) | 1 | GGGGGAGGGGAGGGGTTCTGTACAG GAGCAATAAAGGAGAACTGAGGTAC |
| 4820 | db mining | Hs.278430 | NM_019105 | 14719824 | cytochrome P450, subfamily XXIA (steroid 21-hydroxylase, congenital adrenal hyperplasia), polypeptide 2 (CYP21A2), mRNA /cds=(118,1605) | 1 | GGGGGAGGGGAGGGGTTCTGTACAG GAGCAATAAAGGAGAACTGAGGTAC |
| 4821 | db mining | Hs.159679 | NM_019598 | 9665235 | kallikrein 12 (KLK12), mRNA /cds=UNKNOWN | 1 | ACTTCTTGGAACCTTAACTCCTGCCA GCCCTTCTAAGACCCACGAGCGGG |
| 4822 | db mining | Hs.247808 | NM_019602 | 9624968 | butyrophilin-like 2 (MHC class II associated) (BTNL2), mRNA /cds=(0,1367) | 1 | TGTTCCATCAGCATCCCTTTTGGG CGAGGAGAAAATCGCAACTTTTTC |
| 4823 | db mining | Hs.36989 | NM_019616 | 10518502 | coagulation factor VII (serum prothrombin conversion accelerator) (F7), transcript variant 1, mRNA /cds=(51,1451) | 1 | CAGACTATTCCACCTGCTTCCAG CTTCACAATAACGGCTGCGTCTC |
| 4824 | db mining | Hs.36989 | NM_019616 | 10518502 | coagulation factor VII (serum prothrombin conversion accelerator) (F7), transcript variant 1, mRNA /cds=(51,1451) | 1 | CAGACTATTCCACCTGCTTCCAG CTTCACAATAACGGCTGCGTCTC |
| 4825 | db mining | Hs.289095 | NM_020056 | 11095446 | major histocompatibility complex, class II, DQ alpha 2 (HLA-DQA2), mRNA /cds=(0,767) | 1 | GTCTGTGGGCCTCATGGGCATTGTG GTGGGCACTGTCTTCATCATCCAAG |
| 4826 | db mining | Hs.296552 | NM_020070 | 13399297 | DNA sequence from clone CTA-246H3 on chromosome 22 Contains the gene for IGLL1 (immunoglobulin lambda-like polypeptide 1, pre-B-cell specific), a pseudogene similar to LRP5 (Lipoprotein Receptor Related Protein.), ESTs, Genomic markers (D22S414, D22S925, D22S926), CA repeats, STSs, GSSs and a CpG island /cds=(0,438) | 1 | CTCCAAACAGAGCAACAACAAGTACG CGGCCAGCAGCTACCTGAGCCTGA |
| 4827 | Table 3A | Hs.94395 | NM_020324 | 10947128 | ATP-binding cassette, sub-family D (ALD), member 4 (ABCD4), transcript variant 5, mRNA /cds=(51,1544) | 1 | CCAAAGTCCTCACTCAGACCAGTGCC CCTCCAGTTCAGTTGTCTATGTAT |
| 4828 | db mining | Hs.105509 | NM_020428 | 9966908 | cDNA FLJ14613 fis, clone NT2RP1001113, highly similar to CTL2 gene /cds=UNKNOWN | 1 | TGTCTTCCACCCTCAAGAACTCTTG AACAGACCAACAAGAAGGCAGCG |
| 4829 | literature | Hs.248156 | NM_020530 | 10092620 | oncostatin M (OSM), mRNA /cds=(0,758) | 1 | GCAGGACCAGACCTCCAGGAAAGG CAAGAGACTCATGACCAGGGGACAG |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|---|---|---|
| 4830 | db mining | Hs.105052 | NM_020979 | 10280625 | adaptor protein with pleckstrin homology and src homology 2 domains (APS), mRNA /cds=(127,2025) | 1 | GGTGGGACACGCCAAGCTCTTCAGT GAAGACACGATGTTATTTAAAGCCT |
| 4831 | literature | Hs.1510 | NM_021068 | 10835102 | interferon, alpha 4 (IFNA4), mRNA /cds=(140,709) | 1 | AGCTTGGGTATACCTTGCAGGCACT AGTCCTTTACAGATGACAATGCTG |
| 4832 | db mining | Hs.76293 | NM_021103 | 10863894 | thymosin, beta 10 (TMSB10), mRNA /cds=(65,199) | 1 | AGGAAGAGCCACCTGCAAGATGGAC ACGAGCCACAAGCTGCACGTGTGAAC |
| 4833 | db mining | Hs.3254 | NM_021134 | 10863930 | mitochondrial ribosomal protein L23 (MRPL23), mRNA /cds=(54,515) | 1 | GGGTGCAGCATGGCTCTAACAAGAG AAGAGATCACAGAAACGTGAGGATC |
| 4834 | Table 3A | Hs.7137 | NM_021188 | 10863994 | clones 23667 and 23775 zinc finger protein (LOC57862), mRNA /cds=(182,1618) | 1 | TACATTCTCCCTTTAGCAACCTGAGT AAGAGACTCTCTGCCACTGGGCTG |
| 4835 | db mining | Hs.11090 | NM_021201 | 11139298 | high affinity immunoglobulin epsilon receptor beta subunit (CFFM4), mRNA /cds=(146,868) | 1 | AACTCTTGGCCTCAGAGGAAGGAAAA GCAACTCAACACTCATGGTCAAGT |
| 4836 | db mining | Hs.241587 | NM_021246 | 10864054 | megakaryocyte-enhanced gene transcript 1 protein (MEGT1), mRNA /cds=(3,1151) | 1 | AGGGAACAAGGGAGCAAGGGAACAA GGGACATCTGAACATCTAATGTGAG |
| 4837 | db mining | Hs.110915 | NM_021258 | 10864066 | interleukin 22 receptor (IL22R), mRNA /cds=(23,1747) | 1 | GTGGCCCCCTGGACGGGTACAATAAC ACACTGTACTGATGTCACAACCTTG |
| 4838 | db mining | Hs.210546 | NM_021798 | 11141868 | interleukin 21 receptor (IL21R), mRNA /cds=(68,1684) | 1 | CCCCTACCTGCCCAATTCAATCCT GCCAATAAATCCTGTCTTATTTGT |
| 4839 | Table 3A | Hs.302014 | NM_021803 | 11141874 | interleukin 21 (IL21), mRNA /cds=(46,534) | 1 | ACACGGAAGTGAAAGATTCTGAGGAT CTAAGTTCAGTTGGACACTATGT |
| 4840 | db mining | Hs.82887 | NM_021959 | 11386174 | protein phosphatase 1, regulatory (inhibitor) subunit 11 (PPP1R11), mRNA /cds=(199,579) | 1 | CGGTCCCTTTGCCATACACAGTTACA GAGATCAGTCAAATCCATACCACC |
| 4841 | db mining | Hs.79372 | NM_021976 | 11415051 | retinoid X receptor, beta (RXRB), mRNA /cds=(179,1780) | 1 | ATACCTGTGAGGACTGGTTGTCTCTC TTCGGTGCCCTTGAGTCTCTGAAT |
| 4842 | db mining | Hs.293934 | NM_021983 | 11875206 | major histocompatibility complex, class II, DR beta 4 (HLA-DRB4), mRNA /cds=(58,948) | 1 | TCATCTACTTCAGGAATCAGAAAGGA CACTCTGGACTTCAGCCAAACAGGT |
| 4843 | Table 3A | Hs.96560 | NM_022086 | 11545798 | Homo sapiens, Similar to hypothetical protein FLJ11656, clone MGC:5247, mRNA, complete cds /cds=(149,271) | 1 | TGCTTCTTGAATGGATTAAACAACA GCCAGGAGCTTCCTGTCAAGTAACC |
| 4844 | db mining | Hs.288316 | NM_022107 | 11545816 | chromosome 6 open reading frame 9 (C6orf9), mRNA /cds=(373,855) | 1 | CCCTCCCCACTGCTGCTGAGTCTGTC TGATGTTTTGGTTGTGTGAATAAA |
| 4845 | db mining | Hs.99134 | NM_022110 | 11545822 | DIR1 protein (NG7), mRNA /cds=(268,879) | 1 | AGGAGGAACTGGGGAGGTGGTCAT TCAGGGGAAGAACCAGGATGCAGGG |
| 4846 | Table 3A | Hs.24633 | NM_022136 | 11545870 | SAM domain, SH3 domain and nuclear localisation signals, 1 (SAMSN1), mRNA /cds=(82,1203) | 1 | TGGGAAAGTGTGAGTTAATATTGGAC ACATTTTATCCTGATCCACAGTGG |
| 4847 | literature | Hs.247885 | NM_022304 | 11111111 | histamine receptor H2 (HRH2), mRNA /cds=(525,1604) | 1 | TTAAAGGAGACACATTAATTTCTCA GAGGACTTGGCAAGGGCCGCACAG |
| 4848 | db mining | Hs.271815 | NM_022352 | 11641262 | caspase recruitment domain protein 9 (LOC64170), mRNA /cds=(146,1246) | 1 | GCACACGCCATCTGTGTAACCTCAGG ATCTGTTCTGTTTACCATGTAAC |
| 4849 | db mining | Hs.294030 | NM_022447 | 13937360 | topoisomerase-related function protein 4-2 (TRF4-2), mRNA /cds=(336,869) | 1 | TTTTTCCCAGCTCGCCACAGAATGGA TCATGAAGACTGACAACTGCAAAA |
| 4850 | Table 3A | Hs.15220 | NM_022473 | 11968022 | zinc finger protein 106 (ZFP106), mRNA /cds=(335,5986) | 1 | AAGAGAAATATATGCCCTAGAGCTGC TCCAGCACCCCTTGGTTTCTGATTT |
| 4851 | db mining | Hs.28921 | NM_022482 | 11968149 | DNA sequence from clone RP3- 322G13 on chromosome 20p11.21-12.3 Contains the gene for NTF2-related export protein (NXT1), a gene for a novel zinc finger protein with three isoforms, two isoforms for the 3' part of a novel gene, a gene for a novel protein similar to mouse and bovine beta- soluble NSF attachment protein (SNAP- beta), a novel gene similar to cystatin, another novel gene similar to cystatin 8 (CST8) with two isoforms, ESTs, STSs, GSSs and CpG islands /cds=(0,2135) | 1 | ACAGACAGACTCGATGCCACACAG CTTCACTCTTTGAGCAACATGGAAT |
| 4852 | Table 3A | Hs.161786 | NM_022570 | 13384603 | C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12 (CLECSF12), mRNA /cds=(71,676) | 1 | GCACGGTGTGTTGCCACGATTGACC CTCAACTCTAGCAGTATATCAGT |
| 4853 | db mining | Hs.302036 | NM_022789 | 12232484 | interleukin 17E (IL17E), mRNA /cds=(258,791) | 1 | AGTGTAGTTACTAGTCTTTTGACATG GATGATTCTGAGGAGGAAGCTGTT |
| 4854 | Table 3A | Hs.302981 | NM_024033 | 13162284 | hypothetical protein FLJ11000 (FLJ11000), mRNA /cds=(223,780) | 1 | TCAGTGCATACAGGTTTCCAATAC ACAAGTGCTAGAAAATACACACAA |
| 4855 | db mining | Hs.267194 | NM_024039 | 13128993 | hypothetical protein MGC2488 (MGC2488), mRNA /cds=(553,1170) | 1 | TTGCTTGCCCTCCATGCTTCTCTAAA GAGCAGAACTTGGAGTTTCTCCTT |
| 4856 | Table 3A | Hs.250723 | NM_024104 | 13129111 | hypothetical protein MGC2747 (MGC2747), mRNA /cds=(92,247) | 1 | AGAATGAGCCTGAATGTTGGTGGTTT TTGAAATCCTGACTTGGAGGTTAA |

Table 8

| | | | | | | | |
|------|------------|-----------|-----------|----------|--|---|-----------------------------|
| 4857 | db mining | Hs.71746 | NM_024663 | 13375916 | hypothetical protein FLJ11583 (FLJ11583), mRNA /cds=(371,1606) | 1 | CCTCGGCCCTGACAAACGGGGATCT |
| 4858 | db mining | Hs.94810 | NM_024681 | 13489098 | hypothetical protein FLJ12242 (FLJ12242), mRNA /cds=(185,1057) | 1 | TTTACCTCACTTTGCACTGATTAAT |
| 4859 | Table 3A | Hs.180799 | NM_024835 | 13376244 | C3HC4-type zinc finger protein (LZK1), mRNA /cds=(47,2140) | 1 | TGGCTTGGCCTCTCTTTGGTGATCC |
| 4860 | db mining | Hs.183171 | NM_024838 | 13376250 | hypothetical protein FLJ22002 (FLJ22002), mRNA /cds=(115,783) | 1 | CACCCCGACCCATTTGCACTTGCTG |
| 4861 | db mining | Hs.212839 | NM_024879 | 13376319 | mRNA for KIAA1714 protein, partial cds /cds=(0,3175) | 1 | AATGTTTCTCTTCTGTGAGACTTACT |
| 4862 | db mining | Hs.125034 | NM_025085 | 13376639 | mRNA for putative N-acetyltransferase /cds=(208,2808) | 1 | AAAGCAACTTAGTGGGAAAAAAGT |
| 4863 | db mining | Hs.336937 | NM_025222 | 13489105 | mRNA; cDNA DKFZp434C0814 (from clone DKFZp434C0814) /cds=UNKNOWN | 1 | AGTACTTGAGTAGTCTCAATAGGAGT |
| 4864 | Table 3A | Hs.336937 | NM_025222 | 13489105 | mRNA; cDNA DKFZp434C0814 (from clone DKFZp434C0814) /cds=UNKNOWN | 1 | GTATTTGTAGACAGCAGTTTCCCT |
| 4865 | Table 3A | Hs.336937 | NM_025222 | 13489105 | mRNA; cDNA DKFZp434C0814 (from clone DKFZp434C0814) /cds=UNKNOWN | 1 | ACCCTAGATGAGCTGTCCTGCTCCAG |
| 4866 | db mining | Hs.247879 | NM_025260 | 13376871 | G6B protein (G6B), mRNA /cds=(0,725) | 1 | TAACATTCCTTTTCTAAAATCATT |
| 4867 | db mining | Hs.241586 | NM_025261 | 13376873 | G6C protein (G6C), mRNA /cds=(54,431) | 1 | AACTAGAAGATGTACTTCGACAGCAT |
| 4868 | db mining | Hs.118354 | NM_025263 | 13376877 | CAT56 protein (CAT56), mRNA /cds=(264,1025) | 1 | CCATTTTACTTCAAGGCAGCAAGA |
| 4869 | db mining | Hs.301920 | NM_030651 | 13449284 | chromosome 6 open reading frame 31 (C6orf31), mRNA /cds=(0,602) | 1 | ATTTGAGTTCCTGTGTGTCCAAAAC |
| 4870 | Table 3A | Hs.196270 | NM_030780 | 13540550 | folate transporter/carrier (LOC81034), mRNA /cds=(128,1075) | 1 | GAGGCACCATGTTCTTTGAAAAACA |
| 4871 | db mining | Hs.107149 | NM_030934 | 13569898 | novel protein similar to archaeal, yeast and worm N2,N2-dimethylguanosine tRNA methyltransferase (C1ORF25), mRNA /cds=(194,2395) | 1 | ATTTGAGTTCCTGTGTGTCCAAAAC |
| 4872 | literature | Hs.225946 | NM_031200 | 14043041 | chemokine (C-C motif) receptor 9 (CCR9), transcript variant A, mRNA /cds=(157,1266) | 1 | GAGGCACCATGTTCTTTGAAAAACA |
| 4873 | db mining | Hs.25063 | NM_031268 | 13775167 | PRO0461 protein (PRO0461), mRNA /cds=(779,970) | 1 | GTCCACAGCGGACCCTGCTGATGCC |
| 4874 | Table 3A | Hs.301183 | NM_031419 | 13899228 | molecule possessing ankyrin repeats induced by lipopolysaccharide (MAIL), homolog of mouse (MAIL), mRNA /cds=(48,2204) | 1 | TCCACCATCTATGCAGTTGTAGTTT |
| 4875 | db mining | Hs.283801 | NM_032009 | 14196461 | protocadherin gamma subfamily A, 2 (PCDHGA2), transcript variant 1, mRNA /cds=(185,2983) | 1 | CAGGCTCCCATATGTACCCCATCCCC |
| 4876 | Table 3A | Hs.301104 | NM_032236 | 14149943 | 602313002F1 cDNA, 5' end /clone=IMAGE:4422480 /clone_end=5' | 1 | CATACTCACTCTTTCCATTTTGA |
| 4877 | Table 3A | Hs.193669 | NM_032270 | 14150008 | hypothetical protein DKFZp586J1119 (DKFZp586J1119), mRNA /cds=(27,2153) | 1 | GTTGTATTGGCAAGAGGGAGGGGTG |
| 4878 | db mining | Hs.323662 | NM_032334 | 14150117 | hypothetical protein MGC14595 (MGC14595), mRNA /cds=(101,850) | 1 | AGAGCTGTTGGAGAAGTGAAGTGA |
| 4879 | db mining | Hs.106823 | NM_032335 | 14150119 | mRNA for KIAA1823 protein, partial cds /cds=(52,1185) | 1 | GTACCATCCTCACCGTAGTCATCATC |
| 4880 | db mining | Hs.334639 | NM_032389 | 14150222 | SH3 domain-containing protein 6511 (LOC51165), mRNA /cds=(215,1489) | 1 | ATCGCCGCGCAGCAGCACGAGAAC |
| 4881 | db mining | Hs.248367 | NM_032445 | 14192940 | MEGF11 protein (MEGF11), mRNA /cds=(159,3068) | 1 | ATTTATCGTAAACATCCACGAGTGCT |
| 4882 | db mining | Hs.69233 | NM_032494 | 14210505 | zinc finger protein (LOC84524), mRNA /cds=(92,967) | 1 | GTTGCACTACCATCTATTTGTTGT |
| 4883 | db mining | Hs.28514 | NM_032597 | 14211930 | testes development-related NYD-SP21 (NYD-SP21), mRNA /cds=(76,2115) | 1 | ATCGCTGAATATGTTGATCAGTGATG |
| 4884 | Table 3A | Hs.10056 | NM_032811 | 14249499 | hypothetical protein FLJ14621 (FLJ14621), mRNA /cds=(525,1307) | 1 | AGTTGGGCTTAATGCAAAGATCCT |
| 4885 | Table 3A | Hs.334788 | NM_032815 | 14249507 | hypothetical protein FLJ14639 (FLJ14639), mRNA /cds=(273,689) | 1 | AGGCTATTTACTTCCATGCTTCTCCTT |
| 4886 | Table 3A | Hs.11360 | NM_032839 | 14249551 | hypothetical protein FLJ14784 (FLJ14784), mRNA /cds=(133,1569) | 1 | TTCTACTCTATAGTGGCAACAT |
| 4887 | db mining | Hs.29206 | NM_032895 | 14249657 | hypothetical protein MGC14376 (MGC14376), mRNA /cds=(184,255) | 1 | GGGACCCCCACCCAGTGAGTCAACA |
| 4888 | Table 3A | Hs.154172 | R64548 | 836427 | 602575012F1 cDNA, 5' end /clone=IMAGE:4703258 /clone_end=5' | 1 | TAGGCTCATGTCAAGTTTGAATAA |
| 4889 | db mining | Hs.159386 | S74639 | 807023 | AL560682 cDNA /clone=CS0DL004YM19-(5-prime) | 1 | TGGTGTGATGAACCAAGTCCATTCA |
| 4890 | Table 3A | Hs.172762 | T75153 | 691915 | 16b3 cDNA | 1 | CATTGGAAAACTGATGGTTTTAA |

Table 8

| | | | | | | | |
|------|------------|-----------|----------|---------|--|---|---|
| 4891 | Table 3A | Hs.294092 | T93822 | 726995 | EST375308 cDNA | 1 | TTAGAAAGAAAAGTCTTTTATTAGTAC TGTGTAGGGAAGGCTAAAGAAAT |
| 4892 | db mining | Hs.301365 | U19885 | 642583 | 602462113F1 cDNA, 5' end /clone=IMAGE:4575051 /clone_end=5' | 1 | ACTGTGCGAAACGTACTGTATTACGA TTTTTGAGTGGCCGAAGTAGTCC |
| 4893 | db mining | Hs.318720 | U33547 | 3320135 | Homo sapiens, clone MGC:12387 IMAGE:3933019, mRNA, complete cds /cds=(63,863) | 1 | CAGACCCTGGTGATGCTGGAAACAG TTCCTCGGAGTGGAGAGGTTACAC |
| 4894 | db mining | Hs.287811 | U62824 | 1575443 | mRNA for HLA-C alpha chain (Cw*1701) /cds=(0,1118) | 1 | GTCCAGCAACAGTGGCCAGGGCTCT GATGAGTCTCTCATCGCTGTAAAG |
| 4895 | db mining | Hs.247987 | U80113 | 1791068 | immunoglobulin heavy chain variable region (V4-31) gene, partial cds /cds=(0,356) | 1 | GTGTATTACTGTGCGAGAGCCTTCCG CCATCCCGAGTACGTCCAATATG |
| 4896 | db mining | Hs.289036 | U80180 | 1791202 | immunoglobulin heavy chain variable region (VH4) mRNA, VH4-59 allele, partial cds /cds=(0,353) | 1 | CCCGTCCCTCAAGAGTCGAGTCACC ATATCAGTAGACAAGTCCAAGAACC |
| 4897 | db mining | Hs.247898 | U96393 | 2078365 | partial mRNA for Ig lambda light chain variable region, clone MB91 (331 bp) /cds=(0,330) | 1 | GGCTCCAGGCTCAGGATGAGGCTGA TTATTACTGCTGCTCATATACAAGC |
| 4898 | db mining | Hs.914 | X00457 | 36405 | Homo sapiens, Similar to major histocompatibility complex, class II, DR alpha, clone MGC:14114 IMAGE:4309471, mRNA, complete cds /cds=(40,822) | 1 | CCCTCACTGTCACCTTCCCAGAGAATA CCCTAAGACCAATAAATACTTCAG |
| 4899 | db mining | Hs.296552 | X03529 | 33351 | DNA sequence from clone CTA-246H3 on chromosome 22 Contains the gene for IGLL1 (immunoglobulin lambda-like polypeptide 1, pre-B-cell specific), a pseudogene similar to LRP5 (Lipoprotein Receptor Related Protein.), ESTs, Genomic markers (D22S414, D22S925, D22S926), CA repeats, STSs, GSSs and a CpG island /cds=(0,438) | 1 | TGAATGACTTCTATCTGGGAATCTTG ACGGTGACCTGGAAGGCAGATGGT |
| 4900 | literature | Hs.287797 | X07979 | 31441 | mRNA for FLJ00043 protein, partial cds /cds=(0,4248) | 1 | ACCACTGTATGTTTACTTCTCACCATT TGAGTTGCCCATCTTGTTCACA |
| 4901 | db mining | Hs.247804 | X51887 | 37616 | V108 gene encoding an immunoglobulin kappa orthon | 1 | AGAACAGAGATGATTACACCTACGAA GTCTGAGTTATGGTGTGAGTTGGA |
| 4902 | db mining | Hs.81220 | X58397 | 33615 | CLL-12 transcript of unrearranged immunoglobulin V(H)5 gene /cds=(39,425) | 1 | TTCATCATTGCTTGCTTGCCTTCCTC CCTCCTGTCCGCTCTCACTCACTC |
| 4903 | Table 3A | Hs.275959 | X60656 | 31134 | eukaryotic translation elongation factor 1 beta 2 (EEF1B2), mRNA /cds=(235,912) | 1 | TGGATGTGGCTGCTTTCAACAAGATC TAAATCCATCCTGGATCATGGCA |
| 4904 | db mining | Hs.90093 | X67643 | 2244651 | mRNA for heat shock protein apg-2, complete cds /cds=(278,2800) | 1 | TGAAGAACGACCAAAATTATTTGAAG AATAGGGAACAGATCCAACAGT |
| 4905 | db mining | Hs.300697 | Y14737 | 2765424 | mRNA for immunoglobulin lambda heavy chain /cds=(65,1498) | 1 | GTCTACATACTTCCCAGGCACCCAGC ATGGAAATAAAGCACCCACCACTG |
| 4906 | db mining | Hs.300697 | Y14737 | 2765424 | mRNA for immunoglobulin lambda heavy chain /cds=(65,1498) | 1 | ATACTTCCCAGGCACCCAGCATGGAA ATAAAGCACCCACCACTGCCCTGG |
| 4907 | db mining | Hs.181125 | Y14738 | 2765426 | Homo sapiens, clone MGC:12849 IMAGE:4308973, mRNA, complete cds /cds=(24,725) | 1 | CCCAAGGCATCAAGCCCTTCTCCCTG CACTCAATAAACCTCAATAAATA |
| 4908 | Table 3A | Hs.283770 | Z00008 | 33142 | germline gene for the leader peptide and variable region of a kappa immunoglobulin (subgroup V kappa I) | 1 | AAGGCAGAGATCTTGACACCTAAGGA GTCTAGTTTAGGGCTTTGGTTGGA |
| 4909 | db mining | Hs.37089 | Z00010 | 33146 | germ line pseudogene for immunoglobulin kappa light chain leader peptide and variable region (subgroup V kappa I) | 1 | GTTGACATTAGAAGCAGGATTCTCTG GTACTCCCTCAGAAAATAGAATGC |
| 4910 | db mining | Hs.148661 | Z00022 | 33158 | qg78c05.x1 cDNA, 3' end /clone=IMAGE:1841288 /clone_end=3' | 1 | TTGGAGCGTTTTTGTGTTTGAGATATT AGCTCAGGTCAATTCCAAGAGT |
| 4911 | Table 1 | Hs.181297 | AA010282 | 1471308 | tc35a11.x1 cDNA, 3' end /clone=IMAGE:2066588 /clone_end=3' | 1 | GGTTGTGTCTCTGGTTTCCCCTTTTC CCCGTGGTTTAAATTTTAAAGAAC |
| 4912 | Table 1 | Hs.189468 | AA069335 | 1576904 | tm30a06.x1 cDNA, 3' end /clone=IMAGE:2158066 /clone_end=3' | 1 | ACCATAGCAGACAGGGTCAGATGGA ATATTAGCGGTTTAGGTGAAGAACC |
| 4913 | Table 1 | Hs.13659 | AA115345 | 1670525 | mRNA; cDNA DKFZp586F2423 (from clone DKFZp586F2423) /cds=UNKNOWN | 1 | ATCCACATTCTTACCTTTGGTAGTCA GGTTTGGCTACTTTGACGCTCGCC |
| 4914 | Table 1 | Hs.182278 | AA203528 | 1799239 | Homo sapiens, calmodulin 2 (phosphorylase kinase, delta), clone MGC:1447 IMAGE:3504793, mRNA, complete cds /cds=(93,542) | 1 | TCTGTTACCACCTCTAAAATATTGGG GTGGAATAAAGCTGGGTTCTTGCA |
| 4915 | Table 1 | Hs.100651 | AA251184 | 1886149 | golgi SNAP receptor complex member 2 (GOSR2), mRNA /cds=(0,638) | 1 | AAGGATGAAGGACTGATGGAGGGCA GAGGAACCTGGAGGCAGAGGCACAA |
| 4916 | Table 1 | NA | AA252909 | 1885512 | zr76a03.r1 Soares_NhMPu_S1 cDNA clone IMAGE:669292 5', mRNA sequence | 1 | AGATGTCTGTATAAACAACTTTGGG TAGCAGGTGGTCAGTTAGGCAGGA |

Table 8

| | | | | | | | |
|------|---------|-----------|----------|----------|---|---|--|
| 4917 | Table 1 | Hs.194480 | AA258979 | 1894268 | EST389427 cDNA | 1 | TGCTTGTCTTTTAAACACCTTCACAGA TATCATTTGACCTTGCCAAAGG |
| 4918 | Table 1 | Hs.5241 | AA280051 | 1921589 | fatty acid binding protein 1, liver (FABP1), mRNA /cds=(42,425) | 1 | GGGTAGGCAGCTTGACCCAGTTCT CCTTTATCTCAACTTATTGTCCTGG |
| 4919 | Table 2 | Hs.23128 | AA282304 | 1925220 | Homo sapiens, Similar to RIKEN cDNA 4931428D14 gene, clone MGC:15407 IMAGE:4309613, mRNA, complete cds /cds=(123,1151) | 1 | ACTTGGAAACAGAAAGAACTTCGGCAAC GAGAACACTATCTCAAGCAGAAGA |
| 4920 | Table 1 | NA | AA282774 | 1925825 | zt14g01.r1 NCI_CGAP_GCB1 cDNA clone IMAGE:713136 5', mRNA sequence | 1 | GCGGTGTCCCTGAGTGAGGGCAAAG TTGTAATAACACTTGTCTCTCCTT |
| 4921 | Table 1 | Hs.89072 | AA283061 | 1926050 | hypothetical protein MGC4618 (MGC4618), mRNA /cds=(107,1621) | 1 | ACGGCGTTCTGAAATTTAGCACACTG GGAAGTGCACATGGTTTCATCTGAA |
| 4922 | Table 1 | Hs.291448 | AA290921 | 1938772 | EST388168 cDNA | 1 | AATGAGATCACAGATGGTGACACTGA GCGGAAGGATGCAGTACCTCGGAG |
| 4923 | Table 1 | Hs.211866 | AA290993 | 1938989 | wh99f02.x1 cDNA, 3' end /clone=IMAGE:2388891 /clone_end=3' | 1 | GGCTAGTGGTGTTCAGAGAAATACCA AAACGTGTTTTATCATTGCTGGT |
| 4924 | Table 1 | NA | AA319163 | 1971490 | EST21341 Adrenal gland tumor cDNA 5' end, mRNA sequence | 1 | AGCTGCCTCAGGAGGTTCTTAACATA TAGGAATGTAATTATCAGATTCAA |
| 4925 | Table 1 | Hs.260238 | AA332553 | 1984806 | hypothetical protein FLJ10842 (FLJ10842), mRNA /cds=(39,1307) | 1 | AGGAAACCAAGCCCTCAGAGAAAG AAAGCCTGATTCAAGAAAACAAAGT |
| 4926 | Table 1 | Hs.343557 | AA401648 | 2056830 | 601500320F1 cDNA, 5' end /clone=IMAGE:3902237 /clone_end=5' | 1 | GCTGGGGCTGAGAGAGGGTCTGGGT TATCTCCTCTGATCTTCAAAACAA |
| 4927 | Table 1 | Hs.186674 | AA402069 | 2056860 | qf56f06.x1 cDNA, 3' end /clone=IMAGE:1754051 /clone_end=3' | 1 | TCATGGACACAACTTTGGAGTATAA GCGACATCCCTTAAGCAACAGGCT |
| 4928 | Table 1 | Hs.301985 | AA412436 | 2071006 | 602435787F1 cDNA, 5' end /clone=IMAGE:4553684 /clone_end=5' | 1 | GCCATTTTCCTCCAGAAACAAAACC AAGATAATTTATCCTGAACAGGT |
| 4929 | Table 1 | Hs.9691 | AA418765 | 2080566 | cDNA: FLJ23249 fls, clone COL04196 /cds=UNKNOWN | 1 | TGTTTGTACCACTAGCATTCTTATGTC TGACTTGAACTGTAGTTAGCA |
| 4930 | Table 1 | Hs.24143 | AA426506 | 2106769 | Wiskott-Aldrich syndrome protein interacting protein (WASPIP), mRNA /cds=(108,1619) | 1 | AGGACCATAGGGAAGAGCCAGCCTT GCCTTTCTTATATGATTTTGTTTA |
| 4931 | Table 1 | Hs.89519 | AA429783 | 2112974 | KIAA1046 protein (KIAA1046), mRNA /cds=(577,1782) | 1 | CCTGGGTGCGCTTGTAAATGAAAAGGG AGATCGAGCCATTGTACCACTTA |
| 4932 | Table 1 | NA | AA457757 | 2180477 | aa92c03.r1 Stratagene fetal retina 937202 cDNA clone IMAGE:838756 5', mRNA sequence | 1 | AGCTGTTTAAATGGAATGGAATCGTT CCACTTGGAGCAAGTTTGGAAA |
| 4933 | Table 1 | Hs.82772 | AA460876 | 2185996 | collagen, type XI, alpha 1 (COL11A1), mRNA /cds=(161,5581) | 1 | TCGTTCTACGTTATCTCATCTCCTTGT TTTCAGTGTGCTTCAATAATGCA |
| 4934 | Table 1 | Hs.13809 | AA476568 | 2204779 | mRNA for KIAA1525 protein, partial cds /cds=(0,2922) | 1 | TGTTTTGCTTCCTCAGAACTTTTAA TTGCATCTGCCATCCTTCATTGG |
| 4935 | Table 1 | NA | AL047171 | 5936355 | DKFZp586F2018_r1 586 (synonym: hute1) cDNA clone DKFZp586F2018 5', mRNA sequence | 1 | TGCATTACTCATTAGTTTTAGTTTG AACTCTGCGAGGCTCTAATGT |
| 4936 | Table 1 | Hs.77868 | AL513780 | 12777274 | ORF (LOC51035), mRNA /cds=(135,1031) | 1 | TGGTTCTCTGATGAGCAAGGGAACA ACACTGAGAATGAGGAGGAGAGT |
| 4937 | Table 2 | Hs.30120 | AL533737 | 12797230 | cDNA /clone=CS0DF002YH09-(5- prime) | 1 | AAGCAAGAGATTGTAACCGGGTACA GATCCAAGAGATGAGAGAGGACCC |
| 4938 | Table 1 | Hs.285401 | AL540399 | 12870508 | colony stimulating factor 2 receptor, beta, low-affinity (granulocyte- macrophage) (CSF2RB), mRNA /cds=(28,2721) | 1 | CGTCTACTGCGGAAAAGTCAGGGGA AACTGCCAAACAAAGGAAAATGCC |
| 4939 | Table 1 | NA | AV689330 | 10291193 | AV689330 GKC cDNA clone GKCDJE03 5', mRNA sequence | 1 | GTGTTTGACTTCACTGCTGCGAAATG ACTGTCTCCTGGCTAGTAGGATCT |
| 4940 | Table 1 | Hs.90960 | AV710415 | 10729044 | 602563938F1 cDNA, 5' end /clone=IMAGE:4688769 /clone_end=5' | 1 | ATGTGGGAGGGGCACTGGCAGCTATG AAGACCTCCTACCTCTGGTTCTG |
| 4941 | Table 1 | Hs.237868 | AV716565 | 10813717 | interleukin 7 receptor (IL7R), mRNA /cds=(22,1401) | 1 | CCAGCCTTTGCCTCTTCTTCAATGT GGTTTCCATGGGAATTTGCTTCAG |
| 4942 | Table 1 | Hs.127160 | AV719938 | 10817090 | AV659177 cDNA, 3' end /clone=GLCFUC08 /clone_end=3' | 1 | ACCTTGTAAGTGCCTAAGAAATGAGA CTACAAGCTCCATTTTCAGCAGGAC |
| 4943 | Table 2 | Hs.21536 | AV720984 | 10818136 | yf69a03.s1 cDNA, 3' end /clone=IMAGE:27414 /clone_end=3' | 1 | GCCGAGATCTGCTCAGACTACATGG CTTCCACTATAGGGTTCTACAGTGT |
| 4944 | Table 1 | Hs.22003 | AV730135 | 10839556 | solute carrier family 6 (neurotransmitter transporter, GABA), member 1 (SLC6A1), mRNA /cds=(234,2033) | 1 | ATGTCTATAAATGGTGTCAACTAG AGCACGGGCGTTATGTAAGTTTCT |
| 4945 | Table 1 | Hs.339696 | AV755367 | 10913215 | ribosomal protein S12 (RPS12), mRNA /cds=(80,478) | 1 | TGAGTCGTATTACAATTCAGTGCCG TCGTTTTACAACGTCGTGACTGGG |
| 4946 | Table 1 | Hs.301553 | AW021037 | 5874567 | karyopherin alpha 6 (importin alpha 7) (KPNA6), mRNA /cds=(55,1665) | 1 | ACATAGCGGAAGAAAACATGGCATTG AGTGTGCTGAGTCCAGACAAATGT |
| 4947 | Table 2 | NA | AW402007 | 6920693 | UI-HF-BK0-aao-g-02-0-UI.r1 NIH_MGC_36 cDNA clone IMAGE:3054530 5', mRNA sequence | 1 | GTGCAGTCCATCAGATCCAAGCCTGT CTCTTGAGGAACAACCGCGCAGAC |

Table 8

| | | | | | | | |
|------|---------|-----------|----------|----------|--|---|--|
| 4948 | Table 1 | NA | AW499658 | 7111531 | UI-HF-BR0p-ajj-c-07-0-UI.r1 NIH_MGC_52 cDNA clone IMAGE:3074677 5', mRNA sequence | 1 | TGGTGGCAAATCTGATTTTTGGAAAC GAGTATTGGAGGACTATAAAACAA |
| 4949 | Table 1 | NA | AW499828 | 7111870 | UI-HF-BN0-ake-c-06-0-UI.r1 NIH_MGC_50 cDNA clone IMAGE:3076619 5', mRNA sequence | 1 | ACATTTCTTGTGGCACTACAGCAAC CACATACAGTACAGACAACCTCCA |
| 4950 | Table 1 | Hs.145668 | AW500534 | 7113240 | fmc5 cDNA /clone=CR6-21 | 1 | CCTGGCAGTGTGTCTGGAGTCTGG CACACTGGTTATCAATAGCACATT |
| 4951 | Table 1 | Hs.120996 | AW504293 | 7141960 | serine/threonine kinase 17b (apoptosis- inducing) (STK17B), mRNA /cds=(261,1379) | 1 | CTGTGGTCTGTTATATGAGAGAGATC CTTTAACTAGAGCAAAGAGGGAGT |
| 4952 | Table 1 | Hs.194589 | AW945538 | 8123293 | AV703056 cDNA, 5' end /clone=ADBCMB06 /clone_end=5' | 1 | TCTCTCACTGTTATCATTTTTGCACAG GTGGTTTCAGCAGCTTGATGCCA |
| 4953 | Table 1 | NA | BE177661 | 8656813 | RC1-HT0598-020300-011-h02 HT0598 cDNA, mRNA sequence | 1 | AATCACAGCAGTAACCTCCAGTAGGA AAGATTCTCAAAGGAATAGTTCCT |
| 4954 | Table 2 | NA | BE253336 | 9123402 | 601117146F1 NIH_MGC_16 cDNA clone IMAGE:3357826 5', mRNA sequence | 1 | CCTGGCCTTCAAGAAGTCGTAGTGG CTATTTTCTTTGGACAAAAGTAAGA |
| 4955 | Table 1 | Hs.343565 | BE540808 | 9769453 | 601510248F1 cDNA, 5' end /clone=IMAGE:3912034 /clone_end=5' | 1 | ATAGACAGACGGAGGTCTGATATCC ATGGGCCAACGGCTTGGATTATTC |
| 4956 | Table 2 | NA | BE569141 | 9812861 | 601338954F2 NIH_MGC_53 cDNA clone IMAGE:3681180 5', mRNA sequence | 1 | GATATTGGTAGTAAAGGGTTACCTG TGAACCTCCAAAATTCCTTGGGGC |
| 4957 | Table 1 | Hs.271272 | BE737348 | 10151340 | DKFZp434K1715_r1 cDNA, 5' end /clone=DKFZp434K1715 /clone_end=5' | 1 | GGTGGAGAATCAAACGACCCCGCA AATAAACATGGCGATTGGCTTGGG |
| 4958 | Table 2 | Hs.20225 | BE792125 | 10213323 | tuftelin-interacting protein (TIP39), mRNA /cds=(263,2776) | 1 | GATATCAGACAGCATCGTCTCTGCGA GCACAAAGACTCTGTTTGTCTGAGCA |
| 4959 | Table 1 | Hs.31314 | BE872245 | 10321021 | retinoblastoma-binding protein 7 (RBBP7), mRNA /cds=(287,1564) | 1 | ACATTTTATAAGGCATTTGTGTTAGCC ACTCAGTCATCTTTGGGTGCTGC |
| 4960 | Table 2 | NA | BE884898 | 10333674 | 601506831F1 NIH_MGC_71 cDNA clone IMAGE:3908551 5', mRNA sequence | 1 | ATCTGGAGTGGGACCCCTCAAACCAT GTCTGTGCTTATGCGGGAACAAT |
| 4961 | Table 1 | Hs.250824 | BE887646 | 10343176 | cDNA: FLJ23435 fis, clone HRC12631 /cds=UNKNOWN | 1 | AATTAACGGCCATCACACCCAGACT GACGGTGATCAACAAATTCACAG |
| 4962 | Table 1 | NA | BE896691 | 10361375 | 601440131F1 NIH_MGC_72 cDNA clone IMAGE:3925062 5', mRNA sequence | 1 | GACAGTACTCCTAAGACCCCTGTGTG TGTCCCGATGAGATCATGACTGGG |
| 4963 | Table 1 | Hs.337986 | BF033741 | 10741453 | Homo sapiens, clone MGC:17431 IMAGE:2984883, mRNA, complete cds /cds=(1336,1494) | 1 | CTGTGATATTTTGGTCATGGGCTGGT CTGGTCGGTTTCCCATTTGTCTGG |
| 4964 | Table 1 | Hs.268177 | BF339088 | 11285508 | phospholipase C, gamma 1 (formerly subtype 148) (PLCG1), mRNA /cds=(76,3948) | 1 | CTCATAGCATAGCCAGCATTACAGCAC ACACAAACCTACTGCCACATTTG |
| 4965 | Table 1 | Hs.2554 | BF341359 | 11287850 | sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) (SIAT1), mRNA /cds=(310,1530) | 1 | CACATTTGAAGGCCAAAGGGAAAAACG GGGGAAGCGGAAGGGTTGATTGG |
| 4966 | Table 1 | Hs.334825 | BF530382 | 11617745 | cDNA FLJ14752 fis, clone NT2RP3003071 /cds=(205,1446) | 1 | TACGACCACTGAGAAACGGGCCACC CGGCACACGGATCTTGAACACAAA |
| 4967 | Table 1 | Hs.79530 | BF663116 | 11937011 | M5-14 protein (LOC51300), mRNA /cds=(186,1043) | 1 | CTCAGTGTAGGGCAGAGAGGTCTAA CACCAACATAAGGTACTAGCAGTGT |
| 4968 | Table 1 | Hs.46677 | BF667621 | 11941516 | PRO2000 protein (PRO2000), mRNA /cds=(650,1738) | 1 | AGGTTGTGGGGAGTATGTTTGACCA AAAATTAAATATTGTGGGAGGGA |
| 4969 | Table 1 | Hs.27590 | BF671020 | 11944915 | histone acetyltransferase (MORF), mRNA /cds=(315,6536) | 1 | TGATAGCTCACTTAGTTAATTGTTTG AAGCAAATTTGGGTTGGATGGG |
| 4970 | Table 1 | Hs.71331 | BF691178 | 11976586 | hypothetical protein MGC5350 (MGC5350), mRNA /cds=(189,995) | 1 | ACTACTGCTTGGCTACCTCTCCGCTT TCCCTCTCCTTACTATCGACATA |
| 4971 | Table 1 | Hs.337534 | BF965068 | 12332283 | 602268833F1 cDNA, 5' end /clone=IMAGE:4356776 /clone_end=5' | 1 | GGTCCGACCAATTAATGACTCCATGA TCGGCCTCGGTTTTACAAACCTT |
| 4972 | Table 1 | Hs.334691 | BF965438 | 12332653 | hypothetical protein FLJ22427 (FLJ22427), mRNA /cds=(40,2631) | 1 | AGACAAAGAGAGCATAAATATAGCTC TACTCATGGGTACCATACCAAGTGT |
| 4973 | Table 1 | Hs.279681 | BF965960 | 12333175 | heterogeneous nuclear ribonucleoprotein H3 (2H9) (HNRPH3), transcript variant 2H9, mRNA /cds=(118,1158) | 1 | GCAGGTTATCGCAAGATGTCTTAGAG TAGGGTTACGGTTCTCAGTGACAC |
| 4974 | Table 1 | Hs.5324 | BF966028 | 12333243 | hypothetical protein (CL25022), mRNA /cds=(157,1047) | 1 | AAATGGCTTTACCAAACATTGTCAGT ACCTTTACGTGTTAGAAGGCATTT |
| 4975 | Table 1 | Hs.179902 | BF966049 | 12333264 | transporter-like protein (CTL1), mRNA /cds=(0,1964) | 1 | CTTTCCACAGCAATTGTTTGTACGA GGGGCCTTACAGCGCGGTCCACTT |
| 4976 | Table 1 | Hs.109441 | BF969847 | 12337082 | cDNA FLJ14235 fis, clone NT2RP4000167 /cds=(82,2172) | 1 | CCCTACTTGATTAAAGATTGAGGTGG AATTCTAGATGTGGTCATTCGTGT |
| 4977 | Table 2 | Hs.289721 | BF981634 | 12384446 | cDNA: FLJ22193 fis, clone HRC01108 /cds=UNKNOWN | 1 | ACAGAGAGTCAACCCGAGTACGAA ACAGGCACATTTTGAACACTCACA |
| 4978 | Table 1 | Hs.125819 | BG034799 | 12428456 | putative dimethyladenosine transferase (HSA9761), mRNA /cds=(78,1019) | 1 | AGAAATGGTACGGGGAATGTGAATAA CACGAAATGGTATGGGGAAATGTG |
| 4979 | Table 1 | Hs.34906 | BG111773 | 12605279 | 601820448F1 cDNA, 5' end /clone=IMAGE:4052578 /clone_end=5' | 1 | CACAACGGGTCTTAATGACGACGGAA AGATACATCCATCGGTATGAACGC |

Table 8

| | | | | | | | |
|------|---------|-----------|----------|----------|--|---|---|
| 4980 | Table 1 | NA | BG118529 | 12612035 | 602348464F1 NIH_MGC_90 cDNA clone IMAGE:4443519 5', mRNA sequence | 1 | TGTTCTTGTGCTGCTGTTATCTATACT ATTTTTGTTCTGCTGCCTTCTGACT |
| 4981 | Table 1 | Hs.285729 | BG163237 | 12669951 | 602013364F1 cDNA, 5' end /clone=IMAGE:4149351 /clone_end=5' | 1 | GTCTGGGTGCCAACTTGAGACAGGT GGTCTAGGAAATTGCGGTAAGAGCG |
| 4982 | Table 2 | Hs.111554 | BG164898 | 12671532 | ADP-ribosylation factor-like 7 (ARL7), mRNA /cds=(14,592) | 1 | CCCCTGTTTTCTCGTTCTGCTCCT TTGGACCTGTGTTTGTCTGCT |
| 4983 | Table 1 | Hs.193482 | BG165998 | 12672701 | cDNA FLJ11903 fis, clone HEMBB1000030 /cds=UNKNOWN | 1 | CCCTTAGAATGGTTACTGCCCTTGAA TTAACCTTGACACAACCTGGGTTGG |
| 4984 | Table 1 | Hs.83731 | BG179257 | 12685889 | CD33 antigen (gp67) (CD33), mRNA /cds=(12,1106) | 1 | AGGCTGATTCTTGGAGATTTAACACC CCACAGGCAATGGGTTTATAGACA |
| 4985 | Table 1 | Hs.278428 | BG286817 | 13040034 | progesterone induced protein (DD5), mRNA /cds=(33,8432) | 1 | TCTCCTTTCACTTCTTTGTAGGATTT CTGGGCTTGAAGGATGACTCTTCA |
| 4986 | Table 1 | Hs.173830 | BG289048 | 13044499 | 602383666F1 cDNA, 5' end /clone=IMAGE:4512712 /clone_end=5' | 1 | ATACTGTGTGATTGCGCTTGTCTGC CAACCTGTCTTGTCTGCCATTGA |
| 4987 | Table 1 | Hs.129872 | BG290577 | 13047679 | sperm associated antigen 9 (SPAG9), mRNA /cds=(110,2410) | 1 | AGAATGTCCCACTTGCTGTCTCTTAG AGGCTGAGCTTCATTCTATGAGC |
| 4988 | Table 1 | Hs.170980 | BG387694 | 13281140 | cell cycle progression 2 protein (CPR2), mRNA /cds=(126,1691) | 1 | CAACCTCTGGAGAGTGCCTACTGTTA GAAGCTGAAGGGATGTCAAAGTCA |
| 4989 | Table 1 | Hs.266175 | BG391695 | 13285143 | cDNA FLJ20673 fis, clone KALA4464 /cds=(104,1402) | 1 | CTTTAAATCTTAGATTGCTCCGCACA GATAAAGAGAACCAGGATTGGGGC |
| 4990 | Table 1 | Hs.58643 | BG397564 | 13291012 | 602438603F1 cDNA, 5' end /clone=IMAGE:4564968 /clone_end=5' | 1 | GCCTCAGTACAGAGGGGGCTCTGGA AGTGTGTTGTTGACTGAATAAACGGA |
| 4991 | Table 1 | Hs.24054 | BG489375 | 13450885 | hypothetical protein GL009 (GL009), mRNA /cds=(77,628) | 1 | AGGACTTAACGGGAATACGGGAATAA TCCTCAATTACTTCATCTCTAGGGC |
| 4992 | Table 1 | Hs.29131 | BG497765 | 13459282 | nuclear receptor coactivator 2 (NCOA2), mRNA /cds=(162,4556) | 1 | TGCCTAAGAGCAAGCATCTCTGCGG ACAAAGAAAATTACTGTAGTGGC |
| 4993 | Table 2 | Hs.172089 | BG501063 | 13462580 | mRNA; cDNA DKFZp586l2022 (from clone DKFZp586l2022) /cds=UNKNOWN | 1 | AAACACACAGGAAAAGGGCAAAGGG GGCACCAGGAGAACCGGGAGACAAA |
| 4994 | Table 1 | NA | BG501895 | 13463412 | 602548201F1 NIH_MGC_61 cDNA clone IMAGE:4654344 5', mRNA sequence | 1 | GACATGGAGCCCCCGAAAGCGGG TCTGGACACCAAGTCGATGTGTGAG |
| 4995 | Table 1 | Hs.3280 | BG505961 | 13467478 | caspase 6, apoptosis-related cysteine protease (CASP6), transcript variant alpha, mRNA /cds=(78,959) | 1 | ACAGAATCAGATTTTGCAGGTGTCCA ACCTATAGTGGCTAAGAATTATGT |
| 4996 | Table 1 | Hs.279009 | BG532345 | 13523883 | matrix Gla protein (MGP), mRNA /cds=(46,357) | 1 | AAACTGTTTGGAGAATTTAAGCACTC TCTGATGGGGGACAACTCTATGGA |
| 4997 | Table 1 | Hs.74647 | BG536394 | 13527940 | T-cell receptor active alpha-chain mRNA from JM cell line, complete cds /cds=(136,969) | 1 | AATAATTGGTCTTTTAAACAAACACG GAAGTTTGGTGAATCGTCTATGT |
| 4998 | Table 1 | NA | BG542394 | 13534627 | 602571761F1 NIH_MGC_77 cDNA clone IMAGE:4696046 5', mRNA sequence | 1 | TGTGGCGATTAAGAGAGGTGAAGCAT AACTGATTTCAGGATATGGTTTG |
| 4999 | Table 1 | Hs.83077 | BG547627 | 13546292 | interleukin 18 (interferon-gamma-inducing factor) (IL18), mRNA /cds=(177,758) | 1 | GCAGAACTCTAATTGTACGGGGTCCAC AGAGGCGTGATATGGTATCCAAA |
| 5000 | Table 1 | Hs.301497 | BG566035 | 13573688 | arginine-tRNA-protein transferase 1-1p (ATE1) mRNA, alternatively spliced product, partial cds /cds=(0,1544) | 1 | TGGAGATCCTTCTACTTGGCTGCTGT ATTATGCATTATGTTGGTTTGAG |
| 5001 | Table 1 | Hs.343475 | BG566964 | 13574617 | 601556208T1 cDNA, 3' end /clone=IMAGE:3826392 /clone_end=3' | 1 | ATTTGTACCAAACTTTTGGGATTCAAT GGCAAATAATTCAGTGTGGTGT |
| 5002 | Table 1 | Hs.11050 | BG571068 | 13578721 | mRNA; cDNA DKFZp434C0118 (from clone DKFZp434C0118); partial cds /cds=(0,1644) | 1 | GGTTTTAGCAGTTCTTTAGCCCGTGG TATTTCACTGTTGGGTTTCATAGC |
| 5003 | Table 1 | Hs.194110 | BG571747 | 13579400 | hypothetical protein PRO2730 (PRO2730), mRNA /cds=(183,596) | 1 | GGGAGCCATAAGAACGACTCCAAAAA GAGCCCCAAGGAGGACAAGGGGG |
| 5004 | Table 1 | Hs.306155 | BG572371 | 13580024 | chorionic somatomammotropin hormone 1 (placental lactogen) (CSH1), transcript variant 2, mRNA /cds=(116,886) | 1 | TCAGGGTCTTGATACTCAAGAGAAA GGAGACTTGTGGTTAATGTTTGA |
| 5005 | Table 1 | Hs.301756 | BG573202 | 13580855 | Homo sapiens, clone MGC:17544 IMAGE:3462146, mRNA, complete cds /cds=(256,894) | 1 | TCCTTAGCACACGAAAAAGCCCTTC CCCTGGATTCTGTTTCTTATTTTC |
| 5006 | Table 1 | Hs.79101 | BG575739 | 13583392 | cyclin G1 (CCNG1), mRNA /cds=(187,1074) | 1 | AAGCAAGTAGACACCTTCATAACTAT GAATGAAGCTGCTGAAGTAGTGT |
| 5007 | Table 1 | Hs.172780 | BG611117 | 13662488 | 602343016F1 cDNA, 5' end /clone=IMAGE:4453466 /clone_end=5' | 1 | TCCATTAAAGATCGCAAATGTTGAGG TCCTGTAGCCTGAAAACCTCTCTGC |
| 5008 | Table 1 | Hs.5064 | BG614405 | 13665776 | 602490910F1 cDNA, 5' end /clone=IMAGE:4619835 /clone_end=5' | 1 | CTGATTCAAACAGGTCCAACGTAAA ACGTTCACACTTCCACCATTTCT |
| 5009 | Table 1 | Hs.86437 | BG615272 | 13666643 | 602411368F1 cDNA, 5' end /clone=IMAGE:4540096 /clone_end=5' | 1 | TGATGTTGGTATGCTTGCCCTGTTAC TTATAGACAGTCTTTGTCATAGGC |

Table 8

| | | | | | | | |
|------|---------|-----------|----------|----------|--|---|--|
| 5010 | Table 1 | Hs.111911 | BG617515 | 13668886 | 602540462F1 cDNA, 5' end /clone=IMAGE:4671519 /clone_end=5' | 1 | GGTCTTTGTCCCAGTAGAGTTCATAG TCTATTAGTGTGCATGTTTTTCC |
| 5011 | Table 1 | Hs.326392 | BG618351 | 13669722 | son of sevenless (Drosophila) homolog 1 (SOS1), mRNA /cds=(0,3998) | 1 | TTGTGTCCAAAAGTGTTAACGAAGAC TACTTAACCCAATGATTGGCGCGA |
| 5012 | Table 1 | NA | BG622313 | 13673684 | 602646981F1 NIH_MGC_79 cDNA clone IMAGE:4768413 5', mRNA sequence | 1 | ATGCGTGGATATTGAGAACTTAGGTG TCTAATGGGGAGGATTATTGCTGT |
| 5013 | Table 1 | Hs.173334 | BG674441 | 13905837 | ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA /cds=(0,1922) | 1 | AAGCATTTCCATTTCAACGAGTTTGT CAGCTTTTATTATGTTGGGCAAAA |
| 5014 | Table 1 | Hs.343615 | BG675211 | 13906607 | 602621493F1 cDNA, 5' end /clone=IMAGE:4755166 /clone_end=5' | 1 | AAACCTACCACCTTTAAGAAGACAGCG ATGGGTAATTCCTTATTGGCAGGT |
| 5015 | Table 1 | Hs.250905 | BG675766 | 13907162 | hypothetical protein (LOC51234), mRNA /cds=(0,551) | 1 | ATTCAGCATTAGTTTCTCACATCTTCC CCCAGGTATCCCCAACAGAATTA |
| 5016 | Table 1 | NA | BG676788 | 13908185 | 602623378F1 NCI_CGAP_Skn4 cDNA clone IMAGE:4748322 5', mRNA sequence | 1 | ACACCTCTCTTAGGGCTCCATCAAAAC AGAACTTTAGACTGAGTAACGCT |
| 5017 | Table 1 | Hs.21812 | BG676903 | 13908300 | AL562895 cDNA /clone=CS0DC021YO20-(3-prime) | 1 | AAGTTTGTGCAGCACATTCTGAGTG TACGATATTGACCTGTAGCCCAGC |
| 5018 | Table 2 | Hs.171802 | BG678827 | 13910224 | RST31551 cDNA | 1 | ACCATGAACAGTGTGTTGCTTCAGAC TATTACAAAGAGAATGGGGCAGGT |
| 5019 | Table 1 | Hs.12396 | BG679427 | 13910824 | 602302446F1 cDNA, 5' end /clone=IMAGE:4403866 /clone_end=5' | 1 | TTTTTGAAAAGTATGTTTGGTAGAAAT TAGTTGTATGCCCTCAGGACGGT |
| 5020 | Table 1 | Hs.4248 | BG679662 | 13911059 | vav 2 oncogene (VAV2), mRNA /cds=(5,2841) | 1 | GAAATTAGTGTGAACATGTGGGAAGC CCGATGCATGTGGGTGAGGGATCT |
| 5021 | Table 1 | Hs.182937 | BG681320 | 13912717 | peptidylprolyl isomerase A (cyclophilin A) (PIA), mRNA /cds=(44,541) | 1 | TCCCTGGGTGATACCATTCAATGTCT TAATGTACTTGTGGCTCAGACCTG |
| 5022 | Table 1 | NA | BG682704 | 13914101 | 602629666F1 NCI_CGAP_Skn4 cDNA clone IMAGE:4754273 5', mRNA sequence | 1 | CAGACAGCACAGCCTGAGGGTAGCA GCAGCCACCCATGTTCAAGTAAGTC |
| 5023 | Table 2 | Hs.250465 | BG707615 | 13984138 | mRNA; cDNA DKFZp434E2023 (from clone DKFZp434E2023) /cds=UNKNOWN | 1 | GCCATGAGGTGGAGGACGTGGACCT GGAGCTGTTCAACATCTCGGTGCAG |
| 5024 | Table 1 | Hs.235883 | BG708357 | 13985618 | 602628774F1 cDNA, 5' end /clone=IMAGE:4753483 /clone_end=5' | 1 | TCTGCACCCAAACAAATACCTTTTGA GATTTCTTATAGGCATTCTCTCG |
| 5025 | Table 1 | Hs.119960 | BG709079 | 13987060 | mRNA; cDNA DKFZp727G051 (from clone DKFZp727G051); partial cds /cds=(0,1423) | 1 | GAAGCTCTGCCGACGCCAGGCAC TTCCTACACCACTACTACGTCCAGC |
| 5026 | Table 1 | Hs.87908 | BG709315 | 13987530 | Snf2-related CBP activator protein (SRCAP), mRNA /cds=(210,9125) | 1 | CAGCTCGGACCACCGCCACCTCCCT TTTTATTACAGATCACCCAGTAAG |
| 5027 | Table 1 | Hs.10056 | BG720359 | 13999546 | hypothetical protein FLJ14621 (FLJ14621), mRNA /cds=(525,1307) | 1 | GGTCCCCTCCTGGAGACTCCCTCAC AAAATCTTCCCAAGCTGTTCCCC |
| 5028 | Table 1 | Hs.6986 | BG723274 | 14002461 | glucose transporter pseudogene /cds=UNKNOWN | 1 | TGAATGGGCGTTTATCTTAATGACCA GTTATTGACCAAAGTGTAAGTACAGA |
| 5029 | Table 1 | Hs.181392 | BG740787 | 14051440 | major histocompatibility complex, class I, E (HLA-E), mRNA /cds=(7,1083) | 1 | AGCCTATTCTATTCTAGCCTATTTC CTTACCACCTGTAATCTTGACCA |
| 5030 | Table 2 | Hs.86543 | BG743518 | 14054171 | 602495247F1 cDNA, 5' end /clone=IMAGE:4609330 /clone_end=5' | 1 | GCAATGGGCGGCCAACTATGAACCC TACGTGGTGGTGCCACGAGACTGTC |
| 5031 | Table 1 | Hs.77202 | BG743900 | 14054553 | protein kinase C, beta 1 (PRKCB1), mRNA /cds=(136,2151) | 1 | GCCTGGAGCTTGGCTTTGTATCCAAG TGTATGGTTGCTTTGTCTAAGAGG |
| 5032 | Table 2 | Hs.95835 | BG747862 | 14058515 | RST8356 cDNA | 1 | AGGGAGACTCTCAGCCTTCAGCTTCC TAAATTCTGTGCTGTGACTTTTCG |
| 5033 | Table 1 | Hs.204959 | BG758569 | 14069222 | hypothetical protein FLJ14886 (FLJ14886), mRNA /cds=(111,1169) | 1 | AGCCTACAAGCCACCTCGCCACTGT GAACCTGTCTGCTACTCTGGATGTC |
| 5034 | Table 2 | Hs.37617 | BG760189 | 14070842 | 602144947F1 cDNA, 5' end /clone=IMAGE:4308683 /clone_end=5' | 1 | CCTGCTCACAGACCAGGAAGTCTACA AGCTGGACCTTGACCGGCAGTACC |
| 5035 | Table 1 | Hs.182447 | BG766957 | 14077610 | heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC), transcript variant 1, mRNA /cds=(191,1102) | 1 | AGCAGTTCCACAGTGTTCACACTAC AGGATTTAAATATTTGCTCCAGA |
| 5036 | Table 2 | Hs.301226 | BG768471 | 14079124 | mRNA for KIAA1085 protein, partial cds /cds=(0,1755) | 1 | CCTTTATCCACCTGGATTTTAGGGAC AAACACTGAAAACGAATAAGTCCA |
| 5037 | Table 2 | Hs.301226 | BG768471 | 14079124 | mRNA for KIAA1085 protein, partial cds /cds=(0,1755) | 1 | CCTTTATCCACCTGGATTTTAGGGAC AAACACTGAAAACGAATAAGTCCA |
| 5038 | Table 1 | Hs.124675 | BG772661 | 14083314 | ob13b08.s1 cDNA, 3' end /clone=IMAGE:1323543 /clone_end=3' | 1 | CAGAGAAGCAAGTCAAGTGCAGCG AGTTGGGTGGAAGCTGATAGAGCAA |
| 5039 | Table 2 | Hs.301226 | BG775621 | 14045938 | mRNA for KIAA1085 protein, partial cds /cds=(0,1755) | 1 | CCACAAACCATTCAGATCAGGCACCTT GCTGACCTGTGTTCTTAAGGACAC |
| 5040 | Table 1 | Hs.180450 | BG820627 | 14168214 | ribosomal protein S24 (RPS24), transcript variant 1, mRNA /cds=(37,429) | 1 | AAGAACTATGTAGCATAGTGTCTTA ACACCTCAGTAAAGTAAAGCTGGCC |

Table 8

| | | | | | | | |
|------|----------|-----------|----------|----------|---|----|-----------------------------|
| 5041 | Table 1 | Hs.1432 | BG913430 | 14293906 | protein kinase C substrate 80K-H (PRKCSH), mRNA /cds=(136,1719) | 1 | AGCAGGAGACAGCTTCCTGATCTAGA |
| 5042 | Table 1 | Hs.247474 | BG913498 | 14293974 | hypothetical protein FLJ21032 (FLJ21032), mRNA /cds=(235,1005) | 1 | TGGAACCTAGTCACAATTGAAGTTCCT |
| 5043 | Table 1 | Hs.72988 | BI086609 | 14504939 | signal transducer and activator of transcription 2, 113kD (STAT2), mRNA /cds=(57,2612) | 1 | CCCACACAAGTGGCCACATAAATCT |
| 5044 | Table 1 | Hs.288036 | BI086741 | 14505071 | tRNA isopentenylpyrophosphate transferase (IPT), mRNA /cds=(60,1040) | 1 | GCAAACAAGTCTCAAAGTTGTGGAGA |
| 5045 | Table 1 | Hs.131887 | BI090806 | 14509136 | 602415255F1 cDNA, 5' end /clone=IMAGE:4523725 /clone_end=5' | 1 | GCAAGAAAGAGAAACGTAAAAACAGA |
| 5046 | Table 1 | Hs.287797 | BI091791 | 14510121 | mRNA for FLJ00043 protein, partial cds /cds=(0,4248) | 1 | GAGAGTTGCTGTTGTAATAACGTTT |
| 5047 | Table 1 | Hs.146381 | BI092128 | 14510458 | RNA binding motif protein, X chromosome (RBMX), mRNA /cds=(11,1186) | 1 | GGAATAGTTGATCTACAAAGGCCA |
| 5048 | Table 1 | Hs.75249 | BI092568 | 14510898 | mRNA for KIAA0069 gene, partial cds /cds=(0,680) | 1 | GGTTAACGCTTCTGTGAGGACCTTCT |
| 5049 | Table 1 | Hs.73965 | BI093470 | 14511800 | splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(155,820) | 1 | GGCTCTTGAGATACCTAAATATT |
| 5050 | Table 1 | Hs.104679 | BI094249 | 14512579 | Homo sapiens, clone MGC:18216 IMAGE:4156235, mRNA, complete cds /cds=(2206,2373) | 1 | ACTTTCATTGGTAAATAAGCCTGTCTT |
| 5051 | Table 1 | Hs.7905 | BI193299 | 14648319 | SH3 and PX domain-containing protein SH3PX1 (SH3PX1), mRNA /cds=(43,1830) | 1 | CCTATCTGGATTTTTGGTGTGCA |
| 5052 | Table 1 | Hs.217493 | BI195901 | 14650921 | annexin A2 (ANXA2), mRNA /cds=(49,1068) | 1 | CAGTTATTTAAAGGCTGACAACTGCC |
| 5053 | Table 1 | Hs.33026 | BI198202 | 14653223 | mRNA for FLJ00037 protein, partial cds /cds=(3484,3921) | 1 | TTCCAGACCCGCGCTGTATTAATA |
| 5054 | Table 1 | Hs.179661 | BI222978 | 14676422 | Homo sapiens, tubulin, beta 5, clone MGC:4029 IMAGE:3617988, mRNA, complete cds /cds=(1705,3039) | 1 | TGGTGGGTACAGAAACATTGTACACAG |
| 5055 | Table 1 | Hs.23158 | BI224666 | 14678110 | 600943902F1 cDNA, 5' end /clone=IMAGE:2966352 /clone_end=5' | 1 | GGATCCTGGAACAGAGGAAGAGTT |
| 5056 | Table 1 | Hs.218387 | H03298 | 866231 | tc88c11.x1 cDNA, 3' end /clone=IMAGE:2073236 /clone_end=3' | 1 | TTCTGACCTAATAATTACGGGAAATG |
| 5057 | Table 1 | Hs.178703 | H56344 | 1004988 | AV716627 cDNA, 5' end /clone=DCBBCH05 /clone_end=5' | 1 | GAAAGTCTGGGCCAGCATCAATAA |
| 5058 | Table 1 | NA | H57221 | 1010053 | yr08e08.r1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:204710 5', mRNA sequence | 1 | TGGGTCGGCAAAGCTATTATAACTTT |
| 5059 | Table 1 | Hs.74002 | H81660 | 1059749 | mRNA for steroid receptor coactivator 1e /cds=(201,4400) | 1 | GAATGCTAACCGCATGTTTGACCT |
| 5060 | Table 1 | Hs.5122 | N31700 | 1152099 | 602293015F1 cDNA, 5' end /clone=IMAGE:4387778 /clone_end=5' | 1 | GCTGTGTCTTTCTGGCACAATCGGG |
| 5061 | Table 1 | NA | R11456 | 764191 | yf46a09.r1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:129880 5' similar to gb M87943 HUMAALU4 | 1 | GATTCACCTTTTAGACACTGGAA |
| 5062 | Table 1 | Hs.208603 | R64054 | 835933 | 7f01d11.x1 cDNA, 3' end /clone=IMAGE:3293397 /clone_end=3' | 1 | TTGACAAAGATGACATCGCCCCAAGA |
| 5063 | Table 1 | NA | R85137 | 943543 | yo41c07.r1 Soares adult brain N2b4HB55Y cDNA clone IMAGE:180492 5', mRNA sequence | 1 | GCCAAAATAAATGGGAATTGAAA |
| 5064 | Table 1 | NA | T80378 | 698887 | yd05c01.r1 Soares infant brain 1NIB cDNA clone IMAGE:24693 5', mRNA sequence | 1 | GTAAGATCAGAATACCAAGGCCAGC |
| 5065 | Table 1 | NA | T80654 | 703539 | yd22a08.r1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:108950 5', mRNA sequence | 1 | TAAGGCAACGACTCCCTCCCCAAA |
| 5066 | Table 1 | Hs.44189 | W00466 | 1271875 | yz99f01.s1 cDNA, 3' end /clone=IMAGE:291193 /clone_end=3' | 1 | ATACGGGACAATAAAATCTGCCTTTT |
| 5067 | Table 1 | Hs.306117 | W16552 | 1290934 | capicua protein (CIC) mRNA, complete cds /cds=(40,4866) | 1 | GCTCTGGAGGGAGATACTACCTCT |
| 5068 | Table 1 | Hs.17778 | W19201 | 1295429 | neuropilin 2 (NRP2), mRNA /cds=(0,2780) | 1 | ATGCTGGTGTATGTGACATTGTGTG |
| 5069 | Table 1 | Hs.340717 | W25068 | 1302933 | we58c01.x1 cDNA, 3' end /clone=IMAGE:2345280 /clone_end=3' | 1 | AGTCTCGGGCATGTTACGGTGGG |
| 5070 | Table 1 | Hs.8294 | W80882 | 1391906 | KIAA0196 gene product (KIAA0196), mRNA /cds=(273,3752) | 1 | GGAAATTGTGCCAAACCATGAAAA |
| 5071 | Table 3A | Hs.133543 | AA251316 | 1886279 | EST378950 cDNA | -1 | TATTACTGTGTGTGGGGTGTCTGT |
| 5072 | Table 3A | Hs.96487 | AA524555 | 2265483 | 7q23f06.x1 cDNA, 3' end /clone=IMAGE:3699226 /clone_end=3' | -1 | TTTGTGTGTGAAATATAACATTGATTG |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|----------|--|----|--|
| 5073 | Table 3A | NA | AA628833 | 2541220 | af37g04.s1 Soares_total_fetus_Nb2HF8_9w cDNA clone IMAGE:1033878 3', mRNA sequence | -1 | GACTCGTTACGCCGTAGTTTGTCTTA TCTTGTATCAAATGAATTCGT |
| 5074 | db mining | NA | AA701193 | 2704358 | zj80c03.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:461188 3' similar to gb:M11124 HLA C | -1 | AGCCGCCAGCTACTTAATCCCTCAG TAACATCTATCTAAATCTCCCATG |
| 5075 | Table 3A | Hs.307486 | AA729508 | 2750867 | nx54a03.s1 cDNA /clone=IMAGE:1266028 | -1 | TGGCCTGTGCTTTTACCACACCGTCA AACCCTTGATCATTTCTGTAACA |
| 5076 | Table 3A | Hs.104157 | AA765569 | 2816807 | EST380899 cDNA | -1 | ACATTCTCATAGTCCAGGGGCTCAAC AATTTGGCCTTTTCCAGCACCAC |
| 5077 | db mining | Hs.220649 | AA774984 | 2834318 | QV1-GN0320-051200-552-b08 cDNA | -1 | TCAGCAGTTGTGCCTTTTCTCAGAGA TCCAGCGCTCTTCTCGCTGTAC |
| 5078 | db mining | Hs.192078 | AA884466 | 2993996 | te30h04.x1 cDNA, 3' end /clone=IMAGE:2087479 /clone_end=3' | -1 | TGCAAGCAATAAAATCTGCTTTAATC AGTAACCACTGTCTGACAGGACA |
| 5079 | db mining | Hs.194249 | AA907080 | 3042540 | HOA43-1-G6.R cDNA | -1 | GGTCGTAGAGAAGACAGCAAGGGAG GGGATAAAACCCAGGAAGGACTTAA |
| 5080 | Table 3A | Hs.143254 | AA961072 | 3127626 | EST388440 cDNA | -1 | GGCTCAGCATGACAACCGCCTACGG AAAAACTCTAATTCCTAAACATCTA |
| 5081 | db mining | Hs.163271 | AF343666 | 13591717 | translocation associated fusion protein IRTA1/IGA1 (IRTA1/IGHA1) mRNA, complete cds /cds=(136,402) | -1 | GACAAGCCAGGTGAGCCAGATTGC CAAAGCAGCACTTGCCACACCAGC |
| 5082 | Table 3A | Hs.46476 | AI018105 | 3232624 | EST386846 cDNA | -1 | GGTTCCTTGAAGCAGTGCCAACTTA AATCTACCTCAGGTAAAGTAGTAG |
| 5083 | Table 3A | Hs.238954 | AI031624 | 3249836 | 602637935F1 cDNA, 5' end /clone=IMAGE:4765448 /clone_end=5' | -1 | GCTGACAGTATGGAGGCTAAAGGTG TGGAGGAACGAGGAGATGAGTA |
| 5084 | db mining | Hs.133261 | AI052754 | 3308745 | oy78e01.x1 cDNA, 3' end /clone=IMAGE:1671960 /clone_end=3' | -1 | CAAGTGTGCCGGGCAAGTTGGGAA GGTGAAGCAATCTGTGACTTAAATA |
| 5085 | db mining | Hs.292803 | AI056470 | 3330336 | oy77d03.x1 cDNA, 3' end /clone=IMAGE:1671845 /clone_end=3' | -1 | GAGCTACTCAAGGGGAAAAAGGGC ATATAGTATGCTCTGGTAGTAAAGT |
| 5086 | db mining | Hs.6733 | AI057025 | 3330814 | phosphoinositide-specific phospholipase C PLC-epsilon mRNA, complete cds /cds=(235,7146) | -1 | GCTCAAGATCACCTCTTTGTCTATCTT GAACAATGTTTTCTCTCTAGGT |
| 5087 | db mining | Hs.133930 | AI073993 | 3400637 | oy66d03.x1 cDNA, 3' end /clone=IMAGE:1670789 /clone_end=3' | -1 | TGGTGATAATAGAGATTGTTTCTGCC CTGGGGGTAGTTCAAGGATAACAC |
| 5088 | db mining | Hs.133949 | AI074528 | 3401172 | oy79d05.x1 cDNA, 3' end /clone=IMAGE:1672041 /clone_end=3' | -1 | CTTCAGGTTTGGCCAGCCCTCCTT GAAGACTCCTCCATCCAGTCAAG |
| 5089 | db mining | Hs.134018 | AI076071 | 3405249 | oy80b11.x1 cDNA, 3' end /clone=IMAGE:1672125 /clone_end=3' | -1 | CCCAAGTGAAGTCAAAGTTACTGTGT GGTTGATAGGGAACATGGCTGGAT |
| 5090 | db mining | NA | AI081253 | 3418045 | oy67c02.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:1670882 3' similar to gb:X64707 BREAST BASIC CONSERVED PR | -1 | ACCCGCAGACCAGATGGTTGAAAGG AAAAATTAAGCCTTCTTGGGGATT |
| 5091 | db mining | Hs.134590 | AI081258 | 3418050 | oy67c11.x1 cDNA, 3' end /clone=IMAGE:1670900 /clone_end=3' | -1 | GGAGTTAGATCAACCTTATGGGGAAG GGAAAGCGAGGGCTTGTGACAATT |
| 5092 | Table 3A | Hs.105621 | AI084553 | 3422976 | HNC29-1-B1.R cDNA | -1 | GATGGCTGCTTGCTTAAACCCAG ACAGGGTCTTCCAGTGCATCTGC |
| 5093 | db mining | Hs.230775 | AI085588 | 3424011 | oy68d10.x1 cDNA, 3' end /clone=IMAGE:1670995 /clone_end=3' | -1 | CATTTGTGGGTGGAGGGTTTGAATG TCCTCTTCCATGTCAGGCAAAAGG |
| 5094 | db mining | Hs.146591 | AI086023 | 3424446 | oy70f10.x1 cDNA, 3' end /clone=IMAGE:1671211 /clone_end=3' | -1 | TTCTATGAAGGTTTCCCTGGACAAGA AAGTCCAGAGAGCCCTTAGCTCA |
| 5095 | Table 3A | Hs.23158 | AI097125 | 3446707 | 600943902F1 cDNA, 5' end /clone=IMAGE:2966352 /clone_end=5' | -1 | TGCTGAATGTACCTGAGTGTATGTAT TTAAAGGACTCACATGGGCATCA |
| 5096 | db mining | Hs.150708 | AI122689 | 3538455 | oy79f03.x1 cDNA, 3' end /clone=IMAGE:1672061 /clone_end=3' | -1 | TCTCAACCCTAATATTCATTGTCCAT GAGCATTGTGAGGTTTGGATGG |
| 5097 | db mining | Hs.326995 | AI144314 | 3666123 | oy84f01.x1 cDNA, 3' end /clone=IMAGE:1672537 /clone_end=3' | -1 | ACAAGTGGAAGAGGAAGACAGAAGA ATGGGTGAGGAGATGCAAGGATGG |
| 5098 | db mining | NA | AI144317 | 3666126 | oy84f04.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:1672543 3' similar to gb:X64707 BREAST BASIC CONSERVED PR | -1 | TCCTTAGGGAAAAGAAGATTTTCAA CCCTTCGTTAGTTTCGGTAGGGCC |
| 5099 | db mining | NA | AI187859 | 3739068 | qe07h05.x1 Soares_testis_NHT cDNA clone IMAGE:1738329 3', mRNA sequence | -1 | ACGCAATTTGTTACATACATACACAT GCAAATCCCAAGAAAGGTTTTTA |
| 5100 | Table 3A | Hs.121210 | AI204611 | 3757217 | EST384285 cDNA | -1 | CCCAGCCCTCTATGTACCCGTGTCCC AGCCAGCAATAAATGCCATCTTGG |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|---|----|---|
| 5101 | db mining | Hs.144814 | AI220630 | 3802833 | RST44972 cDNA | -1 | AGCCTGGAATTC TAAGCAGCAGTTTC ACAATCTGTAATTGCACGTTTCTG |
| 5102 | db mining | Hs.126580 | AI222355 | 3804558 | 602691805F1 cDNA, 5' end /clone=IMAGE:4824264 /clone_end=5' | -1 | TGGTTACTCATGTCCTCAAAGACGAC TCATGATGCTGGATGTGAAGAACT |
| 5103 | Table 3A | Hs.36475 | AI243620 | 3839017 | EST372075 cDNA | -1 | AGGCAAAAGTCATTTCTTCCCTATATT TTGTCATGCTTATCTCCTGTCTC |
| 5104 | db mining | NA | AI263168 | 3871371 | qh49e10.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:1848042 3', mRNA sequence | -1 | GTATGAAGGCAAGAAAATTTTCAGGGG AAAACAAGTGGTTATTTTCTGGCC |
| 5105 | Table 3A | Hs.158501 | AI290845 | 3933619 | 7q71b07.x1 cDNA, 3' end /clone=IMAGE:3703644 /clone_end=3' | -1 | GATACCTCTTCTTAAGACTCATCGC GTCTCTCCAGCCTCCTCGCCCCA |
| 5106 | db mining | Hs.150175 | AI301070 | 3960416 | qo16d04.x1 cDNA, 3' end /clone=IMAGE:1908679 /clone_end=3' | -1 | TCTGTATGCTGTGGTCTCATCAGGAA CCTTTCTCTGCACTGCATTTTTC |
| 5107 | db mining | NA | AI356349 | 4107970 | qz26d12.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2028023 3' similar to contains MER7.b2 MER7 repetitive el | -1 | AGAGCTGGTTCAGAAAGGTTCCGGAT GAGTCCTGAATGTTTATGTAGGGCA |
| 5108 | db mining | Hs.157560 | AI356388 | 4108009 | qz26e07.x1 cDNA, 3' end /clone=IMAGE:2028036 /clone_end=3' | -1 | TCCTTAGTCTCCTCAATTTCCACACA CTGAACATGACATTTTACCCTTT |
| 5109 | db mining | NA | AI356470 | 4108091 | qz27b11.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2028093 3', mRNA sequence | -1 | TTTTCTGTTTTCTGTTTTAAGAAATC TGGAACCGCAAGGCCGTCCCTTT |
| 5110 | db mining | Hs.157808 | AI361701 | 4113322 | qz18e09.x1 cDNA, 3' end /clone=IMAGE:2021896 /clone_end=3' | -1 | CCAAAGCCTTTGTTGTTGGTGGCGA GGCCCCCTTTTGAATGGGGTTTTT |
| 5111 | db mining | Hs.327396 | AI361729 | 4113350 | qz24a08.x1 cDNA, 3' end /clone=IMAGE:2027798 /clone_end=3' | -1 | TGCCGCCCCAGGATTCTTTTAAGAA TAAAAAGAAATGAGTGTGGACATG |
| 5112 | db mining | Hs.157811 | AI361733 | 4113354 | qz24b02.x1 cDNA, 3' end /clone=IMAGE:2027787 /clone_end=3' | -1 | CCTACGATATCCTTTTCAAATAGGGG TGGGTCCAGCCCCCTTGTGCCCTG |
| 5113 | db mining | Hs.270193 | AI361773 | 4113394 | qz19c05.x1 cDNA, 3' end /clone=IMAGE:2021960 /clone_end=3' | -1 | CTGGGAGAAAGGTACTTTGGGTAGT GGTAGGGATAGGGATGAACGGGAA |
| 5114 | db mining | NA | AI364677 | 4124366 | qz05h09.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2020673 3', mRNA sequence | -1 | AGCATAATCCTAATGAGGAACCTTGT CTGAAGTCTGAGGCTGAGTTACTT |
| 5115 | db mining | Hs.327411 | AI364926 | 4124615 | qz23b07.x1 cDNA, 3' end /clone=IMAGE:2027701 /clone_end=3' | -1 | TTTTGGAACCTTAGCCCTGTGCAAA TCAAAGGATGTGAGGGGAAAAAGG |
| 5116 | db mining | Hs.157279 | AI364931 | 4124620 | qz23c04.x1 cDNA, 3' end /clone=IMAGE:2027718 /clone_end=3' | -1 | ATTTCCCTACGGATGGGACCAAGAA ACTGATGAGAACGGCCAAAGTGT |
| 5117 | db mining | Hs.157280 | AI364944 | 4124633 | qz23d11.x1 cDNA, 3' end /clone=IMAGE:2027733 /clone_end=3' | -1 | AACACCCGAAACCGTCTTCTGTGGCA TTTGTGAGTTGAAAAAGAACCT |
| 5118 | db mining | Hs.283433 | AI365377 | 4125066 | qz08a02.x1 cDNA, 3' end /clone=IMAGE:2020874 /clone_end=3' | -1 | CCAGTGGCTGGGATGGTGACAGTGA CATCCACAGTAAACAGATGAAATGT |
| 5119 | db mining | Hs.304043 | AI365414 | 4125103 | 7e97a03.x1 cDNA, 3' end /clone=IMAGE:3293068 /clone_end=3' | -1 | GGATTTGAGAAACAGTTGCAGATATT ATTGATTAGCTAGTTGGCAGTGGG |
| 5120 | db mining | Hs.80426 | AI365418 | 4125107 | brain and reproductive organ- expressed (TNFRSF1A modulator) (BRE), mRNA /cds=(146,1297) | -1 | CTTGTTCCAGGCCAGCCCCACACA GTAGGCAGTCATTAAAGTTTGGTGA |
| 5121 | db mining | Hs.157310 | AI365460 | 4125149 | qz09e06.x1 cDNA, 3' end /clone=IMAGE:2021026 /clone_end=3' | -1 | TTTTCCTTCAACTCTTGCGACTTTCTT GGTCTGCCTGTGTGGTTTAATA |
| 5122 | db mining | Hs.157311 | AI365473 | 4125162 | qz09f09.x1 cDNA, 3' end /clone=IMAGE:2021033 /clone_end=3' | -1 | TTCTGTTAATAGCAAACATTGCCTTTG AGTGCTACTACTAAACCTGAGGC |
| 5123 | db mining | NA | AI367021 | 4136766 | qz23h06.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2027771 3' similar to contains MSR1.t1 MSR1 repetitive el | -1 | TCTAGGGATCTGCCCGGCTCAAAATC CCAGGCCGTAGGCTAAGTTGTTT |
| 5124 | db mining | Hs.296281 | AI368512 | 4147265 | interleukin enhancer binding factor 1 (ILF1), mRNA /cds=(197,2164) | -1 | CGGACAAGGGCTGGCAGGTAAATGC CTTCAGTTTGTGTTAAATAGAGGC |
| 5125 | db mining | Hs.327453 | AI378055 | 4187908 | tc79e11.x1 cDNA, 3' end /clone=IMAGE:2072396 /clone_end=3' | -1 | AGCCTTAGCCCCCTTTAAAGCACTTAA AGTTACTACTTCCAAATGTGATTT |
| 5126 | db mining | NA | AI378091 | 4187944 | tc80a09.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2072440 3', mRNA sequence | -1 | ACCTTGTCTAATACAGCTCACTTTGAT TGAACATCTACTCTGTGGCGGTT |
| 5127 | db mining | Hs.158876 | AI378095 | 4187948 | tc80b01.x1 cDNA, 3' end /clone=IMAGE:2072425 /clone_end=3' | -1 | TGGAACGGCTATTTGCCGGTTTAAAA ACCAAAAACCCCGGTTTTTCCAAA |
| 5128 | db mining | Hs.283438 | AI378109 | 4187962 | 7f19b03.x1 cDNA, 3' end /clone=IMAGE:3295085 /clone_end=3' | -1 | GTAAGGCAGACGAGAGAGGCGGAGG TCTCACAGTGAACCACAGGATCTGG |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|---|
| 5129 | db mining | Hs.158956 | AI380117 | 4189970 | tf98b07.x1 cDNA, 3' end /clone=IMAGE:2107285 /clone_end=3' | -1 | TTGCCTGCCATGCCCTTATAAGTGCC CTTTAATGTCATAGCATGTAAAGG |
| 5130 | db mining | Hs.158967 | AI380252 | 4190105 | tf94d05.x1 cDNA, 3' end /clone=IMAGE:2106921 /clone_end=3' | -1 | GGGTTTGTGTCCCCATTAGAACTCTG ATGAAACGGTGGGCTTTCCTTCCT |
| 5131 | db mining | Hs.158969 | AI380283 | 4190136 | tf99g02.x1 cDNA, 3' end /clone=IMAGE:2107442 /clone_end=3' | -1 | CAGAGCCTCCAGAAATTATGTGAACCT GTCTCAAAACATTCTCTAAATGGC |
| 5132 | db mining | Hs.158971 | AI380329 | 4190182 | tf94g05.x1 cDNA, 3' end /clone=IMAGE:2106968 /clone_end=3' | -1 | GAAAGGACCCGAGGGTTGTATTATAA AAAGCCTCCCTGGGCTCAAAAA |
| 5133 | db mining | Hs.309122 | AI380449 | 4190302 | tg02f12.x1 cDNA, 3' end /clone=IMAGE:2107631 /clone_end=3' | -1 | GCCAACTGCTTAGAAGCCCAACACAA CCCATCTGGTCTCTTGAATAAAGG |
| 5134 | db mining | Hs.302447 | AI380514 | 4190367 | tg01e02.x1 cDNA, 3' end /clone=IMAGE:2107514 /clone_end=3' | -1 | TGTCTAGAACAGACTGAGAGTGACAC GCATATTGATTGTGAGGACAGTT |
| 5135 | db mining | Hs.231261 | AI380594 | 4190447 | tf95h06.x1 cDNA, 3' end /clone=IMAGE:2107067 /clone_end=3' | -1 | GTTTGGCCCCAAAGTGTTAGGAGA GCTTCTCCCTAGATCGCCCTGTG |
| 5136 | db mining | Hs.158988 | AI380719 | 4190572 | tg03h03.x1 cDNA, 3' end /clone=IMAGE:2107733 /clone_end=3' | -1 | CCAGGAGGGCCAGAATTTGAAATTC CTTGGGGTGTCTTTTTCCAAAA |
| 5137 | db mining | Hs.159000 | AI381037 | 4190890 | tg20h01.x1 cDNA, 3' end /clone=IMAGE:2109361 /clone_end=3' | -1 | CAGTTTGAGCAAAAGCCTTTGAAATC CAAGACTTTTCCCTTGGGGTGCT |
| 5138 | db mining | Hs.159025 | AI381601 | 4194382 | td05g03.x1 cDNA, 3' end /clone=IMAGE:2074804 /clone_end=3' | -1 | CCAGTTGGTTTTTGACTCCAAAGCC CAGGACCCTTCCAAATCCTGCTTG |
| 5139 | db mining | NA | AI382670 | 4195451 | qz05f05.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2020641 3', mRNA sequence | -1 | AGGCCTTTTCAAAGAAAAACCCCTT TGGGGAAAAAGGGAAAGGGCAAAA |
| 5140 | db mining | Hs.192078 | AI383475 | 4196256 | te30h04.x1 cDNA, 3' end /clone=IMAGE:2087479 /clone_end=3' | -1 | TTTTGCTTGCTGTCGGGAGATAAAG CAGGGAACCTTTATGTAGTAAAA |
| 5141 | db mining | Hs.327467 | AI383510 | 4196291 | td03c10.x1 cDNA, 3' end /clone=IMAGE:2074578 /clone_end=3' | -1 | GGGTTTGGCCCGATTATATTAGGTTG GGTGGGGGAAAAATTTATGGGGG |
| 5142 | db mining | Hs.105125 | AI383774 | 4196555 | 602639120F1 cDNA, 5' end /clone=IMAGE:4762804 /clone_end=5' | -1 | GTGAAGTGGATCTTGAGGCCGTGCT GGAAACCGGAAGGTACACTGCTTGG |
| 5143 | db mining | NA | AI383803 | 4196584 | tc98f01.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2074201 3' similar to gb:J03626 URIDINE 5'- MONOPHOSPHATE | -1 | CAAACTTGAGATAAGGTTAAACTG TGCCAGAGGAAAACTGGTAGTCT |
| 5144 | db mining | NA | AI384024 | 4196805 | td05b02.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2074731 3' similar to contains Alu repetitive element;con | -1 | TGCAGCCAGATTGTTCCAAGGTTGCC AATTACCTAGTGGGTAAATTTCCC |
| 5145 | Table 3A | Hs.107622 | AI391443 | 4217447 | tf96e06.x1 cDNA, 3' end /clone=IMAGE:2107138 /clone_end=3' | -1 | AGTGCTTATCATGAAATGTGCTTCAC TGTTACAGCTCTGTTGTTCCCTTA |
| 5146 | db mining | Hs.160956 | AI391451 | 4217455 | tf96f03.x1 cDNA, 3' end /clone=IMAGE:2107133 /clone_end=3' | -1 | GTTATTTGGGAGACAAATGGACGGG CAGGAAGATTGATGCTCCGCTGTTT |
| 5147 | Table 3A | Hs.160959 | AI391500 | 4217504 | 602086202F1 cDNA, 5' end /clone=IMAGE:4250424 /clone_end=5' | -1 | AGCTGAAGGGCTTCAACTTTGCTTGG ATTTTTAAATATTTCTCTGCATA |
| 5148 | Table 3A | NA | AI392705 | 4222252 | tg23b03.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2109581 3', mRNA sequence | -1 | TGCAGGCTCATTGTGCTCCTTCTTCT GGGTTTCAATTGGATTTCAGTCCT |
| 5149 | db mining | Hs.160978 | AI392745 | 4222292 | tg08b05.x1 cDNA, 3' end /clone=IMAGE:2108145 /clone_end=3' | -1 | ATCTCTAATGAAGCCTAGGATCAGAT TTGTGGCATACCAACAGCACATGT |
| 5150 | db mining | Hs.160981 | AI392793 | 4222340 | tg04g01.x1 cDNA, 3' end /clone=IMAGE:2107824 /clone_end=3' | -1 | CCACAAGGGTTAGTTTGGGCCTTAAA ACTGCCAAGGAGTTTCCAAGGATT |
| 5151 | db mining | Hs.160982 | AI392799 | 4222346 | tg04g09.x1 cDNA, 3' end /clone=IMAGE:2107840 /clone_end=3' | -1 | CGCTTTATTTCCACGAAACCTAGGAC AGTGCCATCAAACCGAGCGCTTT |
| 5152 | Table 3A | Hs.189031 | AI392805 | 4222352 | tg04h03.x1 cDNA, 3' end /clone=IMAGE:2107829 /clone_end=3' | -1 | CCTGTTGTGGCTGGCTGCATAATAAT TTCCAGGAGGCTTTCGGAATGTT |
| 5153 | Table 3A | Hs.221014 | AI392814 | 4222361 | MR2-HT1162-180101-007-d08 cDNA | -1 | CGGTCCAGTCGGCTGCTTCCATTCCC TGAAGAAGAGGCCCTAAAGTTAAA |
| 5154 | Table 3A | Hs.168287 | AI392830 | 4222377 | tg10b09.x1 cDNA, 3' end /clone=IMAGE:2108345 /clone_end=3' | -1 | TTAGCCTCAAAGGGTGGGGAAAAAG CCCATACCTCTGGGCCAGTCCTAG |
| 5155 | db mining | Hs.276774 | AI392845 | 4222392 | tg10d01.x1 cDNA, 3' end /clone=IMAGE:2108353 /clone_end=3' | -1 | CCTTAGAATTAAGTTGAATTTCTCTGC CTTGCTAAGCAAGACTTCTCTGCA |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|---|
| 5156 | Table 3A | Hs.159655 | AI392893 | 4222440 | tg05d07.x1 cDNA, 3' end /clone=IMAGE:2107885 /clone_end=3' | -1 | CAGCCACGGCCCCCTCGCGTCTTCGC GGCACGTTAATTAATATGCGGAAAC |
| 5157 | db mining | Hs.327469 | AI392990 | 4222537 | tg22f02.x1 cDNA, 3' end /clone=IMAGE:2109531 /clone_end=3' | -1 | TTTTACCCAAATTTTAAAGCGCGGAT AAAAGGGTTTTTTGTTTGGAGGGGA |
| 5158 | db mining | Hs.230848 | AI392999 | 4222546 | tg22f11.x1 cDNA, 3' end /clone=IMAGE:2109549 /clone_end=3' | -1 | GGAGGTTAGGGCCTGAAGCTCAAAG CTCCCCCTTTTAAATAGTTTTTCCC |
| 5159 | db mining | NA | AI393006 | 4222553 | tg22g06.x1 cDNA, 3' end /clone=IMAGE:2109562 /clone_end=3' | -1 | CCCCTTTGGGCCCCCCGGGTTTTTCC CTTTTTGGTTTCGGGTGTTTTTTG |
| 5160 | db mining | Hs.228891 | AI393017 | 4222564 | tg22h05.x1 cDNA, 3' end /clone=IMAGE:2109561 /clone_end=3' | -1 | ACGTGGGCCTTTGGACCCCTTATAAG ATGGTCATAAGACCCCAAACTGA |
| 5161 | db mining | Hs.159706 | AI393038 | 4222585 | tg25b07.x1 cDNA, 3' end /clone=IMAGE:2109781 /clone_end=3' | -1 | ATGGCTATAAGGCCAAAAAGTTTGG CGGCATGGGGGATTTTTTGCTCTT |
| 5162 | Table 3A | Hs.160273 | AI393041 | 4222588 | tg25b10.x1 cDNA, 3' end /clone=IMAGE:2109787 /clone_end=3' | -1 | AGAGACGGCCACCTGAGACCAATTA GAATATCCACACCAGTGAAGAGAG |
| 5163 | Table 3A | Hs.126265 | AI393205 | 4222752 | Homo sapiens, Similar to RIKEN cDNA 0610006H10 gene, clone MGC:9740 IMAGE:3853707, mRNA, complete cds /cds=(171,1130) | -1 | GCCTCCCCAACCCCTGGCCTCAATTT CCCTTTCTATAAAATGGAAGATGT |
| 5164 | db mining | Hs.159718 | AI393217 | 4222764 | tg14c09.x1 cDNA, 3' end /clone=IMAGE:2108752 /clone_end=3' | -1 | ACACCAGCCAAAGAAAAGCATACCT GAATCCAAGAGAGTATTACACTG |
| 5165 | db mining | Hs.240635 | AI393223 | 4222770 | tg14d03.x1 cDNA, 3' end /clone=IMAGE:2108741 /clone_end=3' | -1 | CTCAGAGAAGAACAGTGTAGAAACCC GCGCTGTGTGAAGCGAGGTTGGGC |
| 5166 | Table 3A | Hs.160401 | AI393906 | 4223453 | tg05f08.x1 cDNA, 3' end /clone=IMAGE:2107911 /clone_end=3' | -1 | ACTTTCCATTGTTGAGCTGGGGAGTT GGATTTTGTCATTGTTTTTATG |
| 5167 | Table 3A | Hs.340891 | AI393908 | 4223455 | wi30d11.x1 cDNA, 3' end /clone=IMAGE:2391765 /clone_end=3' | -1 | TCCCAGTGATGATTCGCTCCCTTTGT TAATTACTCAGTGTTCTTGTTTT |
| 5168 | Table 3A | Hs.274851 | AI393960 | 4223507 | tg11d04.x1 cDNA, 3' end /clone=IMAGE:2108455 /clone_end=3' | -1 | TGCGTGCTGCTAATACTTAGGTACCC ATAATAGGTCTTTACACTCAGTTT |
| 5169 | Table 3A | Hs.160405 | AI393962 | 4223509 | tg11d08.x1 cDNA, 3' end /clone=IMAGE:2108463 /clone_end=3' | -1 | CCTGACCTTGAGGCATTTTTGATTGT GCAGTTACCTAGGGTATGCTTGTG |
| 5170 | Table 3A | Hs.76239 | AI393970 | 4223517 | hypothetical protein FLJ20608 (FLJ20608), mRNA /cds=(81,680) | -1 | GAGGACTGGGACCGTGATTCCACTA ACCGGAAACCGTCGCCTTCGGGCC |
| 5171 | Table 3A | Hs.160408 | AI393992 | 4223539 | tg06c05.x1 cDNA, 3' end /clone=IMAGE:2107976 /clone_end=3' | -1 | GGGGAAGTCAAGGAGACACACACGC TCTTCAACAGAATCAGCTCTTAAT |
| 5172 | Table 3A | Hs.244666 | AI394001 | 4223548 | tg06d04.x1 cDNA, 3' end /clone=IMAGE:2107975 /clone_end=3' | -1 | AAGTAGATCCTGCCTTAGAAAACCTT TTGCCATGAATGACAAATTCATGT |
| 5173 | db mining | Hs.160410 | AI394009 | 4223556 | tg11e02.x1 cDNA, 3' end /clone=IMAGE:2108474 /clone_end=3' | -1 | TGTCAGCATCTGGAATAGTGTAAGTA TGCAGTGGAGGAAATCTCATCCTT |
| 5174 | db mining | Hs.160423 | AI394303 | 4223850 | tg09g11.x1 cDNA, 3' end /clone=IMAGE:2108324 /clone_end=3' | -1 | TTAACAGGACCTCTGGGCCACCAAG GAGAAAGGGCTGGGGAAGCCAAGAG |
| 5175 | Table 3A | Hs.159678 | AI394671 | 4224218 | tg24a07.x1 cDNA, 3' end /clone=IMAGE:2109684 /clone_end=3' | -1 | GTTCTGTGATAGTTTGTTCCTCAT CTCCCTCACCTCTGCCTGGGTTG |
| 5176 | db mining | Hs.228337 | AI394690 | 4224237 | tg24c06.x1 cDNA, 3' end /clone=IMAGE:2109706 /clone_end=3' | -1 | GGCCCTCCTTTTGCTGGAGAGTTTT TTATAAATGGAGCCCGATTTCAT |
| 5177 | db mining | Hs.159682 | AI394730 | 4224277 | tg24g04.x1 cDNA, 3' end /clone=IMAGE:2109750 /clone_end=3' | -1 | GGGCTTTTTCTTCCCCTAATCAGGGT GACCTGGGCCTTTTGGGCAGGATC |
| 5178 | db mining | Hs.159683 | AI394733 | 4224280 | tg24g09.x1 cDNA, 3' end /clone=IMAGE:2109760 /clone_end=3' | -1 | AAGGAGGGGAGTGAATGATATTGCT GTCATTTCTCAGCAAATCATAGTA |
| 5179 | db mining | Hs.177146 | AI399977 | 4243064 | tg92e06.x1 cDNA, 3' end /clone=IMAGE:2116258 /clone_end=3' | -1 | TAAAATTCTCTGTGGGAAAAAGCCTG CCAATAAATGGGGGTTTTTGGGC |
| 5180 | Table 3A | Hs.225567 | AI400714 | 4243801 | tg93g12.x1 cDNA, 3' end /clone=IMAGE:2116390 /clone_end=3' | -1 | ACAGACTAAGCTGGTTTGGTGGATTCT ATCTTTCATTATGAAGAAAGCAG |
| 5181 | db mining | NA | AI400725 | 4243812 | tg93h12.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2116391 3' similar to contains TAR1.t1 MER22 repetitive e | -1 | CCCAAAGCCTGGGGGGTTTTGGCCCA AACCTTCCCCCTGGTTTTTATAAAA |
| 5182 | db mining | Hs.224409 | AI400796 | 4243883 | IL3-ET0114-011100-330-F11 cDNA | -1 | ACTGCTTTCAAGAAAGTGGGACCAGT GGCATTGTAGCCACCATAATCACT |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|---|----|---|
| 5183 | db mining | Hs.174778 | AI400826 | 4243913 | th10g11.x1 cDNA, 3' end /clone=IMAGE:2117924 /clone_end=3' | -1 | GCCCTTGGCAAATGATTTGAGACCCC TTTTGAAAACCATGTAGGATGAAT |
| 5184 | db mining | Hs.270294 | AI401001 | 4244088 | tm29d11.x1 cDNA, 3' end /clone=IMAGE:2158005 /clone_end=3' | -1 | CACACAGCAGTGGCTTGGGGATGAG GAAGGAAGGGAGAAATCTCAACGGAG |
| 5185 | db mining | Hs.224178 | AI401179 | 4244266 | tg26g11.x1 cDNA, 3' end /clone=IMAGE:2109956 /clone_end=3' | -1 | TTTTTCTGTGAGTTAGGGGCATGGAG GCGGCAGTGTGGGAGCTGGAGCC |
| 5186 | db mining | Hs.175336 | AI401184 | 4244271 | 7o18b08.x1 cDNA, 3' end /clone=IMAGE:3574239 /clone_end=3' | -1 | AGTTGGCTCTAGTTTAAAGATATAAAT ACGTACCTCACTTAAACCCCATGT |
| 5187 | db mining | Hs.327913 | AI401303 | 4244390 | tg92d01.x1 cDNA, 3' end /clone=IMAGE:2116225 /clone_end=3' | -1 | CTTCAGGCCCAAGTTCAACGGGTAA AGAGGTCGCTCCCAAATTATTCT |
| 5188 | db mining | Hs.159693 | AI417000 | 4260504 | th02f02.x1 cDNA, 3' end /clone=IMAGE:2117115 /clone_end=3' | -1 | GTCCCACTAGCCCCATTTAGGGCTT GCTAGTTACATGGGTTTGTGTTTA |
| 5189 | Table 3A | Hs.79968 | AI419082 | 4265013 | splicing factor 30, survival of motor neuron-related (SPF30), mRNA /cds=(0,716) | -1 | GGATGTGTGATGTTTATATGGGAGAA CAAAAAGCTGATGTATAGCCCTGT |
| 5190 | Table 3A | Hs.131067 | AI421806 | 4267737 | yt85b05.s1 cDNA, 3' end /clone=IMAGE:231057 /clone_end=3' | -1 | CAATTTCACCTCTAAGGGGGTCCGG GAAAGGCACGCTGAGGGTGAATATG |
| 5191 | Table 3A | Hs.159103 | AI431873 | 4306229 | tc97d09.x1 cDNA, 3' end /clone=IMAGE:2074097 /clone_end=3' | -1 | GCTTTCAAATGAATTTAGGGCTTTTC TTTGAAGCAGTCTTGTAAGTTGT |
| 5192 | Table 3A | Hs.254006 | AI432340 | 4309500 | tg54e06.x1 cDNA, 3' end /clone=IMAGE:2112610 /clone_end=3' | -1 | TCCTTTCTGGATACCAGGAATCACTT AAAAATCTGTGTATAATGCCCCA |
| 5193 | db mining | Hs.283442 | AI435240 | 4301796 | ti02a08.x1 cDNA, 3' end /clone=IMAGE:2129270 /clone_end=3' | -1 | AAACAGGGAACGACAGGAAAAAGAT GACCGTGATACACTCTGCTAAAAGC |
| 5194 | db mining | Hs.327548 | AI435268 | 4301992 | ti02d10.x1 cDNA, 3' end /clone=IMAGE:2129299 /clone_end=3' | -1 | CCCCCCCCGGCTTCCCCCTTTTTTCCC CGCCCGTTTTTTGGGGGAATGGG |
| 5195 | Table 3A | NA | AI436418 | 4281540 | ti01h02.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2129235 3' similar to SW:SYB2_HUMAN P19065 SYNAPTOBREVIN | -1 | GGCCATGCCGGGCCAGCCCCACCTG AAGCTCAGTGAAGCTGATTAATAA |
| 5196 | Table 3A | Hs.165703 | AI436561 | 4282683 | ti03b03.x1 cDNA, 3' end /clone=IMAGE:2129357 /clone_end=3' | -1 | CGCAGGACTCTAAAGATCCAAGCTCA CAAAACACTCCAAATCCACCTCGA |
| 5197 | Table 3A | Hs.111377 | AI436587 | 4282890 | AL582032 cDNA /clone=CS0DL003YA06-(3-prime) | -1 | AACTTTACTTCTGTCTTGGCAGGAC ATGGAGAGAGGGAGGGATTCCAAA |
| 5198 | db mining | Hs.283443 | AI436589 | 4282906 | 7f34g01.x1 cDNA, 3' end /clone=IMAGE:3296592 /clone_end=3' | -1 | GGGTGATAATTGAGGGTGCCGCTGG GAAGGTCCGAGAATGGGTTTTCATG |
| 5199 | Table 3A | Hs.257066 | AI438957 | 4300957 | UI-H-BI3-aka-h-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733930 /clone_end=3' | -1 | GTTTCATTGCTGTTTCTGAGTGTGCTG CTGTGGTGCTATAAATGCTCCAG |
| 5200 | db mining | Hs.165701 | AI438979 | 4301111 | tc89d11.x1 cDNA, 3' end /clone=IMAGE:2073333 /clone_end=3' | -1 | TATTCACCAAGTGAGCTACACTCCCG GCCCTTTAGTGTGTTGTAAC |
| 5201 | db mining | Hs.165702 | AI438980 | 4301118 | tc89d12.x1 cDNA, 3' end /clone=IMAGE:2073335 /clone_end=3' | -1 | CCGTGTTGTGGCAAAATGGTCCCTG GAGTTTTGACCCTGTGTTAAAGA |
| 5202 | db mining | Hs.327566 | AI439020 | 4301397 | tc89e05.x1 cDNA, 3' end /clone=IMAGE:2073344 /clone_end=3' | -1 | TTTTTTGGGGCCGAAAACCCCCAATG AGGGGGATTAAAGCTGTTTTCCCC |
| 5203 | db mining | Hs.327567 | AI439044 | 4301565 | tc89h03.x1 cDNA, 3' end /clone=IMAGE:2073365 /clone_end=3' | -1 | GGGGTTGTCTTTTCCACCCTGATG GGGAATTTATGGATGGGTTTCCTT |
| 5204 | db mining | Hs.165704 | AI439060 | 4301677 | tc84f07.x1 cDNA, 3' end /clone=IMAGE:2072869 /clone_end=3' | -1 | AAATGAGTGACCAAAACACTTCTGTA CCACTTCTGTGAGCTGAGGTCCAG |
| 5205 | Table 3A | Hs.165681 | AI439580 | 4305318 | QV3-DT0043-211299-044-d03 cDNA | -1 | AGGAACCTAAAGAACTGCCAAGTGT AGATAAGCATTGAGTATGTTACCC |
| 5206 | db mining | NA | AI439601 | 4305465 | tc85d10.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2072947 3', mRNA sequence | -1 | GGTTGTCCAGTTTTCGGTTTTTAACG CCCCCATAGGGGATTTGGCCCCC |
| 5207 | Table 3A | Hs.192463 | AI439633 | 4305688 | 7q86c05.x1 cDNA, 3' end /clone=IMAGE:3705201 /clone_end=3' | -1 | GTTTTGAATGAGGAATGATTTTCTA AGCCTGACATCAGATGTCTGACA |
| 5208 | db mining | Hs.165732 | AI439643 | 4305758 | tc91e08.x1 cDNA, 3' end /clone=IMAGE:2073538 /clone_end=3' | -1 | GAAATCTCCCCCTTTTCCCCCTCTCCTT CCCTTCTGCTGACCTGTTCTCAG |
| 5209 | Table 3A | Hs.255490 | AI439645 | 4305772 | tc91e08.x1 cDNA, 3' end /clone=IMAGE:2073542 /clone_end=3' | -1 | CACAGAGGGAGTGTGCAGGGCCAGA TTTCATCCTGGGGCCACGCTGAAAT |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|---|----|--|
| 5210 | Table 3A | Hs.9614 | AI440234 | 4281195 | Nucleophosmin (probe bad, mutations, wrong clone used) (nucleolar phosphoprotein B23, numatrin) | -1 | TGATAGGACATAGTAGTACGGGTGGT CAGACATGAAATGGTGGGGAGCC |
| 5211 | Table 3A | Hs.309279 | AI440337 | 4282020 | tc88b03.x1 cDNA, 3' end /clone=IMAGE:2073197 /clone_end=3' | -1 | CAATACCTACCCCCAGTGGCAGCCG CCTGCTCCTCATGACCCAAGTAAGT |
| 5212 | Table 3A | Hs.89104 | AI440491 | 4300600 | 602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5' | -1 | TGTTTTAAACAACCTCTTCTCAACATTTT GTCCAGGTTATTCCTGTAAACCA |
| 5213 | Table 3A | Hs.59844 | AI440512 | 4300747 | tc83f09.x1 cDNA, 3' end /clone=IMAGE:2072777 /clone_end=3' | -1 | TAAGTGTCTAGGTTTGTGGGGAAGGTT ATTCTTGCCTTGTGTATTTTGCC |
| 5214 | Table 3A | Hs.327610 | AI452611 | 4286566 | tj27g07.x1 cDNA, 3' end /clone=IMAGE:2142780 /clone_end=3' | -1 | CAAACCCCTATCCCCATTCTCCTCC TATCCCTCAACCCGACATCATTA |
| 5215 | Table 3A | Hs.121973 | AI458739 | 4311318 | 602428025F1 cDNA, 5' end /clone=IMAGE:4547239 /clone_end=5' | -1 | CCTGCAACAGCTAAGGCCAAGCCAA ACTTACCGTGGACTCAAACACTTTG |
| 5216 | Table 3A | Hs.86437 | AI469584 | 4331674 | 602411368F1 cDNA, 5' end /clone=IMAGE:4540096 /clone_end=5' | -1 | TGAATTTGGAGTCCCTGGCACAATAA TCTACCTTCAAATCAGAGGTCCTT |
| 5217 | Table 3A | Hs.149095 | AI471866 | 4333956 | ti67d04.x1 cDNA, 3' end /clone=IMAGE:2137063 /clone_end=3' | -1 | TCCCACCCCTTTTCTACTGAATTTGT GGGGATCCTATAATAAAAGTGAAT |
| 5218 | Table 3A | Hs.303662 | AI472078 | 4334168 | tj85h03.x1 cDNA, 3' end /clone=IMAGE:2148341 /clone_end=3' | -1 | ACTACCAGAGCCCTAGGACTTCTGAG CACATTTAGAAAAATACCAGAGGCA |
| 5219 | db mining | Hs.170772 | AI472326 | 4334416 | tj87c09.x1 cDNA, 3' end /clone=IMAGE:2148496 /clone_end=3' | -1 | CATGTCAGAGTTCTTAACAGAAAGCA AAGGTTTCCAAACAGCACTTGCAAT |
| 5220 | Table 3A | Hs.78746 | AI474074 | 4327119 | cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds /cds=(0,2141) | -1 | ATGAAATCTCATGGGGCCAACTGCA CATCAGCTACTGCTACCTTCTTGC |
| 5221 | db mining | NA | AI475527 | 4328572 | tc85g07.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2072988 3', mRNA sequence | -1 | CCCTGTGGCAACTTGTGGGTACGGTT TAACTGGACCACGCTGAGCTCTCG |
| 5222 | db mining | Hs.292501 | AI475611 | 4328656 | 7f03g08.x1 cDNA, 3' end /clone=IMAGE:3293630 /clone_end=3' | -1 | AGAAATAGTGTTTCTCGGAAGCTCAG TTTGGAGCTGACTGCACACGTTGC |
| 5223 | Table 3A | Hs.300759 | AI475653 | 4328698 | ribosomal protein L36 (RPL36), mRNA /cds=(145,462) | -1 | GTTGCTGGCTGCCCTCCCCTGCACT CTCCCTGAAATAAAGAAGAGCTTGG |
| 5224 | db mining | Hs.300759 | AI475653 | 4328698 | ribosomal protein L36 (RPL36), mRNA /cds=(145,462) | -1 | GTTGCTGGCTGCCCTCCCCTGCACT CTCCCTGAAATAAAGAAGAGCTTGG |
| 5225 | Table 3A | NA | AI475666 | 4328711 | tc93c08.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2073710 3', mRNA sequence | -1 | ACGTGTCAGACACAATCCTGAGCCTT CTACAAGTGTTCCCTCTTACTCCT |
| 5226 | db mining | NA | AI475678 | 4328723 | tc93d10.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2073715 3' similar to gb:M92287 G1/S-SPECIFIC CYCLIN D3 (| -1 | AAGCCCTGTTTACCAGGTTTTTCTT AAGGCGAGAAGGTTTAGGGTGGTG |
| 5227 | Table 3A | Hs.105676 | AI475680 | 4328725 | tc93d12.x1 cDNA, 3' end /clone=IMAGE:2073719 /clone_end=3' | -1 | GAGAAAGCTCCCAGTCTGTCTTTCCC AACATCCCTTCAGTTTCAATAAGC |
| 5228 | db mining | Hs.170338 | AI475682 | 4328727 | tc93e03.x1 cDNA, 3' end /clone=IMAGE:2073724 /clone_end=3' | -1 | TTCAGGTGAGTGTGCCTGGAGGTGG AGAACTATGGTTTGTATAACTTGGC |
| 5229 | Table 3A | Hs.236030 | AI475694 | 4328739 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2 (SMARCC2), mRNA /cds=(22,3663) | -1 | AAGGTGCCATGTATTGAAAGTGTGCG TCAAAGAACATAATATCAGTGGA |
| 5230 | db mining | NA | AI475735 | 4328780 | tc86g02.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2073074 3', mRNA sequence | -1 | TGTAATTATTTCTGTATGTTCAAGAA GGTAAAGGAAAGGACAGCTATGGGA |
| 5231 | db mining | Hs.327640 | AI475806 | 4328851 | tc94g03.x1 cDNA, 3' end /clone=IMAGE:2073844 /clone_end=3' | -1 | ATTTATTTGGGGTGGTCCCCCCTTT GGGCCCCCCGGGTTTCCCTTTTTT |
| 5232 | db mining | Hs.170586 | AI475815 | 4328860 | tc94h02.x1 cDNA, 3' end /clone=IMAGE:2073843 /clone_end=3' | -1 | AACCATAAAAGGCCCGTTTGGTTAGT TTTCCTGTTTCTGTTTGGGCT |
| 5233 | Table 3A | Hs.105052 | AI475827 | 4328872 | adaptor protein with pleckstrin homology and src homology 2 domains (APS), mRNA /cds=(127,2025) | -1 | TTATGGGGTAACTCACTTTGGGCGGC ACGAAGAACTCCAGGCGGAAGCGT |
| 5234 | db mining | Hs.258864 | AI475833 | 4328878 | tc87b01.x1 cDNA, 3' end /clone=IMAGE:2073097 /clone_end=3' | -1 | TCTCTCCCCATCCCAAGTCATCCAGC CCTTTTCTACCTCAATAAACCC |
| 5235 | Table 3A | Hs.170587 | AI475884 | 4328929 | tc95c12.x1 cDNA, 3' end /clone=IMAGE:2073910 /clone_end=3' | -1 | CCCCCTGATGGACTTCAAATATGTCT CATCAACTACAGTATTAAATGCCA |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|--|
| 5236 | Table 3A | Hs.170588 | AI475905 | 4328950 | tc95f06.x1 cDNA, 3' end /clone=IMAGE:2073923 /clone_end=3' | -1 | CGAGAATGCCTAGGGAAACCAGCTA CGCTTACAAGCCAGCTACGCAGCCC |
| 5237 | db mining | Hs.170589 | AI475909 | 4328954 | tc95f10.x1 cDNA, 3' end /clone=IMAGE:2073931 /clone_end=3' | -1 | GGAAACATTGGCCCTGGGGGTGTCCC CCAAAAGGGGGCCGTTTTTAAAGGG |
| 5238 | db mining | NA | AI475926 | 4328971 | tc95h10.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2073955 3' similar to gb:M59849 FIBRILLARIN (HUMAN);, mRN | -1 | TGGGTTGACATTGTTTCGCACGGGGT GTTTCTTATATTAAGAACTCACT |
| 5239 | Table 3A | NA | AI478556 | 4371782 | tm53e03.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2161852 3', mRNA sequence | -1 | CTTCCACAAAAATAATCGATAACCTTG GGGGATTGTTTTATGGCTTGACA |
| 5240 | db mining | NA | AI479016 | 4372184 | tm29h05.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2158041 3' similar to gb:X58141_rna1 ERYTHROCYTE ADDUCIN | -1 | CCGCCTTGGGGAGACAGGTCTTGAT TGCTTTTTCCCACTGAACATTGTT |
| 5241 | Table 3A | Hs.170784 | AI479022 | 4372190 | tm30a05.x1 cDNA, 3' end /clone=IMAGE:2158064 /clone_end=3' | -1 | TCCCAGACTTTCAGGAAAGTAACTGT AGCACTGTTAATATCACAACAACA |
| 5242 | db mining | Hs.187200 | AI479029 | 4372197 | tm30b06.x1 cDNA, 3' end /clone=IMAGE:2158067 /clone_end=3' | -1 | TTTTAGCTGGGAGTGGGGGGACTAT GGGAATAACTTTCCTTCATTTAAT |
| 5243 | Table 3A | Hs.337139 | AI479075 | 4372243 | tm30h01.x1 cDNA, 3' end /clone=IMAGE:2158129 /clone_end=3' | -1 | ACATGTGTGTGTTTTCCATGAGGCAC TGCTTTTTATGCATTTCCCTCCCC |
| 5244 | db mining | NA | AI479094 | 4372262 | tm31b02.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2158155 3' similar to contains TAR1.t1 MER22 repetitive e | -1 | CTGTATTGGAAGTCAGCAGGGCTCAG CAGGATTGACCAGCAGTTACCTC |
| 5245 | db mining | Hs.185498 | AI479659 | 4372827 | tm32h04.x1 cDNA, 3' end /clone=IMAGE:2158327 /clone_end=3' | -1 | TGGTTTATAGATGCACCTTCTTTCATA GGCAGTCCCTGGCACTTCTTTC |
| 5246 | Table 3A | Hs.170909 | AI492034 | 4393037 | tg06f12.x1 cDNA, 3' end /clone=IMAGE:2108015 /clone_end=3' | -1 | AGGAGCTGGTATTATTGGAGGGTATT ATAGATCCAGTGATTGTGACTGT |
| 5247 | db mining | NA | AI492041 | 4393044 | tg06g08.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2108030 3' similar to gb:L23320 ACTIVATOR 1 140 KD SUBUNI | -1 | GCAGTAGTGCTAAGGCCTCTTTTGTA GGCTTTAGATTTTGTCGTTATGGC |
| 5248 | Table 3A | Hs.119923 | AI492066 | 4393069 | tg12b03.x1 cDNA, 3' end /clone=IMAGE:2108525 /clone_end=3' | -1 | GCTTGTCAGAACAGATATTTCCTCA CCCTGCCTAGTAGATGTGTTTCAG |
| 5249 | db mining | Hs.327698 | AI492127 | 4393130 | tg07d04.x1 cDNA, 3' end /clone=IMAGE:2108071 /clone_end=3' | -1 | CCCCCGTTTTAGGTTAGGGCCTTGG GCAGGGGTTGCCCCCTGTTACCCC |
| 5250 | db mining | Hs.170912 | AI492164 | 4393167 | tg12h01.x1 cDNA, 3' end /clone=IMAGE:2108593 /clone_end=3' | -1 | TTGGTTTTATTATCCAAAAGTGGCC TTCTCATAGGCTTTACACCCGGA |
| 5251 | Table 3A | Hs.341634 | AI492181 | 4393184 | wt85e01.x1 cDNA, 3' end /clone=IMAGE:2514264 /clone_end=3' | -1 | GGCAGGCTCTAGCCACCCTGTGCGGT TCCCAATAAGCCATTTATTGAATAA |
| 5252 | Table 3A | Hs.276903 | AI492640 | 4393643 | qz18a06.x1 cDNA, 3' end /clone=IMAGE:2021842 /clone_end=3' | -1 | TTTTTGACCAGTCTACATTTCTGATCT GTGGGATCTGCATTTGTGAATTC |
| 5253 | db mining | Hs.170933 | AI492648 | 4393651 | qz18b06.x1 cDNA, 3' end /clone=IMAGE:2021843 /clone_end=3' | -1 | TCTGGACAATGTTGATGCTAACCTTG ATGATATCCATCCCTATTACTGGG |
| 5254 | db mining | NA | AI492653 | 4393656 | qz18c02.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2021858 3' similar to contains Alu repetitive element; m | -1 | AGGACATGAAGGTCTGAAAAAGAAAC AGGAAAATACAGACATCCCCGCTT |
| 5255 | Table 3A | Hs.170331 | AI492865 | 4393868 | th78a05.x1 cDNA, 3' end /clone=IMAGE:2124752 /clone_end=3' | -1 | AAGTCAAGGAACCCCTCTCGGGTCTCT GAGATCCAGGCCAACAGTAAACAG |
| 5256 | db mining | Hs.327702 | AI493426 | 4394429 | tg91a07.x1 cDNA, 3' end /clone=IMAGE:2116116 /clone_end=3' | -1 | AGGGGGCTTTAAAAATTTAAAAATTGC CTTTTGTTTTAAAAAGGCCCATGT |
| 5257 | Table 3A | Hs.276907 | AI493726 | 4394729 | qz12f08.x1 cDNA, 3' end /clone=IMAGE:2021319 /clone_end=3' | -1 | CCCCCTCCACCCAAAGAAAAAGAAA TGGTAACCTACCTGGACAAAACATT |
| 5258 | db mining | Hs.342652 | AI493740 | 4394743 | yi60c05.r1 cDNA, 5' end /clone=IMAGE:143624 /clone_end=5' | -1 | CCCTTGCTCTTATTGTTCTTGCTGG TGTGGTATGTTCCCGGCTGAAAAA |
| 5259 | db mining | NA | AI494343 | 4395346 | qz14a10.x1 cDNA, 3' end /clone=IMAGE:2021466 /clone_end=3' | -1 | TTCCCCTTTTTTCCGCCCTTTTTTAAAA AGCCCCCTTTTTTAAATGGGGCGC |
| 5260 | db mining | Hs.283456 | AI494542 | 4395545 | 7f12b08.x1 cDNA, 3' end /clone=IMAGE:3294423 /clone_end=3' | -1 | AAGGACAGCTTGCTTGCTGATGAACA CTTCCACAGTCTTTTGAGCTAAGT |
| 5261 | Table 3A | Hs.171009 | AI494612 | 4395615 | RST42450 cDNA | -1 | ACATGAGAATTAACCATGTCCAGTAG TTAAGTTCATTTTCTACAGTGTGC |
| 5262 | Table 3A | Hs.342008 | AI498316 | 4390298 | UI-H-BI1-aeq-b-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2720186 /clone_end=3' | -1 | GCCAGAATGGTACAGAGTGGAGGGT GTTCTGCTAATGACTTCAGAGAAGT |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|---|
| 5263 | Table 3A | Hs.169541 | AI523598 | 4437733 | th08g11.x1 cDNA, 3' end /clone=IMAGE:2117732 /clone_end=3' | -1 | GCACAACCTTCTGGGAATCTAGTGGCT GTATGTTAAAGCATCGGTAAAGA |
| 5264 | db mining | Hs.171098 | AI523617 | 4437752 | tg95b03.x1 cDNA, 3' end /clone=IMAGE:2116493 /clone_end=3' | -1 | AAAAAGGCCCTTGTGTTGTTGTTT TGGCCCGTTGGGAAAAATGCCTGT |
| 5265 | db mining | Hs.264120 | AI523641 | 4437776 | 601436078F1 cDNA, 5' end /clone=IMAGE:3921187 /clone_end=5' | -1 | TTTAGGAGCTGACCATACATGATGAG TGATACAGCCTGTACTTTGCTCAT |
| 5266 | Table 3A | Hs.309484 | AI523766 | 4437901 | tg94f07.x1 cDNA, 3' end /clone=IMAGE:2116453 /clone_end=3' | -1 | GGTTTCCACGGAACGGGAGGCTGCT GAAGAGTCAAAGCCTGGGCAGACTC |
| 5267 | db mining | NA | AI523780 | 4437915 | tg94h09.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2116481 3' similar to gb:M15059 LOW AFFINITY IMMUNOGLOBUL | -1 | CAGGTGATGAGTATTCCAAGCTCAGG TGGTGAGTCCTCCTCACCGGGATG |
| 5268 | db mining | Hs.171108 | AI523790 | 4437925 | tg96b01.x1 cDNA, 3' end /clone=IMAGE:2116585 /clone_end=3' | -1 | AAAGGGAACTGGCTCTGGCACCAC CTACTGGAGACCAAACCTTACCACAA |
| 5269 | Table 3A | Hs.194054 | AI523854 | 4437989 | HA0669 cDNA | -1 | GACAAAATAGTTACCTATGCTTTCCTT CTGGCACCCCGAATGTACGCAGG |
| 5270 | Table 3A | Hs.228926 | AI523873 | 4438008 | tg97c12.x1 cDNA, 3' end /clone=IMAGE:2116726 /clone_end=3' | -1 | ATCTGACCTGAGGGAGATCACAATG CCTTCTGTATTGGGTGGTAATGAT |
| 5271 | db mining | Hs.207993 | AI523884 | 4438019 | tg97e12.x1 cDNA, 3' end /clone=IMAGE:2116750 /clone_end=3' | -1 | TCCGTTGTAACACATCTAATGTGAAC GCATTATAAACATGGACCTGTACT |
| 5272 | db mining | NA | AI523904 | 4438039 | tg97h03.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2116757 3' similar to SW:MKK2_HUMAN P49137 MAP KINASE-ACT | -1 | ACATAACTATTCCGTTGATGAATAGC ATCAGGACTTAAATGGTGACCTTGT |
| 5273 | db mining | Hs.337129 | AI523973 | 4438108 | tg98h03.x1 cDNA, 3' end /clone=IMAGE:2116853 /clone_end=3' | -1 | AACGGGTTTGGGTTTGGGGGGTTT GTTCTTTTATTGAATCCATTTAAGT |
| 5274 | db mining | Hs.340482 | AI523988 | 4438123 | tg99b05.x1 cDNA, 3' end /clone=IMAGE:2116881 /clone_end=3' | -1 | TATAGGAGATGGGATACTATTCCCG CTGCTATTGATAAGGTGCGAGGCG |
| 5275 | db mining | Hs.283457 | AI523989 | 4438124 | 7f27b07.x1 cDNA, 3' end /clone=IMAGE:3295861 /clone_end=3' | -1 | CAGAACGTCCTCAAGGACACACTCCT CCCTCGGGCCTCACTCTGGAGCAC |
| 5276 | db mining | Hs.229405 | AI524004 | 4438139 | tg99d01.x1 cDNA, 3' end /clone=IMAGE:2116897 /clone_end=3' | -1 | CTGGACATGTTGTTTCCATGTTTCAGT CCCTTCCCGGTTTGGGTGTTTT |
| 5277 | db mining | Hs.283458 | AI524006 | 4438141 | tg99d05.x1 cDNA, 3' end /clone=IMAGE:2116905 /clone_end=3' | -1 | AAAGTAGCCATCCTGAGTCTCCAGGG TGATGAGCGGACTTGGGTGTGGAT |
| 5278 | db mining | Hs.327719 | AI524013 | 4438148 | tg99e03.x1 cDNA, 3' end /clone=IMAGE:2116924 /clone_end=3' | -1 | CCTTCCATCTCATCGGTGGCCTCTCA CTGTGGCTCACTGTTTAACACATG |
| 5279 | Table 3A | Hs.252359 | AI524022 | 4438157 | tg99f02.x1 cDNA, 3' end /clone=IMAGE:2116923 /clone_end=3' | -1 | TGTTCAAGGTCACATAGTTTAGGTAA GAAGCTCAAACCTGAGTTTTAGGT |
| 5280 | Table 3A | Hs.192524 | AI524039 | 4438174 | tg99h02.x1 cDNA, 3' end /clone=IMAGE:2116947 /clone_end=3' | -1 | CACCTGATTCCCCCTCTGCCACAG GACTCTGCTGTTGTTTTCATTCTG |
| 5281 | db mining | Hs.283459 | AI524046 | 4438181 | th01a01.x1 cDNA, 3' end /clone=IMAGE:2116968 /clone_end=3' | -1 | TCTCGTGAGGTGATGTGTTGCTGCA GACTTAAGCTATCTGCCTTGAAGAT |
| 5282 | db mining | Hs.171119 | AI524139 | 4438274 | th09f04.x1 cDNA, 3' end /clone=IMAGE:2117791 /clone_end=3' | -1 | AACAAGCCTGGAATAATGCCCCAAA GATTGAGTGGAATCGCCCTTTT |
| 5283 | db mining | NA | AI524156 | 4438291 | th09h01.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2117809 3' similar to contains Alu repetitive element;con | -1 | CAGGACCAGATGGCCAGGAGGAAG TGGATGCTTTCTTGGTAGGGAATGG |
| 5284 | Table 3A | Hs.171122 | AI524202 | 4438337 | th10d11.x1 cDNA, 3' end /clone=IMAGE:2117877 /clone_end=3' | -1 | CCTCCTGCTAGAAGACAGATTTCTTC CTTGGCTGACAGGCTGAATTAAGC |
| 5285 | db mining | Hs.171123 | AI524214 | 4438349 | th11b04.x1 cDNA, 3' end /clone=IMAGE:2117935 /clone_end=3' | -1 | AATTTCCAAAAACAAAACAAACAAG CAGGTTTCATGGAGCCCGAGTCCA |
| 5286 | db mining | Hs.171124 | AI524233 | 4438368 | th11d04.x1 cDNA, 3' end /clone=IMAGE:2117959 /clone_end=3' | -1 | CCTTTATGCAAGTTGTAAGGGGTTGA CCAGTAAAGAGGAAGTTTGTCC |
| 5287 | Table 3A | Hs.174193 | AI524263 | 4438398 | th11g07.x1 cDNA, 3' end /clone=IMAGE:2118012 /clone_end=3' | -1 | AGTATTAGCTACAAACAAGCCTTGT TCCTCTGGCTGTCAGGCACTGCT |
| 5288 | db mining | Hs.230874 | AI524266 | 4438401 | th11g12.x1 cDNA, 3' end /clone=IMAGE:2118022 /clone_end=3' | -1 | AAGCCCCAGTAAGGTGTTTCAGGACT GGTAAACGACTGTCTCAAGTAAGG |
| 5289 | Table 3A | Hs.12315 | AI524624 | 4438759 | hypothetical protein FLJ11608 (FLJ11608), mRNA /cds=(561,1184) | -1 | TGGTTCAGGTAGTAAATGCTTTTGGT CACATCAGAACTCTAGATCTGGGG |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|---|
| 5290 | db mining | Hs.327722 | AI524626 | 4438761 | td11c03.x1 cDNA, 3' end /clone=IMAGE:2075332 /clone_end=3' | -1 | GCCTGGGCTGTTTTGCTATATGTAA ATAAAGCCCTTGGGTCTTTATTTT |
| 5291 | db mining | Hs.231512 | AI524700 | 4438835 | th12c05.x1 cDNA, 3' end /clone=IMAGE:2118056 /clone_end=3' | -1 | GGAGGTTAGGAAGCCCTTTTAAAGTA CAAACCCCGGCATGGGGAATTTT |
| 5292 | db mining | Hs.171140 | AI524720 | 4438855 | th12e10.x1 cDNA, 3' end /clone=IMAGE:2118090 /clone_end=3' | -1 | AACGGGAGTGATCGGGAAGTGAACA GTTTCATCATCTGCTGCTGCTATTTC |
| 5293 | db mining | Hs.292520 | AI524724 | 4438859 | th12f03.x1 cDNA, 3' end /clone=IMAGE:2118077 /clone_end=3' | -1 | CTGGTATGTTGCTTTGTAGGGGAAAA ACTAATTTTGTGGGTGAGGGACA |
| 5294 | db mining | Hs.283462 | AI538419 | 4452554 | td06a02.x1 cDNA, 3' end /clone=IMAGE:2074826 /clone_end=3' | -1 | CCGGACAAGCCATTGTGTTCTAGT TTGCAATTACTCCACGCAAGTGG |
| 5295 | db mining | Hs.231292 | AI538420 | 4452555 | td06a03.x1 cDNA, 3' end /clone=IMAGE:2074828 /clone_end=3' | -1 | TTTGGGCATCAACTTCAACAACACT ACCAGGACGCCTGAGGGTGCTTTT |
| 5296 | db mining | Hs.171216 | AI538445 | 4452580 | td06d02.x1 cDNA, 3' end /clone=IMAGE:2074851 /clone_end=3' | -1 | TGAAGAAAGTACCTGTAAATGTAGA GTAATTGCGAAGCTGTGAGGAATA |
| 5297 | Table 3A | Hs.203784 | AI538474 | 4452609 | td06h08.x1 cDNA, 3' end /clone=IMAGE:2074911 /clone_end=3' | -1 | TCCTAGACCCTGCATTGTGAAATGGG GCTTGAAATTTAGTTCTGAAATTT |
| 5298 | Table 3A | Hs.306024 | AI538546 | 4452681 | FK506-binding protein 3 (25kD) (FKBP3), mRNA /cds=(23,697) | -1 | CTAAAGCAGTGTCTGACCTGGATTTC CTGCCAATTTGTAAGCTTTCATGA |
| 5299 | Table 3A | Hs.192534 | AI538554 | 4452689 | EST384032 cDNA | -1 | GGAGCTGAGCAGGGATGCAAAACCA TCCAGTCTGTAAGATTACAGAGAC |
| 5300 | db mining | Hs.171260 | AI540044 | 4457417 | td08e06.x1 cDNA, 3' end /clone=IMAGE:2075074 /clone_end=3' | -1 | AAACGGTGTGTTGAGCTGCTTTGGGAA AACCCATGTTGCAGATTTTCAGGT |
| 5301 | db mining | Hs.283463 | AI540109 | 4457482 | 7f10e03.x1 cDNA, 3' end /clone=IMAGE:3294268 /clone_end=3' | -1 | CAGAGCTGTGTTTCTCAACAAGTGT GCGAGCGGTGCTGTGCGCCATGAG |
| 5302 | Table 3A | Hs.171261 | AI540125 | 4457498 | MR1-BN0212-280600-001-c06 cDNA | -1 | AAATCGCTTCTGTATTGTTAATAGCAA TATATGACCTCTGCTGTCTCTCT |
| 5303 | db mining | NA | AI540130 | 4457503 | td09g11.x1 NCL_CGAP_CLL1 cDNA clone IMAGE:2075204 3' similar to gb:X64707 BREAST BASIC CONSERVED PR | -1 | GAAAGGATAATTTGCAACCCCTTGCA AGTTTCGGTATGGGCCGTGCCAAC |
| 5304 | Table 3A | Hs.171264 | AI540161 | 4457534 | td10c10.x1 cDNA, 3' end /clone=IMAGE:2075250 /clone_end=3' | -1 | CCCTCTTGAAGTGCCTGCTTAAGAA ATGTTGGTTCATGGAGACATATT |
| 5305 | Table 3A | Hs.222186 | AI540165 | 4457538 | td10d05.x1 cDNA, 3' end /clone=IMAGE:2075241 /clone_end=3' | -1 | TCTGCCTTATTTGGCTTGAAGAGAA ACCGATAAAGTCTCCGTGCTAGT |
| 5306 | Table 3A | Hs.170935 | AI540204 | 4457577 | MYE6493a cDNA | -1 | AAACAGCAGAAAGTAATTTCTGGTG AACTGATGAGAATTCCTATTGCA |
| 5307 | db mining | Hs.327797 | AI540784 | 4458157 | tc87e08.x1 cDNA, 3' end /clone=IMAGE:2073158 /clone_end=3' | -1 | AGGTTGTTTGGAAAAATTTTGTGTT TGTCCTAAGGGGTCTGCCACC |
| 5308 | db mining | Hs.327798 | AI540789 | 4458162 | tc87f03.x1 cDNA, 3' end /clone=IMAGE:2073149 /clone_end=3' | -1 | CCTCCGGAACGTTTTTAAAAAGGAAA AAGCCCGGTTTTCCCTTGGGAAAAA |
| 5309 | Table 3A | Hs.170577 | AI540813 | 4458186 | 602574255F1 cDNA, 5' end /clone=IMAGE:4702644 /clone_end=5' | -1 | CAGACCTGTGGGCTGATCCAGACT GAGAGTTGAAGTTTGTGTGCATCA |
| 5310 | Table 3A | Hs.173182 | AI554733 | 4487096 | tn27f08.x1 cDNA, 3' end /clone=IMAGE:2168871 /clone_end=3' | -1 | ACCAAGTTTGAATTTGTCAAATCCCA AGTCAATCCAGGATGTTCAATTTCT |
| 5311 | Table 3A | Hs.282963 | AI557431 | 4489794 | 602583968F1 cDNA, 5' end /clone=IMAGE:4711721 /clone_end=5' | -1 | AGTGATCTGCCTTTCAGCAACTGTCT TATTTTGGTTCTTTGAAACTGTGA |
| 5312 | db mining | Hs.104679 | AI559444 | 4509649 | Homo sapiens, clone MGC:18216 IMAGE:4156235, mRNA, complete cds /cds=(2206,2373) | -1 | TTTGAATGGCTGAAGCTAAGGCAACG TTAGTTTCTCCTTACTCTGCTTTT |
| 5313 | db mining | Hs.118392 | AI560561 | 4510902 | RST42466 cDNA | -1 | ACCTTTGTGATTCTGTCTAGTGAAAT GGGACATTTTAAATAGTGCCAGA |
| 5314 | Table 3A | NA | AI560651 | 4510992 | tq60f01.x1 NCL_CGAP_Ut1 cDNA clone IMAGE:2213209 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A | -1 | GAACTTGCCCTAAACTGGGTTAAAT GGACCCTGTTGAGTTTCTGGACA |
| 5315 | db mining | Hs.327874 | AI568374 | 4531748 | th13e03.x1 cDNA, 3' end /clone=IMAGE:2118172 /clone_end=3' | -1 | TAAATTGGGCAAAGTTTTTATGGAAT TTCCGGGGCAAGGTTTTGGGGGC |
| 5316 | Table 3A | Hs.340517 | AI568459 | 4531833 | tn39e07.x1 cDNA, 3' end /clone=IMAGE:2170020 /clone_end=3' | -1 | AAATCTCATTGCAAGTTCTCCCATTA AGCAAGGGAGTAGTTTACTAGGA |
| 5317 | Table 3A | Hs.143951 | AI568622 | 4531996 | tn41e10.x1 cDNA, 3' end /clone=IMAGE:2170218 /clone_end=3' | -1 | AAGAAAGGCCCATACAGATGGCAAA ATAGAGGATTGGTGAGGGATATGC |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|---|----|---|
| 5318 | db mining | Hs.75969 | AI568695 | 4532069 | proline-rich protein with nuclear targeting signal (B4-2), mRNA /cds=(113,1096) | -1 | AAAACCATTCCAGCTTAATGCCTTTAA TTTTAATGCCAACAAATTGGGG |
| 5319 | Table 3A | NA | AI568725 | 4532099 | th15a01.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2118312 3', mRNA sequence | -1 | TGCAACCTTCTTAAATGTGGGCTAC TGGAGATCATGCCACTGCACTCCA |
| 5320 | Table 3A | Hs.159014 | AI568751 | 4532125 | th15d09.x1 cDNA, 3' end /clone=IMAGE:2118353 /clone_end=3' | -1 | AGCTCAGATGGGTCCCCAAAGAGG CATAGGAAAGCGCGACCTCACTGCC |
| 5321 | db mining | Hs.174242 | AI568753 | 4532127 | th15e04.x1 cDNA, 3' end /clone=IMAGE:2118366 /clone_end=3' | -1 | CAAATAAAAGGCTGGGGCCAAAGG TGGGCACCAAAAGTCTCTATGTG |
| 5322 | Table 3A | NA | AI568755 | 4532129 | th15f03.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2118365 3', mRNA sequence | -1 | TGCAGCTCCCATTTCTGAGCGTCTA CCAGGTACTAGGAGAACTCTTACA |
| 5323 | db mining | Hs.327876 | AI568771 | 4532145 | th15h04.x1 cDNA, 3' end /clone=IMAGE:2118391 /clone_end=3' | -1 | ATTATCCTTTTCCCCAGGAAGCCCTC GGCCCCCAAAAGGAAACAGTTT |
| 5324 | db mining | Hs.179070 | AI568773 | 4532147 | th15h09.x1 cDNA, 3' end /clone=IMAGE:2118401 /clone_end=3' | -1 | CATGAGCCCAGGGGTTTCATGACAAA CATTACTAGCATGTTCAACTGCCC |
| 5325 | Table 3A | NA | AI569898 | 4533272 | tr57c12.x1 NCI_CGAP_Pan1 cDNA clone IMAGE:2222422 3' similar to gb:D16234 PROBABLE PROTEIN DISULFID | -1 | GCCCCGTTTATGAAAAACAGGAC CAGTTTATGTTTGGGGTTTGGGAA |
| 5326 | Table 3A | Hs.92448 | AI570295 | 4533669 | EST390664 cDNA | -1 | GCTTGGTACTGTCATAGTGATTACAA ATTTTCATGGAATCGGAAGAGCAAC |
| 5327 | Table 3A | Hs.5637 | AI570531 | 4533905 | 602998983F1 cDNA, 5' end /clone=IMAGE:5141013 /clone_end=5' | -1 | TTTTCTCCCCCTCTCTCCCCCTCCAC GAAGTGCATACCACTGTAACCTTGG |
| 5328 | Table 3A | Hs.14623 | AI571519 | 4534893 | interferon, gamma-inducible protein 30 (IFI30), mRNA /cds=(40,951) | -1 | AAGCCCAGATACACAAAATCCACCC CATGATCAAGAATCCTGCTCCACT |
| 5329 | db mining | Hs.8882 | AI572757 | 4536131 | tu43c07.x1 cDNA, 3' end /clone=IMAGE:2253804 /clone_end=3' | -1 | CATGTGTTGACTCTGTAATGGATTAT GTAGCCCACTTCAGTCTGCAAAT |
| 5330 | Table 3A | Hs.230430 | AI579979 | 4564355 | tq45a01.x1 cDNA, 3' end /clone=IMAGE:2211720 /clone_end=3' | -1 | AGGGGTGTCCTCTTTTCCCTTCATGT AAAATCTAACTGGGGCTACCACT |
| 5331 | Table 3A | NA | AI581199 | 4565575 | ti94h10.x1 NCI_CGAP_Co14 cDNA clone IMAGE:2154787 3' similar to SW:ATP6_HUMAN P00846 ATP SYNTHASE A | -1 | TCTACTGACTATCCTAGAAATCGCTG TCGCCTTAATCCAAGCTACGTTT |
| 5332 | Table 3A | Hs.327922 | AI581383 | 4565759 | to71c02.x1 cDNA, 3' end /clone=IMAGE:2183714 /clone_end=3' | -1 | TGAAGAACTGCCCTTTCTGTGATGT TTTTGAATACTACCAACAGCCAA |
| 5333 | Table 3A | Hs.229918 | AI581732 | 4567629 | ar74f03.x1 cDNA, 3' end /clone=IMAGE:2128349 /clone_end=3' | -1 | CTTCCTAGCCCTAAGTTTGGCCTTTG GGTGGCTCCAAAAGGATTAGGTT |
| 5334 | Table 3A | Hs.292553 | AI582954 | 4568851 | tr98e07.x1 cDNA, 3' end /clone=IMAGE:2227140 /clone_end=3' | -1 | TCCCCCTCGTTTTGTAGGGTTTGATC ATAATAAAACAATGGGGTGGGGCC |
| 5335 | Table 3A | Hs.340925 | AI590337 | 4599385 | wh96a06.x1 cDNA, 3' end /clone=IMAGE:2388562 /clone_end=3' | -1 | TGTAAAGTGAGGTTTTCTGAACCC TAGCAGAAGGACTTTTAATGTTT |
| 5336 | Table 3A | Hs.101617 | AI597917 | 4606976 | 601513709F1 cDNA, 5' end /clone=IMAGE:3914786 /clone_end=5' | -1 | AGTTCCACTGCTGTCTCTTACCTT GATTAATGCTATGCATGTACTT |
| 5337 | db mining | Hs.13646 | AI611245 | 4620412 | 601287348F1 cDNA, 5' end /clone=IMAGE:3621754 /clone_end=5' | -1 | AGTTCTGTTGTGTAATCTGGTGCTGG TTCCCTGGGCATATGTATTCTGTG |
| 5338 | Table 3A | NA | AI619574 | 4628700 | ty50c09.x1 NCI_CGAP_Ut2 cDNA clone IMAGE:2282512 3' similar to gb:M23613 NUCLEOLAR PHOSPHOPROTEIN B | -1 | CCCCCTTGCTTGGTTTTAAGTAGGTA TGGAATGTTATTATAGGCCATAGT |
| 5339 | db mining | Hs.340564 | AI625119 | 4650050 | ts47b12.x1 cDNA, 3' end /clone=IMAGE:2231711 /clone_end=3' | -1 | TCAGTGTAACATAATTAGGCCGTGA GTTTTTGCTCTTACTCCAGGTTT |
| 5340 | Table 3A | Hs.188365 | AI625368 | 4650299 | ts37c10.x1 cDNA, 3' end /clone=IMAGE:2230770 /clone_end=3' | -1 | TGTAAACTTGTTTTAACAACCTTTTTT AACATTTTGGCCGGGGTATTCCC |
| 5341 | Table 3A | Hs.278554 | AI627495 | 4664295 | chromobox homolog 3 (Drosophila HP1 gamma) (CBX3), mRNA /cds=(111,662) | -1 | TGCTGAAAGTGTCCTCAAGGGGTA CTAGTTTTTAAGCTCCCACTCCCC |
| 5342 | Table 3A | Hs.171262 | AI628893 | 4665693 | ty95h02.x1 cDNA, 3' end /clone=IMAGE:2286867 /clone_end=3' | -1 | TTCCCAAGTTGCCACAGACCGTTTATA TGAAGAAATGCTAAAGAAGTCCCC |
| 5343 | Table 3A | NA | AI628930 | 4665730 | ty40d03.x1 NCI_CGAP_Ut2 cDNA clone IMAGE:2281541 3' similar to SW:ATP6_HUMAN P00846 ATP SYNTHASE A | -1 | TCTACTGACTATCCTAGAAATCGCTG TCGCCTTAATCCAAGCTACGTTT |
| 5344 | db mining | Hs.264154 | AI630176 | 4681506 | ad06a03.r1 cDNA /clone=ad06a03-(random) | -1 | AGTTCTAAAGCCGGGAATTCCTAAGG ATATACTAAATGAGATTATGTGTGG |

Table 8

| | | | | | | | |
|------|------------|-----------|----------|---------|---|----|--|
| 5345 | Table 3A | Hs.340604 | Al631850 | 4683180 | wa36h07.x1 cDNA, 3' end /clone=IMAGE:2300221 /clone_end=3' | -1 | GCCTGGGGGAGGAGAAGTCCCTTCC CATTCCAGCTCGATCAATCTTGCTG |
| 5346 | Table 3A | Hs.256729 | Al634652 | 4685982 | wx27c05.x1 cDNA, 3' end /clone=IMAGE:2544872 /clone_end=3' | -1 | GGAGTAGAGAGAGTCTTGCTACATGC GGGAAGTGAATTACATCACTGCG |
| 5347 | Table 3A | Hs.319825 | Al634972 | 4686302 | 602021477F1 cDNA, 5' end /clone=IMAGE:4156915 /clone_end=5' | -1 | AAGAAGTTTCATTGATATCCACTGGT CACATCATACCTGTCTATAGGGCA |
| 5348 | Table 3A | Hs.176920 | Al638800 | 4691034 | tt32e01.x1 cDNA, 3' end /clone=IMAGE:2242488 /clone_end=3' | -1 | TGCTTCAAGCACAGGATTTATGGAAT AGTTGGCAAATTAACAACATGCT |
| 5349 | Table 3A | Hs.197028 | Al650871 | 4734850 | 602643870F1 cDNA, 5' end /clone=IMAGE:4774817 /clone_end=5' | -1 | CGGCAGCCTTATGGAATGAGTTTCTT GTGATGAATGTTGTCCCAAAGCT |
| 5350 | Table 3A | Hs.4283 | Al651212 | 4735191 | 602621616F1 cDNA, 5' end /clone=IMAGE:4755315 /clone_end=5' | -1 | ACAGTTACTTTGGAGCTGCTAGACTG GTTTTCTGTGTTGGTAAATTGCCT |
| 5351 | db mining | Hs.203064 | Al651922 | 4735901 | hy16b12.x1 cDNA, 3' end /clone=IMAGE:3197471 /clone_end=3' | -1 | TGTGAAGAATCCCTACCATTAAATACC CTGGGTGGGATAAATAAAATGGG |
| 5352 | Table 3A | Hs.195378 | Al653766 | 4737745 | ty01b06.x1 cDNA, 3' end /clone=IMAGE:2277779 /clone_end=3' | -1 | CCCAAAATTTGTTTAAAGTCCGACTT CCAAAAGGGGCCAATAAAAGGG |
| 5353 | db mining | Hs.111941 | Al660405 | 4763975 | qd92a04.x1 cDNA, 3' end /clone=IMAGE:1736910 /clone_end=3' | -1 | CACCGCCTCTGCCTCCGCCTCTTCCA CTGGAGAGCCCGAGGTCAAAGGTC |
| 5354 | Table 3A | Hs.200442 | Al669591 | 4834365 | tw34b09.x1 cDNA, 3' end /clone=IMAGE:2261561 /clone_end=3' | -1 | CCCTCACCTAGCAGTACTACCACAAT AATGCTATCATGGTGCCAGGGAAT |
| 5355 | Table 3A | Hs.101150 | Al672433 | 4852164 | Homo sapiens, clone IMAGE:4054156, mRNA, partial cds /cds=(0,526) | -1 | TCTCCTTCCCCATTGGGCCGCCTTTA TCAATTGCCTGTTTTGTTTTGTTT |
| 5356 | Table 3A | Hs.341178 | Al678004 | 4888186 | xa30a04.x1 cDNA, 3' end /clone=IMAGE:2568270 /clone_end=3' | -1 | TTTTTATCTTTCTTGGTGGGGGTGTG GTGGTGGTGAAGAGGACCTAAAAA |
| 5357 | Table 3A | Hs.324507 | Al678099 | 4888281 | hypothetical protein FLJ20986 (FLJ20986), mRNA /cds=(182,2056) | -1 | CGCCAGAGGTCAGAACATGTCTATTT TGAATTGGATCGTTACAAATGAGC |
| 5358 | Table 3A | Hs.178784 | Al681868 | 4892050 | 602587746F1 cDNA, 5' end /clone=IMAGE:4716442 /clone_end=5' | -1 | GCAGGCACTGACATTTTTGAGCAAAG ACGTGATGTTATGAGATAAATATC |
| 5359 | Table 3A | Hs.90744 | Al684022 | 4895316 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA /cds=(0,1268) | -1 | TTCTGACACGATTACACAACGAGGCT TTAATGCCATTTGGGTAGGTGAGC |
| 5360 | db mining | Hs.328323 | Al684369 | 4895663 | tc96e09.x1 cDNA, 3' end /clone=IMAGE:2074024 /clone_end=3' | -1 | TTTTAAAGGGGAGGGGCCGGGGTTT GGTCCCCGGTCCCAAAGGTAAAAAGTT |
| 5361 | Table 3A | Hs.58774 | Al684437 | 4895731 | Homo sapiens, Similar to zinc finger protein 175, clone MGC:12651 IMAGE:4301632, mRNA, complete cds /cds=(367,522) | -1 | GAGTGAGAAGAGGCTTTTAAAGGACCA TGTGAAGAGGCTTTTAAACACTTT |
| 5362 | db mining | Hs.182817 | Al684847 | 4896141 | 602290551F1 cDNA, 5' end /clone=IMAGE:4385293 /clone_end=5' | -1 | GGGTTGGGATAAAGCTTAGATGTT TGCCACTTGTCCAGTGAAATTAC |
| 5363 | Table 3A | NA | Al688560 | 4899854 | wd39f08.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2330535 3', mRNA sequence | -1 | ACTGAAAAGTTGAAAGACTTTTGCAG TGAACATTTATATAACTCCCCGCT |
| 5364 | Table 3A | Hs.201789 | Al693179 | 4970519 | MR1-C10181-061100-001-a01 cDNA | -1 | ATTCATAGGTAGTGCCAGAGAGAGT ACAAGCTCTGACTCATATGGCAGT |
| 5365 | literature | Hs.202407 | Al697497 | 4985397 | we14b06.x1 cDNA, 3' end /clone=IMAGE:2341043 /clone_end=3' | -1 | ACATGTTACCTGGAGTAGCTGTGTCA ACAGATTAATATGGAATGCTACTA |
| 5366 | Table 3A | Hs.177708 | Al697756 | 4985656 | 602369210F1 cDNA, 5' end /clone=IMAGE:4477370 /clone_end=5' | -1 | TGGTTCTGTGCTACCATAGGGCTG GTGTACATTGGGCCATTAATAAAC |
| 5367 | Table 3A | Hs.206654 | Al700738 | 4988638 | EST368531 cDNA | -1 | ACAGATCCCTATTGCCAGACACATCA TTCTCTCCATCCAGAAAGCAAACA |
| 5368 | Table 3A | Hs.80887 | Al701165 | 4989065 | v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), mRNA /cds=(297,1835) | -1 | TCTGGGAAAGACATTTTTAAGCTGCT GACTTCACCTGCAAAATCTAACAG |
| 5369 | Table 3A | Hs.102793 | Al707589 | 4997365 | RST17769 cDNA | -1 | AGTCACGATAAACCTGGTCACCTGAA AATTGAAATTGAGCCACTTCCTTG |
| 5370 | Table 3A | Hs.309433 | Al707809 | 4997585 | as28g09.x1 cDNA, 3' end /clone=IMAGE:2318560 /clone_end=3' | -1 | AAACTGGCGGCCCAACAAACAGTG GGTTAAATGGTCCCTGGGTGACAT |
| 5371 | Table 3A | Hs.107369 | Al707896 | 4997672 | as34a10.x1 cDNA, 3' end /clone=IMAGE:2319066 /clone_end=3' | -1 | AGTGTTCCTCCACATCTAAAGAAAG CCCATTTTGAAACTGGATACTGCA |
| 5372 | Table 3A | Hs.176430 | Al708327 | 4998103 | at04c02.x1 cDNA, 3' end /clone=IMAGE:2354114 /clone_end=3' | -1 | CCCAGGTGGCCCTCTCCATCAGAT GTTATTGCTCTTCCCAATTTATTTA |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|---|----|---|
| 5373 | Table 3A | Hs.300710 | AI709236 | 4999012 | RC0-MT0059-200600-021-g05 cDNA | -1 | AAGATGCCTAAGCGTTAACCAGGTGA AACAGGGGTGGGAGAGAGAAAGAA |
| 5374 | Table 3A | Hs.297184 | AI720536 | 5037792 | 601502712F1 cDNA, 5' end /clone=IMAGE:3904539 /clone_end=5' | -1 | GTCATACACCTATCCCCATTTTCT CCTATCCCCTCAACCCGGACATCAT |
| 5375 | Table 3A | Hs.313929 | AI733018 | 5054131 | oh60h01.x5 cDNA, 3' end /clone=IMAGE:1471441 /clone_end=3' | -1 | GCAGGTGGCAGAATGGGGTGCATGA AGGTTTCTGAAAATTAACACTGCTT |
| 5376 | Table 3A | Hs.310333 | AI735206 | 5056730 | at07f03.x1 cDNA, 3' end /clone=IMAGE:2354429 /clone_end=3' | -1 | ACAGAGAGGCAGCATTTGTTTCCAG TTAAAATTTGACCTCACTGTGATT |
| 5377 | Table 3A | Hs.277201 | AI740667 | 5108955 | wg07b07.x1 cDNA, 3' end /clone=IMAGE:2364373 /clone_end=3' | -1 | CCCCCTTTTGTGTGGTTTTATATTGG AACCCCTTTTCTTTTGAACTA |
| 5378 | Table 3A | Hs.204656 | AI741246 | 5109534 | wg26g09.x1 cDNA, 3' end /clone=IMAGE:2366272 /clone_end=3' | -1 | CTGACCCCTTCTCACCCCTGCCAAC AGTGGTGGCATATATCACAATGG |
| 5379 | Table 3A | Hs.299883 | AI742850 | 5111138 | hypothetical protein FLJ23399 (FLJ23399), mRNA /cds=(282,1769) | -1 | TGTTTTACCTCACTGTTGGACATACAT TCCAAGCTTTTCAACTCTAGGAG |
| 5380 | Table 3A | Hs.6187 | AI745230 | 5113518 | wg10e05.x1 cDNA, 3' end /clone=IMAGE:2364704 /clone_end=3' | -1 | CAGAACATGCCCAAAGAGCCTATAT CTTGCTGCTGGGAAATGTAAAGCA |
| 5381 | Table 3A | Hs.293842 | AI748827 | 5127091 | 601571679F1 cDNA, 5' end /clone=IMAGE:3838675 /clone_end=5' | -1 | CAAACACCGGCAGTTGAAAGGAAAA GGACGGGAATGTGATGGAAGAG |
| 5382 | Table 3A | NA | AI749435 | 5127699 | at24b04.x1 Barstead aorta HPLRB6 cDNA clone IMAGE:2356015 3' similar to gb:X55715 40S RIBOSOMAL PRO | -1 | CCCCCTCCCTGCCCGGTGAGCTTT GGGGAACCCAAAAATTAGATTTTGC |
| 5383 | Table 3A | Hs.204929 | AI749444 | 5127708 | at24c03.x1 cDNA, 3' end /clone=IMAGE:2356036 /clone_end=3' | -1 | CCCAAATCCAAGGACCAATGCTGTTG TAAACAAGGGGTAAAGGCCCTAAA |
| 5384 | Table 3A | Hs.205071 | AI760018 | 5175685 | wh83b02.x1 cDNA, 3' end /clone=IMAGE:2387307 /clone_end=3' | -1 | ACTCCACCAAGACTGTGAACCTCCACC GGGGTAGGAAGCATATTTTACTCA |
| 5385 | Table 3A | Hs.160951 | AI760020 | 5175687 | wh83b05.x1 cDNA, 3' end /clone=IMAGE:2387313 /clone_end=3' | -1 | GAGAACTCGTTTCAAGGAACCTCGATG TTTCCGGGGACCAAGCCCGCCAG |
| 5386 | Table 3A | Hs.340921 | AI760026 | 5175693 | wh83c05.x1 cDNA, 3' end /clone=IMAGE:2387336 /clone_end=3' | -1 | CCAGCGAATTTCCAGCTTTTGAAACT CAGATTTCTTTTTCGACCCAGGT |
| 5387 | Table 3A | Hs.26873 | AI760224 | 5175891 | wh62g06.x1 cDNA, 3' end /clone=IMAGE:2385370 /clone_end=3' | -1 | GATGCGCGGCAAGAATGTACCTGTA GATGTGTACATACCACAGTGCTGTA |
| 5388 | Table 3A | Hs.14373 | AI760353 | 5176020 | yx26h11.r1 cDNA, 5' end /clone=IMAGE:262917 /clone_end=5' | -1 | TTTATCTCAGAATCTTGATGAACCTCG AAATGACCCCTGATGGGGGCATG |
| 5389 | db mining | Hs.204598 | AI760374 | 5176041 | wh87d12.x1 cDNA, 3' end /clone=IMAGE:2387735 /clone_end=3' | -1 | GGCCCCCTGTCTTACCTGTTTTCGG CCCCCTTAATTTTAAACCCCGGG |
| 5390 | db mining | Hs.283496 | AI760389 | 5176056 | wh87f08.x1 cDNA, 3' end /clone=IMAGE:2387751 /clone_end=3' | -1 | GTCACAGTGTAGACACATGGTGCTTC CATAGTGAGTAGAATATCCATTGT |
| 5391 | db mining | Hs.340927 | AI760556 | 5176223 | wi10d09.x1 cDNA, 3' end /clone=IMAGE:2389841 /clone_end=3' | -1 | GTGGCCTGGCCTGGCTCTCACAGAC CCAAGGCTTCCGTGTAGATATGTC |
| 5392 | db mining | Hs.205803 | AI760674 | 5176341 | wh96b04.x1 cDNA, 3' end /clone=IMAGE:2388559 /clone_end=3' | -1 | GGATTGTGGCAGGAAGTGTTCCTCCT CCCAGCCTAAATTTTCTGTGT |
| 5393 | db mining | Hs.283497 | AI760699 | 5176366 | 7f34c12.x1 cDNA, 3' end /clone=IMAGE:3296566 /clone_end=3' | -1 | AAACCCACACCTCAGTGAATTTAAAA GAGTAGATGTTTTAAAGACCGGA |
| 5394 | db mining | Hs.264654 | AI760835 | 5176502 | wh96f11.x1 cDNA, 3' end /clone=IMAGE:2388621 /clone_end=3' | -1 | TGCCATTGGTATTTTTCTGAAACA TTACATAATAAGATGCAGCATGC |
| 5395 | Table 3A | NA | AI760901 | 5176568 | wi09h06.x1 NCI_CGAP CLL1 cDNA clone IMAGE:2389787 3', mRNA sequence | -1 | GCCTGAAACCATCTGCCTTCTAGGA AGACAGCAATTCTGGAAGACGAAG |
| 5396 | db mining | Hs.230931 | AI760991 | 5176658 | wh97b11.x1 cDNA, 3' end /clone=IMAGE:2388669 /clone_end=3' | -1 | GGTGGTTCCCGAGCCCTTTCCCTGG CCCTGGGTTGAAAAATTTGTTTC |
| 5397 | db mining | Hs.328494 | AI761029 | 5176696 | wi10d06.x1 cDNA, 3' end /clone=IMAGE:2389835 /clone_end=3' | -1 | AAAACCTTTCGCCCGGCTTAAATTT ACCGGGGTTTGGTTTATTTGGTTT |
| 5398 | Table 3A | Hs.98531 | AI761058 | 5176725 | wi69b03.x1 cDNA, 3' end /clone=IMAGE:2398541 /clone_end=3' | -1 | CTCCTTGGTGTGATGCAACTGAGGAA CCTAATTGGCTGGGTGGGTGTTTC |
| 5399 | Table 3A | Hs.205452 | AI761141 | 5176808 | wh97g08.x1 cDNA, 3' end /clone=IMAGE:2388734 /clone_end=3' | -1 | GTTTGTAAAAGAACCTGCCACATTTG TTGAAAGTTAGAGCCATCACAGC |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|---|----|---|
| 5400 | Table 3A | NA | AI761144 | 5176811 | wh97h01.x1 NCL_CGAP_CLL1 cDNA clone IMAGE:2388721 3', mRNA sequence | -1 | CTCTTGGCTGCTGGCCTTTTGTCTT GTCATGGCTCATTAGCTCCCTAAA |
| 5401 | db mining | Hs.328495 | AI761468 | 5177135 | wh98e07.x1 cDNA, 3' end /clone=IMAGE:2388804 /clone_end=3' | -1 | CCAGGGGTTTTTAAATTTTCTGAAGTT TTTGGGGCCATTTTGGTTGTTGG |
| 5402 | Table 3A | Hs.80887 | AI761622 | 5177289 | v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), mRNA /cds=(297,1835) | -1 | CCCCGCTTGCCTTTTATTTTCAGAACCC CCAAGTATTACCAATATGTTACA |
| 5403 | Table 3A | Hs.289834 | AI761924 | 5177591 | wg68h03.x1 cDNA, 3' end /clone=IMAGE:2370293 /clone_end=3' | -1 | GCCGAAGCTCACAGAGGCTAAGTTA CACGCTTAGGTGTTCTTATTCTCTAC |
| 5404 | Table 3A | Hs.204610 | AI762023 | 5177690 | wh89f04.x1 cDNA, 3' end /clone=IMAGE:2387935 /clone_end=3' | -1 | AACCAGGTTTATGATGCTGTAATAAAA CCATGGCATTAAAGAGGGCAAGAG |
| 5405 | db mining | NA | AI762156 | 5177823 | wh90e05.x1 NCL_CGAP_CLL1 cDNA clone IMAGE:2388032 3' similar to gb:X64707 BREAST BASIC CONSERVED PR | -1 | GGGTAAAGGAGGGCCGCTCCAAAAT TTTCCTTTTCCAGGAAGCCCTTG |
| 5406 | db mining | Hs.204771 | AI762177 | 5177844 | wh90g09.x1 cDNA, 3' end /clone=IMAGE:2388064 /clone_end=3' | -1 | ATGCTGTGAGTGGTACACATGGCTGA GGTTATGATCTGTTAAATATGTA |
| 5407 | Table 3A | Hs.205327 | AI762557 | 5178224 | wh92f07.x1 cDNA, 3' end /clone=IMAGE:2388229 /clone_end=3' | -1 | TTCATTAATTCCTCAACCCAATACTGT CTGGCTTCCACCAACAGGAGCGG |
| 5408 | db mining | Hs.328503 | AI762707 | 5178374 | wh93d06.x1 cDNA, 3' end /clone=IMAGE:2388299 /clone_end=3' | -1 | TGGTTTCTATTTTAAAAACCTGGGTTA GGCCAAGGTTTGGGGTTCGCCCT |
| 5409 | db mining | Hs.204477 | AI762719 | 5178386 | wh93e10.x1 cDNA, 3' end /clone=IMAGE:2388330 /clone_end=3' | -1 | CAACATTGCCTACCAGTTGCAGTTCA TTAGCCCCGTCGCCCCAGCATTG |
| 5410 | db mining | Hs.205815 | AI762739 | 5178406 | wh93g11.x1 cDNA, 3' end /clone=IMAGE:2388356 /clone_end=3' | -1 | CCTTTGGGGTGGGGGCTTTTCTTTT TTGGCCGGTTCATTAAGGTTTTT |
| 5411 | Table 3A | NA | AI762741 | 5178408 | wh93h02.x1 NCL_CGAP_CLL1 cDNA clone IMAGE:2388339 3', mRNA sequence | -1 | CCCACTCCGGCTGTTTTAGAAAGTTTT CCCGAATCCGTGATCCCTTTACAA |
| 5412 | db mining | NA | AI762797 | 5178464 | wi04c12.x1 NCL_CGAP_CLL1 cDNA clone IMAGE:2389270 3' similar to TR:Q61655 Q61655 EUKARYOTIC TRANSLA | -1 | AATGGGCAAATTTTACCCAAAACCTTA AGCTTGCCTATTCCGTTTGAGGCA |
| 5413 | Table 3A | Hs.333513 | AI762870 | 5178537 | wi63c07.x1 cDNA, 3' end /clone=IMAGE:2397996 / | -1 | GAAGGAGAGGCACACAAAATACAC ACACTCACACAAAACCAACAACCA |
| 5414 | db mining | Hs.204480 | AI762931 | 5178598 | wh94e08.x1 cDNA, 3' end /clone=IMAGE:2388422 /clone_end=3' | -1 | GGATACCCCTTTATCCCGAGGGAAT TTTTACCCTTTGGATGCCTTTAAA |
| 5415 | db mining | Hs.289836 | AI762955 | 5178622 | wh94g12.x1 cDNA, 3' end /clone=IMAGE:2388454 /clone_end=3' | -1 | CAAATTACAAACCTAAAAATACAGAA CATCAGCGGAGAAGACAGGAGAGC |
| 5416 | db mining | Hs.277238 | AI763079 | 5178746 | wh95a12.x1 cDNA, 3' end /clone=IMAGE:2388478 /clone_end=3' | -1 | CTCCTCCCTTGGGTGGGACCTGGGT TGGGGGTTTGATAGAAAAATTAACC |
| 5417 | Table 3A | Hs.173904 | AI763121 | 5178788 | wi06d12.x1 cDNA, 3' end /clone=IMAGE:2389463 /clone_end=3' | -1 | GGTTAAACTAGATCCCTGCAAGGCCA TCACCTCCATTCCAAGTTGTTACT |
| 5418 | Table 3A | Hs.190453 | AI763206 | 5178873 | wh95e09.x1 cDNA, 3' end /clone=IMAGE:2388520 /clone_end=3' | -1 | AGTGGGTTATTTTAGATCTTTTCTCTG GGGTTGAGGTACATAGCTTAAC |
| 5419 | db mining | Hs.283500 | AI763225 | 5178892 | UI-H-BW1-anj-a-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082282 /clone_end=3' | -1 | TGTTTGGGTATATTGTTTGGGTTTTG GGCACTAGGATGGGTGACTCAGGG |
| 5420 | Table 3A | Hs.130059 | AI763262 | 5178929 | wi66c04.x1 cDNA, 3' end /clone=IMAGE:2398278 /clone_end=3' | -1 | GCCAGTGAATCTAGTTTTGGCTATTC TGTATTTTGCCAGTTTTTCCCAT |
| 5421 | db mining | Hs.328504 | AI763414 | 5179081 | wh92a11.x1 cDNA, 3' end /clone=IMAGE:2388188 /clone_end=3' | -1 | AACCATTTTCCCCGGGAACCCGTTT TGCCTGGTTTCGGATTTTTTACCC |
| 5422 | Table 3A | Hs.36137 | AI765153 | 5231662 | hepatocyte nuclear factor 3, gamma (HNF3G), mRNA /cds=(0,1043) | -1 | CCGGGAAGCGGGGTACTGGCTGTGT TTAATCATTAAAGGTACCGTGTCCG |
| 5423 | db mining | Hs.340947 | AI766625 | 5233134 | wi01f06.x1 cDNA, 3' end /clone=IMAGE:2388995 /clone_end=3' | -1 | TTTTCCCTCCCAAATTCAGTGCAT TACAGTTTTTGAACAGAACGGG |
| 5424 | Table 3A | NA | AI766638 | 5233147 | wi02a10.x1 NCL_CGAP_CLL1 cDNA clone IMAGE:2389050 3', mRNA sequence | -1 | TACGAGAAGTCAGGAAGTTTTGAAAT GGCAGTGACAGGAGACGGGGGAAG |
| 5425 | db mining | Hs.210276 | AI766656 | 5233165 | wi02d04.x1 cDNA, 3' end /clone=IMAGE:2389063 /clone_end=3' | -1 | AAGGGCAGGCAAATCAATTAATAA GCCGTAACAACAACCTCGGGGGTG |
| 5426 | Table 3A | Hs.223935 | AI766706 | 5233215 | wi02g11.x1 cDNA, 3' end /clone=IMAGE:2389124 /clone_end=3' | -1 | AGTACACGGCCCTCAAAAGTTATATG TGCTGAATGTAACCTACTTAGCGA |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|---|
| 5427 | Table 3A | Hs.89104 | AI766963 | 5233472 | 602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5' | -1 | TTGTTTTAACAACTCTTCTCAACATTT TGCCAGGTATTCTACTGTAACCA |
| 5428 | Table 3A | Hs.209511 | AI768880 | 5235389 | wh71e04.x1 cDNA, 3' end /clone=IMAGE:2386206 /clone_end=3' | -1 | CTTCTCCACCTCGGCCAGGTATAGG GCCAGCTTCTCGTCTCTGGGATCCG |
| 5429 | Table 3A | Hs.203594 | AI796317 | 5361780 | uncharacterized gastric protein ZA43P mRNA, partial cds /cds=(0,134) | -1 | GCCAGGTCATTGTATAGGGAGTAAGA TGAAGGTGAATTTGCAGCTAGTTG |
| 5430 | Table 3A | Hs.230939 | AI796419 | 5361882 | wj17f02.x1 cDNA, 3' end /clone=IMAGE:2403099 /clone_end=3' | -1 | TGTGTTTTGTTTTCTGGTCCCAGGG CACCGTTGTTTTGTGAACCTCTC |
| 5431 | db mining | Hs.291079 | AI797561 | 5363033 | 602437732F1 cDNA, 5' end /clone=IMAGE:4555638 /clone_end=5' | -1 | CATGGCTCTAAAATTTGGAATTAACCT CTCTTGCCCTAAGAGCTGCTTGT |
| 5432 | Table 3A | Hs.159577 | AI797788 | 5363260 | wh78b11.x1 cDNA, 3' end /clone=IMAGE:2386845 /clone_end=3' | -1 | GCTGGTGGGAAGTTGAGCCATGTTTA TCTCTAGTGAATCCTTACCTTGT |
| 5433 | db mining | Hs.207473 | AI797813 | 5363370 | wh79c04.x1 cDNA, 3' end /clone=IMAGE:2386950 /clone_end=3' | -1 | CATGTTTACACAAATTCCTTCAAAGC CCCTTAACATGGGGCCGGGCCCC |
| 5434 | db mining | Hs.171110 | AI797852 | 5363409 | 7e88g03.x1 cDNA, 3' end /clone=IMAGE:3292276 /clone_end=3' | -1 | ACCCTAATAGCTAGGCTGGGTATATT TTCAAAGTGATAGCGAAACCCACG |
| 5435 | db mining | NA | AI797901 | 5363296 | wh78f12.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2386895 3' similar to contains Alu repetitive element, m | -1 | CAGTTGGCCTCTACAATTGGGAATT CTACCAAGCTCCAAGTTGACCTGG |
| 5436 | db mining | Hs.226571 | AI797916 | 5363311 | DKFZp434G046_s1 cDNA, 3' end /clone=DKFZp434G046 /clone_end=3' | -1 | GGATTCCCGACAAAGGCTTGATGTGT ACTTGAAAGTGAGCAAAGGGTTTGT |
| 5437 | db mining | Hs.223520 | AI797988 | 5363460 | wh80a02.x1 cDNA, 3' end /clone=IMAGE:2387018 /clone_end=3' | -1 | GGGTGGGAGACAGGCTAATCCTTTC CCCTTGTTCACGTCTTTATGAC |
| 5438 | db mining | Hs.207062 | AI798027 | 5363499 | wh80e09.x1 cDNA, 3' end /clone=IMAGE:2387080 /clone_end=3' | -1 | ACAACCTTCTTAATATATTAGAGACCC GCAGGAAACATTTAGTGGTGAAAC |
| 5439 | db mining | Hs.341012 | AI798028 | 5363500 | wh80f11.x1 cDNA, 3' end /clone=IMAGE:2387085 /clone_end=3' | -1 | GTACATGTTTGTGTGCTAAATTGCTC ATTTGGCAGTGATAGATTGAAAAAC |
| 5440 | db mining | Hs.229494 | AI798100 | 5363583 | wh81d01.x1 cDNA, 3' end /clone=IMAGE:2387137 /clone_end=3' | -1 | GGGGGTCAAAGAGGGTACAAATGTA TGGGGGTATATTGAATGCTAAACAT |
| 5441 | db mining | Hs.328535 | AI798101 | 5363584 | wh81d02.x1 cDNA, 3' end /clone=IMAGE:2387139 /clone_end=3' | -1 | GGGAGCCCGTTTTAGAAGGAAGGGC AAAAGTAGGGTTTTTAACCCAAACG |
| 5442 | db mining | Hs.210307 | AI798114 | 5363576 | wh81c01.x1 cDNA, 3' end /clone=IMAGE:2387136 /clone_end=3' | -1 | TCCGTCCCATTCCCCCGGAAAAACAAG GTTTTGAATTGGCCCGTAAAGGG |
| 5443 | Table 3A | Hs.209609 | AI798144 | 5363616 | wh81g12.x1 cDNA, 3' end /clone=IMAGE:2387206 /clone_end=3' | -1 | ACGTCCTTATACAATGCACTGTTTGA TTTTTAAACAATACCTGAAGGGCT |
| 5444 | Table 3A | Hs.158989 | AI799909 | 5365381 | 602666595F1 cDNA, 5' end /clone=IMAGE:4806358 /clone_end=5' | -1 | ACTCAATACTCGGGAAGGCTTCACA TTTCTGGGACTCAGCATTATCCAA |
| 5445 | Table 3A | Hs.135167 | AI802181 | 5367664 | AV712376 cDNA, 5' end /clone=DCAAND12 /clone_end=5' | -1 | TTGAGAGGCAACACTTAAACACTAGG GCTACTGTGGCATCTATGTAGACA |
| 5446 | Table 3A | Hs.195175 | AI802547 | 5368019 | mRNA for CASH alpha protein /cds=(481,1923) | -1 | AGCCCTTCTTGTGTGCTGTATGTTTA GATGCTTCCAATCTTTGTACT |
| 5447 | Table 3A | Hs.25648 | AI803065 | 5368537 | tumor necrosis factor receptor superfamily, member 5 (TNFRSF5), mRNA /cds=(47,880) | -1 | GGGGTATGGTTAGTAATATCCACCA GACCTCCGATCCAGCAGTTTGGT |
| 5448 | Table 3A | Hs.301209 | AI804629 | 5370101 | myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 (MLLT10), mRNA /cds=(183,3266) | -1 | AACAACAACAGCAAAATCCCTTAGT GCGTAACTTGAAATTCCTTCGGC |
| 5449 | db mining | Hs.209261 | AI805106 | 5391760 | tc90g10.x1 cDNA, 3' end /clone=IMAGE:2073474 /clone_end=3' | -1 | TTGTAAGTGGGTGCATAAGAAGATCT CTTCAATTAATGCCCGCTGGT |
| 5450 | Table 3A | Hs.187698 | AI805111 | 5391765 | cytomegalovirus partial fusion receptor mRNA, partial cds /cds=(0,1037) | -1 | ATAATTAAGAAATCAGCCGTGTGCTT CTCACGTTTGGGCTCCGAGACGTG |
| 5451 | Table 3A | Hs.167206 | AI805131 | 5391785 | 602727149F1 cDNA, 5' end /clone=IMAGE:4866348 /clone_end=5' | -1 | GTCAGTCTCCTCACCTGCCTCTGCTC CTCGCTTAGCCCATTTGATTGCATC |
| 5452 | db mining | NA | AI805144 | 5391798 | td11g08.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2075390 3' similar to gb:L24038_ma1 A-RAF PROTO- ONCOGENE | -1 | GGGAAGAAGCCCGTGCCCCACCCA ATAAATGTTGGTTTGGCCCTGATG |
| 5453 | db mining | NA | AI805257 | 5391750 | tc90f09.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2073449 3', mRNA sequence | -1 | CAGAACTTCTGGCGAAGGCCATGTAA GAACTACTCCAAGGAGGAAGAGGC |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|---|----|--|
| 5454 | Table 3A | NA | AI807278 | 5393844 | wf38h03.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2357909 3', mRNA sequence | -1 | CTCTACCATAAGGCACTATCAGAGAC TGCTACTGGAGTGTATATTTGGTT |
| 5455 | db mining | NA | AI808039 | 5394527 | wf52h02.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2359251 3' similar to TR:Q62845 Q62845 NEURAL CELL | -1 | ACTGCTACAGCTTAACCATTGTTCCA AGCTAATTAATTAACCTTTGGGGA |
| 5456 | Table 3A | Hs.87912 | AI808931 | 5395497 | EST379776 cDNA | -1 | CAATTGTGATTTGGAAGGTTAACTG GGTCTGCCAGATGTTTACGAATA |
| 5457 | db mining | Hs.209989 | AI809181 | 5395747 | wh75d05.x1 cDNA, 3' end /clone=IMAGE:2386569 /clone_end=3' | -1 | TCCAAGCAAAAGTTATGCAATAAGAC AGAATATAAAGTCTCCGAGAGCCT |
| 5458 | db mining | Hs.230485 | AI809184 | 5395750 | wh75d08.x1 cDNA, 3' end /clone=IMAGE:2386575 /clone_end=3' | -1 | GGGTGGGGTGGGGTGAGAGTGTGTG GAGTAAGGACCTTCAGAATTAATAT |
| 5459 | db mining | Hs.292761 | AI809305 | 5395871 | wh75g11.x1 cDNA, 3' end /clone=IMAGE:2386628 /clone_end=3' | -1 | TGCAGTTCTTATTTTCTTTGCTGTG ATAATTGCAAAATCCGTCAATAGAA |
| 5460 | Table 3A | Hs.210385 | AI809310 | 5395876 | wh75h08.x1 cDNA, 3' end /clone=IMAGE:2386623 /clone_end=3' | -1 | TGCAAGTTTCTGAGACTGTGAAAAGT GTTTTGCTTCTTTGTTACCCAAT |
| 5461 | db mining | Hs.90463 | AI809378 | 5395944 | wa27e12.x1 cDNA, 3' end /clone=IMAGE:2299342 /clone_end=3' | -1 | TCCCAGCGAATGTGAATCATTTAGTG TGCTACTCAAAATTAGGTGTCCAC |
| 5462 | Table 3A | Hs.257466 | AI809475 | 5396041 | UI-H-BI3-ald-e-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2736471 /clone_end=3' | -1 | TAAGATGTAGGGGCCACCGGCCAGC AGTACCCAGCAATGACCACTATCAG |
| 5463 | db mining | Hs.208153 | AI809564 | 5396130 | wh76e01.x1 cDNA, 3' end /clone=IMAGE:2386680 /clone_end=3' | -1 | ATAAATGAAAGCATACCAAGTGCTGT CCATTCCATAGGTACAACATATGGA |
| 5464 | db mining | Hs.310486 | AI809746 | 5396312 | 7e96g11.x1 cDNA, 3' end /clone=IMAGE:3293060 /clone_end=3' | -1 | CTGGTATTCTGAGGTGAGATGTAGGC TGTTGCTCGCTCCGGCTGGGTCTC |
| 5465 | Table 3A | Hs.277293 | AI811065 | 5397631 | tr03f05.x1 cDNA, 3' end /clone=IMAGE:2217249 /clone_end=3' | -1 | CCATCGGGGGTATTGGGGTTTTGGG CTGAATTTACTTGATTATTGAAAA |
| 5466 | Table 3A | Hs.86693 | AI817153 | 5436320 | EST380760 cDNA | -1 | GCCAGATTGTGGCAGGTAAAGAGAC AATGTAATTTGCACTCCCTATGATA |
| 5467 | Table 3A | Hs.230492 | AI818596 | 5437675 | wk74d04.x1 cDNA, 3' end /clone=IMAGE:2421127 /clone_end=3' | -1 | TTTAAAAAGGAGGGAGGATTCTGGG TTAAACCTTTTATTTGGCCCCCAT |
| 5468 | Table 3A | Hs.229990 | AI818777 | 5437856 | wl11f10.x1 cDNA, 3' end /clone=IMAGE:2424619 /clone_end=3' | -1 | TAAACCCCAAGACTTCAGATTACGCC GAATTGTGGTGTTCACAAGGCCG |
| 5469 | Table 3A | NA | AI818951 | 5438030 | wj89e12.x1 NCI_CGAP_Lym12 cDNA clone IMAGE:2410030 3' similar to WP:C11H1.7 CE18492 ;contains Alu r | -1 | CTAAGCATGGGGAAGGGGGCAGAGT GAGGACTGTGCCATTGATTAAAGTG |
| 5470 | Table 3A | Hs.51039 | AI823541 | 5444212 | KIAA0076 gene product (KIAA0076), mRNA /cds=(86,5182) | -1 | GTACAGAAACATATTTCCATGCTTTGA AATAAAGGGAAGTGCTCTCTGTT |
| 5471 | Table 3A | Hs.211535 | AI823649 | 5444320 | wi85g03.x1 cDNA, 3' end /clone=IMAGE:2400148 /clone_end=3' | -1 | GAAGCCTTTTCTTTTCTGTTACCCCTC ACCAAGAGCACAACTTAAATAGG |
| 5472 | Table 3A | Hs.304477 | AI824522 | 5445193 | bx71d03.x1 cDNA, 3' end /clone=IMAGE:2275013 /clone_end=3' | -1 | ACCGATCGTTTTTAGGATAATATGCA TGTTTCAAGTGGTATTGAAACCCCC |
| 5473 | db mining | Hs.270624 | AI825096 | 5445859 | 7b65e05.x1 cDNA, 3' end /clone=IMAGE:3233120 /clone_end=3' | -1 | TGAGGGACAGGCTGCCTAAAGTCTAA TTGGAGAGTTAACCTAATGTCTGT |
| 5474 | Table 3A | Hs.117906 | AI825645 | 5446316 | wb75b09.x1 cDNA, 3' end /clone=IMAGE:2311481 /clone_end=3' | -1 | CACCATCGTGGCTCTGAGAAGTACGAC GCCGTGAATGTTGACCTGAGTGCCG |
| 5475 | Table 3A | Hs.229993 | AI827451 | 5448122 | wl17d11.x1 cDNA, 3' end /clone=IMAGE:2425173 /clone_end=3' | -1 | GGGGAGAGACCACCTAGACATTG CATTTTTGTAAGTTAGCCAGCCAAT |
| 5476 | Table 3A | Hs.181400 | AI827911 | 5448669 | 602650370T1 cDNA, 3' end /clone=IMAGE:4761353 /clone_end=3' | -1 | TGGATAAATCTGAGCAACTTTCTTCTT TGTGCTCCAGGAACCTACGCACT |
| 5477 | Table 3A | Hs.342617 | AI827950 | 5448708 | ha15h10.x1 cDNA, 3' end /clone=IMAGE:2873827 /clone_end=3' | -1 | TGTGGGTTTTGATTGACATACTGTTG TTCATGCTGAAGTTTGAGTGTCTG |
| 5478 | Table 3A | Hs.132238 | AI829569 | 5450240 | wf28e02.x1 cDNA, 3' end /clone=IMAGE:2356922 /clone_end=3' | -1 | GGTGTGCAGTCCGCCTGAAAGCCTT CCCTTTAGCTATTAGGAATTGAGTC |
| 5479 | db mining | Hs.289878 | AI831819 | 5452490 | wh84f12.x1 cDNA, 3' end /clone=IMAGE:2387471 /clone_end=3' | -1 | ACATTGGAAGAAACCCACAACTGT AATGAATATGAAAAGAAATTGTCTAAAA |
| 5480 | Table 3A | Hs.341177 | AI832038 | 5452709 | wj99e02.x1 cDNA, 3' end /clone=IMAGE:2410970 /clone_end=3' | -1 | AAAACCGTTTTCCCATACATAAAGA ACAGGGGTACTCCGCCCTGATGG |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|---|----|---|
| 5481 | Table 3A | Hs.210995 | AI832182 | 5452853 | td13h11.x1 cDNA, 3' end /clone=IMAGE:2075589 /clone_end=3' | -1 | TTTGGTGAAGTGAAAGAGAGAAGTTG CTCTAAAAGGTTGGAACACGAGCC |
| 5482 | Table 3A | Hs.249031 | AI832183 | 5452854 | wh80g09.x1 cDNA, 3' end /clone=IMAGE:2387104 /clone_end=3' | -1 | TGGACTGTTGTAATGTTTTCGCTTAT CAAAATGAAACTGCCAAATGAGA |
| 5483 | Table 3A | Hs.63908 | AI858771 | 5512387 | hypothetical protein MGC14726 (MGC14726), mRNA /cds=(21,653) | -1 | GCTTTGAGTTTTGGGATGGTCACATG ACACAATCCAGCACTTGAACCTGA |
| 5484 | Table 3A | Hs.252259 | AI859076 | 5512692 | ribosomal protein S3 (RPS3), mRNA /cds=(22,753) | -1 | AGAGCCATCCCCACAAAGTAAATGTG CAGTGCCCATGTTTCTTGTGTTTA |
| 5485 | Table 3A | NA | AI860120 | 5513736 | wh39e01.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2383128 3', mRNA sequence | -1 | GACTCTGAGAGAGAGCGACGGCCAT CATAGAACAGCGAAGGCAGTCGATC |
| 5486 | db mining | Hs.156811 | AI862332 | 5526439 | hz33g10.x1 cDNA, 3' end /clone=IMAGE:3209826 /clone_end=3' | -1 | ATCGATGAGAAGAGTCTGCAAAACAC TTCATCCTCAGGACGTGCTGTCT |
| 5487 | db mining | Hs.304508 | AI862595 | 5526702 | wh99g01.x1 cDNA, 3' end /clone=IMAGE:2388912 /clone_end=3' | -1 | ATATATTAACCACAGGTATTAGAGA CATGAATTGCACCAACACAAGCT |
| 5488 | Table 3A | NA | AI862623 | 5526730 | wh99h10.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2388931 3', mRNA sequence | -1 | ATTCATTCGGGTCTTCTTTCTTCCG CCCCCTTCTTCCATTGGCACCTC |
| 5489 | Table 3A | Hs.181426 | AI865427 | 5529523 | EST367815 cDNA | -1 | TCAGTTTTGTGGAATCTGGTGTTCG ACTATAGGTTAAGAGTTGCCATTT |
| 5490 | Table 3A | Hs.341208 | AI865603 | 5529710 | wk47g03.x1 cDNA, 3' end /clone=IMAGE:2418580 /clone_end=3' | -1 | TGTGTGGTGGGGGTGCTTTGAGGTT GGAGGAAAGTAGAGACAGCGAAAC |
| 5491 | Table 3A | Hs.9788 | AI866194 | 5530301 | hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5 (MGC10924), mRNA /cds=(104,769) | -1 | TGTGCTTTTTGCCAAGTGGAATTC ATCTTGGTTTGCTATGTTAAACT |
| 5492 | Table 3A | Hs.224760 | AI874107 | 5548156 | wm49b01.x1 cDNA, 3' end /clone=IMAGE:2439241 /clone_end=3' | -1 | CTTTGGGGACCTAAACCCAGGTGG TCTCTGGTGTTAATAATGCTGGAA |
| 5493 | Table 3A | NA | AI880542 | 5554591 | at80h05.x1 Barstead colon HPLRB7 cDNA clone IMAGE:2378361 3' similar to SW:ATP6_HUMAN P00846 ATP SY | -1 | AAATCGCGGTCGCCCTTAATCCAAGCC TAGGTTTTCACACTTTTAGTAAGC |
| 5494 | Table 3A | Hs.220850 | AI880607 | 5554656 | ym91d11.r1 cDNA, 5' end /clone=IMAGE:166293 /clone_end=5' | -1 | TGGGGCACTTTGAAACTTCACAGGC CCACTGCTGCTTGCTGAAATAAAA |
| 5495 | Table 3A | Hs.89414 | AI884548 | 5589712 | chemokine (C-X-C motif), receptor 4 (fusin) (CXCR4), mRNA /cds=(88,1146) | -1 | GACATTCATCTGTTCCACTGAGTCT GAGTCTTCAAGTTTTCACTCCAGC |
| 5496 | Table 3A | Hs.23096 | AI884671 | 5589835 | 602254146F1 cDNA, 5' end /clone=IMAGE:4346626 /clone_end=5' | -1 | TGGCGAGGATAAATAGAGGCATTGTT TTTGCTACTTTCATATCATTGGC |
| 5497 | db mining | Hs.34650 | AI885574 | 5590738 | 602286784T1 cDNA, 3' end /clone=IMAGE:4375724 /clone_end=3' | -1 | TGGCTCTCCTCTTTGTAATATACAGG GTGAACCTCTTACTGATACACACA |
| 5498 | Table 3A | Hs.121572 | AI886313 | 5591477 | EST387650 cDNA | -1 | CCAGTGTCTGCTGATGGGTGCTAGGC TGAATTATTTGTAATTGTGCTTAGG |
| 5499 | Table 3A | Hs.213385 | AI912585 | 5632440 | we11d07.x1 cDNA, 3' end /clone=IMAGE:2340781 /clone_end=3' | -1 | ACCGCTTTTTGTGATTCCCTGGAAAC CCTTAATTCAATAGTCTGACTGA |
| 5500 | Table 3A | Hs.228486 | AI917348 | 5637203 | ts83d10.x1 cDNA, 3' end /clone=IMAGE:2237875 /clone_end=3' | -1 | AGCCCTGGGTAGCCAAGTGATTTTCC CATTCCTCAAAGTTAGTAAACCTTT |
| 5501 | Table 3A | Hs.179391 | AI917642 | 5637497 | wi52d11.x1 cDNA, 3' end /clone=IMAGE:2393877 /clone_end=3' | -1 | GCAGGAAAGATGGGGTGGTGGACTG TTTTTGCTACTTTTTGTTTTTGAA |
| 5502 | Table 3A | Hs.337286 | AI922889 | 5658853 | wn64g11.x1 cDNA, 3' end /clone=IMAGE:2450276 /clone_end=3' | -1 | CCCCCTGAAACTGGCATTGTTGTAAAT GTGGTTTGACTATTTTTGTATGTT |
| 5503 | Table 3A | Hs.212553 | AI922921 | 5658885 | wn81c05.x1 cDNA, 3' end /clone=IMAGE:2452232 /clone_end=3' | -1 | ACCTGGAGAATTCCTAAGGCCAAAG CAAGGTAACAGGGACTTCAGTTTT |
| 5504 | Table 3A | Hs.58643 | AI926251 | 5662139 | 602438603F1 cDNA, 5' end /clone=IMAGE:4564968 /clone_end=5' | -1 | GCCTCAGTACAAAGGGGGCTTTGGA AGTGTGTTGTTGGCTGAATAAAGGAA |
| 5505 | Table 3A | Hs.40328 | AI927454 | 5663418 | nab63b04.x1 cDNA, 3' end /clone=IMAGE:3272383 /clone_end=3' | -1 | ACCCATGCCAATTGAAGAACGTGTTA AAGATGAGGAGGAGAGATGTACCA |
| 5506 | db mining | Hs.154366 | AI934956 | 5673826 | ng40b06.s1 cDNA, 3' end /clone=IMAGE:937235 /clone_end=3' | -1 | GCACATTCCTTCTTATATCCTGGAA GCACCCAGATATTCTTCATGTCCC |
| 5507 | Table 3A | Hs.101370 | AI936516 | 5675386 | AL583391 cDNA /clone=CS0DL012YA12-(3-prime) | -1 | TTAAGTCATCTGCTGAGCAGTGTGCT GTGTCAACCTCCTCCTAGGTAACC |
| 5508 | Table 3A | Hs.180446 | AI948513 | 5740823 | importin beta subunit mRNA, complete cds /cds=(337,2967) | -1 | CAGGGTATCAGATATTGTGCCTTTTG GTGCCAGGTTCAAAGTCAAGTGCC |
| 5509 | Table 3A | Hs.71245 | AI954499 | 5746809 | zl17f11.r1 cDNA, 5' end /clone=IMAGE:502221 /clone_end=5' | -1 | TGGTAATAGTGTGACTCCAGGGAA GAACAGATGGGTGCCAGAGTGAAA |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|----------|--|----|---|
| 5510 | Table 3A | Hs.118820 | AI955314 | 5747624 | Homo sapiens, clone IMAGE:3357862, mRNA, partial cds /cds=(0,325) | -1 | TCAAGTATACCATTTAAATATTTTCAT CAGGCAGAGCCCTGACCAGGAAA |
| 5511 | db mining | NA | AI961962 | 5754664 | wt40g09.x1 NCI_CGAP_Pan1 cDNA clone IMAGE:2509984 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION | -1 | CTTTTCCGGTTCGCCGAGGATGCTTG GGAAGGAACCCGCTCCTCTCTTC |
| 5512 | Table 3A | Hs.341528 | AI962127 | 5754840 | wx77f07.x1 cDNA, 3' end /clone=IMAGE:2549701 /clone_end=3' | -1 | TCCCCAAACCCCTTAAAGGTTTTTA AATTGTTTCAAATCTGGGCAAGTT |
| 5513 | Table 3A | Hs.37121 | AI968387 | 5765205 | phospholipase C, beta 3 (phosphatidylinositol-specific) (PLCB3), mRNA /cds=(0,3704) | -1 | GACTCGGAGAGCCAGGAGGAGAACA CGCAGCTCTGAACTGGCTGAGCGAG |
| 5514 | db mining | Hs.13034 | AI969716 | 5766534 | hv63f09.x1 cDNA, 3' end /clone=IMAGE:3178121 /clone_end=3' | -1 | CTGTTGTGAATCATTTGTGTCCTTTTC AAGTGTCTTTCAGAGGAAAGGTA |
| 5515 | Table 3A | Hs.193247 | AI978581 | 5803611 | hypothetical protein DKFZp434A171 (DKFZp434A171), mRNA /cds=(113,2584) | -1 | AAGAAGCAACCACAGCTAATTTTAGA ACATGCACTCTGACAGAAAAGACA |
| 5516 | Table 3A | Hs.153 | AI984074 | 5811293 | ribosomal protein L7 (RPL7), mRNA /cds=(10,756) | -1 | GCTTTTGAGGACCTTTCTGGAGGAAA GGAAAAGCCTGTTTTGGGGAGTCT |
| 5517 | Table 3A | Hs.7557 | AL042081 | 5421426 | FK506-binding protein 5 (FKBP5), mRNA /cds=(153,1526) | -1 | AGGCTGCATATGGATTGCCAAGTCAG CATATGAGGAATTAAGACATTGT |
| 5518 | Table 3A | Hs.133262 | AL044498 | 5432716 | DKFZp434I082_s1 cDNA, 3' end /clone=DKFZp434I082 /clone_end=3' | -1 | AAGACTAGAGCTACACTAGGCCACTA TCTTATTACACGACAGCACACAATC |
| 5519 | Table 3A | Hs.39911 | AL138429 | 6855110 | mRNA for FLJ00089 protein, partial cds /cds=(62,1111) | -1 | TTAAGAACCCCAAAGATTAAAGGAAA CAATGTTAAGGGCTTTTGTGAGGA |
| 5520 | Table 3A | Hs.89986 | AL515381 | 12778874 | cDNA /clone=CL0BB017ZH06-(3-prime) | -1 | CGGAAGTCGAAATCAAATCTATGCTT TTAATTGAAACCGTGCCTGAAACG |
| 5521 | Table 3A | Hs.9096 | AL520535 | 12784028 | hypothetical protein FLJ20473 (FLJ20473), mRNA /cds=(57,1472) | -1 | TCTTCACCAGGTTCAAGCTCCGTGGG CCCACTGCTGCTGTGCCAAGAAG |
| 5522 | Table 3A | Hs.13144 | AL521097 | 12784590 | HSPC160 protein (HSPC160), mRNA /cds=(53,514) | -1 | GATACACTGTCCAGCCAGGTCAG GCCCTAGGTTCTTTACTCTAGCTAC |
| 5523 | Table 3A | Hs.118142 | AL522477 | 12785970 | AL522477 cDNA /clone=CS0DB008YK14-(3-prime) | -1 | TGGAATTTACTAAATTTGTGAAATTAAC GTAACCGAAGCAACACCGGCCAA |
| 5524 | Table 3A | Hs.295112 | AL528020 | 12791513 | KIAA0618 gene product (KIAA0618), mRNA /cds=(1041,4040) | -1 | GCGGGAGGCTGGGACTTTCCATTAC AAATAGAGACTTCATTCTGTGTAG |
| 5525 | Table 3A | Hs.26670 | AL540260 | 12870241 | AL540260 cDNA /clone=CS0DF032YF03-(3-prime) | -1 | ACTCAGGTGGTGTGGTGTAGTGAT GCTGGAGAGAGAAATATTACTGGT |
| 5526 | Table 3A | Hs.285013 | AL543900 | 12876379 | putative HLA class II associated protein I (PHAP1), mRNA /cds=(148,897) | -1 | CAGGTTGCTTTCGTGTCCTCTTCTG GTTGCTTTAGAAGTGACGTGTAAT |
| 5527 | Table 3A | Hs.183232 | AL561892 | 12909772 | hypothetical protein FLJ22638 (FLJ22638), mRNA /cds=(12,476) | -1 | AAACACAGCCCACCCCATTTTCAGACC GCCTTCCTGAGGAGAAAATGACAG |
| 5528 | Table 3A | Hs.21812 | AL562895 | 12911771 | AL562895 cDNA /clone=CS0DC021YO20-(3-prime) | -1 | GCTAACTGGATAAAGTTTGTGCAGAC ATTCCTGAGTGTACGATATTGACC |
| 5529 | Table 3A | Hs.21812 | AL562895 | 12911771 | AL562895 cDNA /clone=CS0DC021YO20-(3-prime) | -1 | GCTAACTGGATAAAGTTTGTGCAGAC ATTCCTGAGTGTACGATATTGACC |
| 5530 | Table 3A | Hs.181165 | AL565736 | 12917408 | eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(53,1441) | -1 | AGCTGGCTTCACTGCTCAGGTGATTA TCCTGAACCAACAGGCCAAATAAG |
| 5531 | Table 3A | Hs.77393 | AL567986 | 12921892 | farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDPS), mRNA /cds=(114,1373) | -1 | AGTCAGGACTGTCTAGGTCAGGGAA GCCAAGATGTCTGAAGAGAGAGGAA |
| 5532 | Table 3A | Hs.13256 | AL570416 | 12926702 | AL570416 cDNA /clone=CS0DI020YK05-(3-prime) | -1 | ATTCAACCAAGTAATGGTACCTGAGGA ATTGAAATGGGTATTGTTTCTGT |
| 5533 | Table 3A | Hs.180546 | AL571386 | 12928631 | AL571386 cDNA /clone=CS0DI009YL09-(3-prime) | -1 | AGTGGAGAGGCCCTGTGTTTACTT TTCATATTGAGTGATGATGAGCT |
| 5534 | Table 3A | Hs.21732 | AL573787 | 12933363 | AL573787 cDNA /clone=CS0DI055YM17-(3-prime) | -1 | GCATTCTATTTAAAAAGGGAGTGGGG AGCAAATGAAAATTAATGTGGGG |
| 5535 | Table 3A | Hs.23294 | AL574514 | 12934790 | hypothetical protein FLJ14393 (FLJ14393), mRNA /cds=(60,1454) | -1 | TCACCAGGAAAACATGCTTGTGAATT GTGCAGTAAAAGGTGGTAATGACT |
| 5536 | Table 3A | Hs.181392 | AL575666 | 12937052 | major histocompatibility complex, class I, E (HLA-E), mRNA /cds=(7,1083) | -1 | CCTTTTCTCTCCCATGACCCCTTAACA GCATCTGCTTCATTCCCCTCACC |
| 5537 | Table 3A | Hs.85258 | AL575755 | 12937231 | CD8 antigen, alpha polypeptide (p32) (CD8A), mRNA /cds=(65,772) | -1 | CTGAGAGCCCAAACCTGCTGCCAAA CATGCACTTCCTTGCTTAAGGTAT |
| 5538 | Table 3A | Hs.169610 | AL576149 | 12938006 | mRNA for transmembrane glycoprotein (CD44 gene) /cds=(178,2406) | -1 | TGAGTGAACAAAGCTGTGAAACATTC TGCGTTTATGCAACTTCCTTGCCCT |
| 5539 | Table 3A | Hs.174905 | AL577970 | 12941605 | mRNA for KIAA0033 gene, partial cds /cds=(0,1008) | -1 | CAAGAAGACAAGCATCTGTGGTGCG GAGGCAAGCAGGCTAAGTAGGATT |
| 5540 | Table 3A | Hs.5057 | AL578975 | 12943566 | AL578975 cDNA /clone=CS0DK012YN01-(3-prime) | -1 | TTGGCCAGTGTGATTGATTGCTTTA TCTTTGGTACTTTTACTTGAATGG |
| 5541 | Table 3A | Hs.279555 | AL582047 | 12949649 | AL582047 cDNA /clone=CS0DL003YD01-(3-prime) | -1 | CATCCAGCACTAATTTTCATGCATTTA TGAAAGGATGCCCTGAGGACCCCT |
| 5542 | Table 3A | Hs.198296 | AL582354 | 12950255 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), mRNA /cds=(297,5015) | -1 | AGCCTGAGGCAAAATAAATCCAGTA ATTTGGAAGAATGGGTGTTGGCAA |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|----------|--|----|---|
| 5543 | Table 3A | Hs.101370 | AL583391 | 12952309 | AL583391 cDNA /clone=CS0DL012YA12-(3-prime) | -1 | AGGACCTTGACAAGCCGTTTGAGATG GAATGTAGGCCCTGATGTTATGCT |
| 5544 | Table 3A | Hs.101370 | AL583391 | 12952309 | AL583391 cDNA /clone=CS0DL012YA12-(3-prime) | -1 | AGGACCTTGACAAGCCGTTTGAGATG GAATGTAGGCCCTGATGTTATGCT |
| 5545 | Table 3A | Hs.7187 | AU158636 | 11020157 | mRNA for KIAA1757 protein, partial cds /cds=(347,4576) | -1 | AGTGGAGTGTTTACACCTTGCTGTAA CATTTGAACCTTTCACAAGAGATGT |
| 5546 | Table 3A | Hs.86671 | AV648638 | 9869652 | 602079785F2 cDNA, 5' end /clone=IMAGE:4254068 /clone_end=5' | -1 | ATATCATATTATTTGATGCCATTAGGC GGCCTGGATCACCAATTCTAAGT |
| 5547 | Table 3A | Hs.343475 | AV648670 | 9869684 | 601556208T1 cDNA, 3' end /clone=IMAGE:3826392 /clone_end=3' | -1 | GCCACCAGACAGAAGGACCAGAGTT TCTGATTATAAACAATGATGCTGGG |
| 5548 | Table 3A | Hs.2730 | AV650434 | 9871448 | heterogeneous nuclear ribonucleoprotein L (HNRPL), mRNA /cds=(28,1704) | -1 | TGTTGGTGAGCAATGTGCAGAGGCA GAGCCGCTGAAGTATGGTTCCTGAG |
| 5549 | Table 3A | Hs.312582 | AV651615 | 9872629 | 601439711F1 cDNA, 5' end /clone=IMAGE:3924482 /clone_end=5' | -1 | GGCTGCTGTTGACTGAAATTCCTATC CTCAAATTAAGTCTAGACTGAAGCT |
| 5550 | Table 3A | Hs.5897 | AV653169 | 9874183 | cDNA FLJ13388 fis, clone PLACE1001168 /cds=UNKNOWN | -1 | CTTTTGTAGAGCAAGGTTCTTCTTC CTCCTCTTTTGGTGCAGGGACGC |
| 5551 | Table 3A | NA | AV654188 | 9875202 | AV654188 GLC cDNA clone GLCDTC01 3', mRNA sequence | -1 | GCCTGTATGTGGGATGCCATAGGTG TGACTGTAGAGTCATTCTTCTCTCC |
| 5552 | Table 3A | Hs.38218 | AV659358 | 9880372 | 602569369F1 cDNA, 5' end /clone=IMAGE:4693744 /clone_end=5' | -1 | TGTAAGTTGACTTTCAAAGTCTCTG GAAACACTGGACTTTAGCTGGTCC |
| 5553 | Table 3A | Hs.133333 | AV661783 | 9882797 | AV661783 cDNA, 3' end /clone=GLCGXE12 /clone_end=3' | -1 | GAAGCGTGGCAGAGAACTATGGATC AGGCAGCCCTCTCATCTTTACCAT |
| 5554 | Table 3A | Hs.85844 | AV700210 | 10302181 | neurotrophic tyrosine kinase, receptor, type 1 (NTRK1), mRNA /cds=(0,2390) | -1 | TTGGTCCAAACTCTGGAGCCTTGTTG GAGAACATAGGGCATAACGTGTTT |
| 5555 | Table 3A | Hs.285173 | AV700298 | 10302269 | 602632207F1 cDNA, 5' end /clone=IMAGE:4777537 /clone_end=5' | -1 | CCCTTCTTAGTAAAGAGACATCTTCT ACAGTAACCAGAGAGAAGAAGTGG |
| 5556 | Table 3A | Hs.238730 | AV700542 | 10302513 | hypothetical protein MGC10823 (MGC10823), mRNA /cds=(63,1235) | -1 | TGGACATAACCTGGGTGAGAAGAGAA ACTTTTGAAGCTACACGAACAAGC |
| 5557 | Table 3A | Hs.284674 | AV700636 | 10302607 | AV700636 cDNA, 3' end /clone=GKBAGH12 /clone_end=3' | -1 | CGGCTCAAATAAACCTTTACCGGATT TTTGGGGTTATGCCACACCCTTG |
| 5558 | Table 3A | Hs.240077 | AW002624 | 5849540 | wu80d10.x1 cDNA, 3' end /clone=IMAGE:2524435 /clone_end=3' | -1 | GGACCACTAGTACTCCAGAACCATAA TATAACTAGACATGCCTGGAATGC |
| 5559 | Table 3A | Hs.301704 | AW002985 | 5849991 | eomesodermin (Xenopus laevis) homolog (EOMES), mRNA /cds=(0,2060) | -1 | AACAAGCCATGTTTGGCCTAGTCCAG GATTGCCTCACTTGAGACTTGCTA |
| 5560 | Table 3A | NA | AW004905 | 5853768 | wz82d03.x1 NCI_CGAP_Gas4 cDNA clone IMAGE:2565317 3' similar to SW:ATP6_HUMAN P00846 ATP SYNTHASE A | -1 | TCTACTGACTATCCTAGAAATCGCTG TCGCCTTAATCCAAGCCTACGTTT |
| 5561 | Table 3A | Hs.173280 | AW005376 | 5854154 | ws94a12.x1 cDNA, 3' end /clone=IMAGE:2505598 /clone_end=3' | -1 | GAGAAACTTCCGTGCATGAAGGTTTC CTCCTTGACTCGGCAGCAGCGGCC |
| 5562 | Table 3A | Hs.233560 | AW006045 | 5854823 | wz81b09.x1 cDNA, 3' end /clone=IMAGE:2565209 /clone_end=3' | -1 | CCAAGTAGGTTTTAACTCTGGTATGG TCTCGTGTTTTCAATTGTTGTGCA |
| 5563 | Table 3A | Hs.159643 | AW006352 | 5855130 | wt04d12.x1 cDNA, 3' end /clone=IMAGE:2506487 /clone_end=3' | -1 | GTTCCCACGGAGCTGACTTCTCCGG GGTGCCGTGTGCCCTACATTAAACCC |
| 5564 | Table 3A | Hs.231987 | AW006867 | 5855645 | 602320903F1 cDNA, 5' end /clone=IMAGE:4424065 /clone_end=5' | -1 | CCGTAACCTCCGACAAACGCAGAACTT CTTGAGGCTTTCTTCTTCTAAGGA |
| 5565 | db mining | Hs.157118 | AW009081 | 5857859 | ws76g10.x1 cDNA, 3' end /clone=IMAGE:2503938 /clone_end=3' | -1 | TCTGGACCCTGCTTGGGTTTACAGCA TTGGTGGAGGTAAGTAGTATTCTC |
| 5566 | Table 3A | Hs.134272 | AW009671 | 5858449 | ws85g09.x1 cDNA, 3' end /clone=IMAGE:2504800 /clone_end=3' | -1 | GAAGAGGAAGCTCATCCGAAGTCTTC CGACAGAGTGAGCCGTATGCCCG |
| 5567 | db mining | Hs.131887 | AW009730 | 5858508 | 602415255F1 cDNA, 5' end /clone=IMAGE:4523725 /clone_end=5' | -1 | AGTGTGTATTCTTGATGTTTATTGGCT CATGTGGACAGAAATGTACAGGG |
| 5568 | Table 3A | Hs.232000 | AW016002 | 5864759 | UI-H-BI0p-abh-h-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2712035 /clone_end=3' | -1 | AGATGAGGCTGCTCTGAAGATTTCAGT AATTAGGATGGACAGTCAGCTACT |
| 5569 | Table 3A | Hs.233261 | AW026667 | 5880120 | wv15d09.x1 cDNA, 3' end /clone=IMAGE:2529617 /clone_end=3' | -1 | TGGGCTTTGGGGTTTCAGTTTGTACC TTTGGAGACTTATTTAATGAAACC |
| 5570 | Table 3A | Hs.101340 | AW026713 | 5880166 | EST380762 cDNA | -1 | CAGTGGTTCCTGAGAGAATCTTAGTT CAAAGGACTGCCCCCGCCAAACCC |
| 5571 | Table 3A | NA | AW027160 | 5885916 | wt72b08.x1 Soares_thymus_NHFT cDNA clone IMAGE:2512983 3' similar to contains Alu repetitive eleme | -1 | ACCGCCAAAGCCAATCATCCACTTTC AGTACTTACCTAACCAATCTCCCA |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|---|----|---|
| 5572 | Table 3A | Hs.233564 | AW027530 | 5886286 | wv74c06.x1 cDNA, 3' end /clone=IMAGE:2535274 /clone_end=3' | -1 | CAGGATGTTATTGACAGGGTGGCCTT TGTGATTCCTCCGGTGGTGGCAGC |
| 5573 | Table 3A | Hs.311783 | AW043857 | 5904386 | wy81g04.x1 cDNA, 3' end /clone=IMAGE:2554998 /clone_end=3' | -1 | GCCATTTTCATTTGCTGTGTGGTTAGA CTTCCAGGAGGCTGTTAGTCTA |
| 5574 | Table 3A | Hs.277672 | AW050975 | 5913245 | wz25f04.x1 cDNA, 3' end /clone=IMAGE:2559103 /clone_end=3' | -1 | CCTTTGTGAAAAGTCACCTGTGACTG TCAGGGGTATGCTATGGGCCTTTT |
| 5575 | db mining | Hs.279066 | AW063114 | 8887051 | TN0103 cDNA, 3' end /clone_end=3' | -1 | GATCCACTTTGGGGTTCGGCGGCAG ATTATTCCGCTGGTAGAGCCGGATG |
| 5576 | db mining | Hs.279082 | AW063120 | 8887169 | TN0257 cDNA, 3' end /clone_end=3' | -1 | AATAAGGGACTCATTTCATTATGCAGC AAATGTTGTTTGTATTGGCTTGC |
| 5577 | db mining | Hs.279083 | AW063153 | 8887202 | TN0786 cDNA, 3' end /clone_end=3' | -1 | CTTCATGGTCTCCAGCCAGGACTCCA TCAGCGCCACGGCTTCATCCGAAC |
| 5578 | db mining | Hs.279127 | AW063155 | 8887204 | DP1003 cDNA, 3' end /clone_end=3' | -1 | TTGATGCTCATCATCTGCTCGAGGTG ATTGATGCCAGGTTGACGCCACCAT |
| 5579 | db mining | Hs.279104 | AW063156 | 8887205 | TN0974 cDNA, 3' end /clone_end=3' | -1 | TCCTTTGGATAAGGTCCAAAACCTGT AACACATGACCCTCAGAGCCCTTT |
| 5580 | db mining | Hs.279085 | AW063158 | 8887207 | TN0311 cDNA, 3' end /clone_end=3' | -1 | CCCGCGGACTTCACCACCCGCTATCT GGGCACCAAGACTATATCTAGAT |
| 5581 | db mining | Hs.279086 | AW063159 | 8887208 | TN0312 cDNA, 3' end /clone_end=3' | -1 | CGCAATAGTCCTCGACAAGTCGCCAA CCCTCCCACTTCGGTCGATCAGCT |
| 5582 | db mining | Hs.279092 | AW063191 | 8887240 | TN0359 cDNA, 3' end /clone_end=3' | -1 | CGTCGGGTACTTCGCCGATAAAATC GCTGATGGCCTGGTCGATCCTGAAG |
| 5583 | db mining | Hs.279093 | AW063196 | 8887245 | TN0360 cDNA, 3' end /clone_end=3' | -1 | ATCTTATCCCTCTGTTACTCAATGTGA GTGCATACATTTACATTGCCTACT |
| 5584 | db mining | Hs.279102 | AW063210 | 8887259 | TN0377 cDNA, 3' end /clone_end=3' | -1 | GGTCCTTGAAGATGACGCGGATGAT CGAGGTCTCTGCGCGGTAGGCCGATG |
| 5585 | db mining | Hs.279067 | AW063230 | 8887055 | TN0107 cDNA, 3' end /clone_end=3' | -1 | ATGATGAAGCTGCTGTCCAACGCCCT CGCTCGCCAGTTTCTGCTGGTGTG |
| 5586 | db mining | Hs.279069 | AW063239 | 8887064 | TN0018 cDNA, 3' end /clone_end=3' | -1 | TCCTTGGCAGAGCCTTCGGGTTCTAC GATTTGATCGACGACGCTGGTGTG |
| 5587 | db mining | Hs.279070 | AW063242 | 8887067 | TN0138 cDNA, 3' end /clone_end=3' | -1 | TCGAACATGGGCAGCTCCGTTTCAAG ATGGCTCAAGACTAGCGGATTGGG |
| 5588 | db mining | Hs.279071 | AW063246 | 8887071 | TN0358 cDNA, 3' end /clone_end=3' | -1 | AGTGATAGAGACAAAGACTGCTTTT TAATTTTGTGGGGGAGGGGGTGA |
| 5589 | db mining | Hs.279072 | AW063252 | 8887077 | TN0149 cDNA, 3' end /clone_end=3' | -1 | CGGGTCACTCATGTTGGCTACTAACCC CTTTTCGTGCGCGGGCATTCTAG |
| 5590 | db mining | Hs.279087 | AW063267 | 8887092 | TN0331 cDNA, 3' end /clone_end=3' | -1 | CTTGCTCTTGATCGCTTCTCTCTG CAAGGAGAGCTTCTGGACCTTCA |
| 5591 | db mining | Hs.279073 | AW063271 | 8887096 | TN0156 cDNA, 3' end /clone_end=3' | -1 | CTTGTTTGACATCAGCGCCATCTCGA CAGCGTATTCCGCTATGACTGTTT |
| 5592 | db mining | Hs.279074 | AW063274 | 8887099 | TN0792 cDNA, 3' end /clone_end=3' | -1 | CACGAAGCCTTCGATCAGTTGCAGCA CGCGGCCAGAGCGGTGATAGAAC |
| 5593 | db mining | Hs.279122 | AW063299 | 8887124 | TN0185 cDNA, 3' end /clone_end=3' | -1 | CATTTTGCCATCTGCGAGCATCTGGG TATTGACATGATCCCCAGTGGAGC |
| 5594 | db mining | Hs.279076 | AW063319 | 8887144 | TN0230 cDNA, 3' end /clone_end=3' | -1 | CACCAAGCTGGTCAACATCCAGGCG AATGGCTATTACGTGGATGAGATGA |
| 5595 | db mining | Hs.279078 | AW063325 | 8887150 | TN0236 cDNA, 3' end /clone_end=3' | -1 | TTGCTGATACGGCCTTTGATCATGTT TTCAACGATGTTTTCCGGCTTGCC |
| 5596 | db mining | Hs.279079 | AW063327 | 8887152 | TN0238 cDNA, 3' end /clone_end=3' | -1 | CCTCGACAACTAAATGTTGATTGA ATTGGCCTGTTATCATCTTGATCAC |
| 5597 | db mining | Hs.302423 | AW063352 | 8887289 | TN0725 cDNA, 3' end /clone_end=3' | -1 | GTTTCAGATCGGGCGCTCCCGCCG GGTACCTATAGCGGAATCGAATTTT |
| 5598 | db mining | Hs.279095 | AW063358 | 8887295 | TN0979 cDNA, 3' end /clone_end=3' | -1 | GAAAACAGAAATGATGCTCGGCACAT TCTCGTCCAGCACCTCGGCAACGG |
| 5599 | db mining | Hs.279096 | AW063371 | 8887308 | TN0746 cDNA, 3' end /clone_end=3' | -1 | AACTGTATTTCGATCACCGTGGCGCTG ATGGTGTCAGCAGTCGCCTTGTTT |
| 5600 | db mining | Hs.279097 | AW063372 | 8887309 | TN1085 cDNA, 3' end /clone_end=3' | -1 | AGTTGACATATAACCCACTTTACATAC ATTCCAAAATTGCGAGTAGTGAGT |
| 5601 | db mining | Hs.279075 | AW063428 | 8887365 | TN0121 cDNA, 3' end /clone_end=3' | -1 | ATATCGTACCGAGAACTAGTCCGGA TATCTGACCAGGTATGGCGGTTGG |
| 5602 | db mining | Hs.279099 | AW063436 | 8887373 | TN0922 cDNA, 3' end /clone_end=3' | -1 | GTGGATGACCTGATCCAGGTCGGCC TGATCGGCCTGACTGATGAGCTGTC |
| 5603 | db mining | Hs.279100 | AW063458 | 8887395 | TN0949 cDNA, 3' end /clone_end=3' | -1 | ATGATGACCAGATGCTCTGGCACCGT GTCGAGTTTCGAGGATGCCGACATT |
| 5604 | db mining | Hs.279103 | AW063469 | 8887406 | TN0961 cDNA, 3' end /clone_end=3' | -1 | GATCTGGGACGCATGGCCGAAGCTG AAAAGCTGGCTGTAGAAGACCTCGA |
| 5605 | db mining | Hs.279101 | AW063474 | 8887411 | TN0354 cDNA, 3' end /clone_end=3' | -1 | AACATGGCAATATTTATTGTCCTAAT ACTGTCACTGGCAAGGTTGGTGT |
| 5606 | db mining | Hs.279821 | AW063497 | 8887434 | TN0113 cDNA, 3' end /clone_end=3' | -1 | GAGGCAGAGGTGTAGCGAGTCCAGG CTCTCTTCAACGTTGCACCCGACG |
| 5607 | db mining | Hs.279105 | AW063509 | 8887446 | TN1012 cDNA, 3' end /clone_end=3' | -1 | GTCCACACGTTCCGGCCTGACTCT GCTGTGTTCCAGGAGACAATCTCG |
| 5608 | db mining | Hs.279089 | AW063534 | 8887471 | TN1054 cDNA, 3' end /clone_end=3' | -1 | CATGACGTTGTGCTGCACACCCCAAC AGATCACGTAATCAGCCTGGTGGA |
| 5609 | db mining | Hs.279080 | AW063546 | 8887483 | TN0243 cDNA, 3' end /clone_end=3' | -1 | TAGGCTATAGAGATGTGAGGGATTAT TATTAGTCACACCTCTAGTCATGCC |
| 5610 | db mining | Hs.279108 | AW063552 | 8887489 | TN1055 cDNA, 3' end /clone_end=3' | -1 | GGCTGCCGGATGTGTAGGTCTTCCC ATGTTGTGAAGTAACGGTGCTCCAC |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|--|
| 5611 | db mining | Hs.279109 | AW063556 | 8887493 | TN1059 cDNA, 3' end /clone_end=3' | -1 | TGCCCTGTATAGTGTGTAATAAATTA GAATGTTTCACCCAAACCATCTGG GTCTTTTCAATCGCTCTTTAGCTCGT GCGGGCTGTTGTCCCACTTGTGG CTATGCGCTGCGCTACAAGCTGGAC CTGTATTTCGGAAGCTTCACTACTACC TTCGAAGCGACGCTGCGTGCGCTGC TCGTCCAATTGCAGCATGGATAAGG CCTTCCGCTGTCCCTTCAGTAGCTGT TTCTGTTCCCTGACGCCCACTTCT CAATGCAGCGGCTGATCGCATCAC CCACGAGATGCAGGACGAAGGCGAG |
| 5612 | db mining | Hs.279110 | AW063561 | 8887498 | TN1066 cDNA, 3' end /clone_end=3' | -1 | |
| 5613 | db mining | Hs.279090 | AW063572 | 8887509 | TN1079 cDNA, 3' end /clone_end=3' | -1 | |
| 5614 | db mining | Hs.279111 | AW063598 | 8887535 | DP0133 cDNA, 3' end /clone_end=3' | -1 | |
| 5615 | db mining | Hs.302424 | AW063600 | 8887537 | DP0925 cDNA, 3' end /clone_end=3' | -1 | |
| 5616 | db mining | Hs.279124 | AW063609 | 8887546 | DP0922 cDNA, 3' end /clone_end=3' | -1 | |
| 5617 | db mining | Hs.279113 | AW063630 | 8887567 | DP0154 cDNA, 3' end /clone_end=3' | -1 | TCATTCACTCTGAGTAGGAGGAAAGA GGACAGGTTGTTGGAGAGTTGGTT TAATTGCCGCTGAAGCACGAATCCTC GAAATGCGTCACCTTCGGATTGAC AAATGTGGTGACAAAGTACCAGCAAG AACTGGACTGTGTTTCTGGAGCCT GTTTCATCGTCTCGCGTCGCAAGAAGT AAGGGCTAGGCCATGACTCGTTCCG CTCTTGGCAGCCTGCTCTCGTGGG TCAGCATCGTCGCGTGCTCCGCTGG GTGCTCGCTGAGCTGGTCCAGAAAT CCGTGCACTGAGGCGATGGCGGCTG CATGAACAAGGGCCGATCATCCTG ATGCCCAACACACTGGACTTCGGTG CACCCGTTGTAGGCGACGAGCGTGA ACGAAAACGTGTGCGACGCGTTGTA CATATCGCGCTGTGCCATAGCCGGA TGTTCTTCGTGCGTGCTACCCCGG TTCTTCCGTCGCGCATCGGAATGCG AAACTCGTACTTCGTGTAGAACTC GCCAGGGGCTTTATCACTTCCATGGC CGCAGCGATGACCAGGTCAAGCTG CGCCGACCAAGCTTACCAGCTTCTCG CCGATCTACTCGCAGCAAGAAGGC GGTAGTGACGTGCTGAATGACGGTG CCGTCCATCATCGGCTCGGAGTAAG TTCAGGACTCGTTTACGTAAGCAAC GCTGTCTAAAGTTCCTCAAGGGATT CTCTTTACCCGGAACAGGTTGGGGA GATGACACGACAGAAATCATACGC CTTTGGATATATCGAGAAAGGCCAGG GCCTGAACAAGGAAAGCTTCCAGG AAGGCTGGTCAAGAATCTTGACACG GAATTGCACAGTCTCGGCTGATCC GATCGATTCCGGGGTGACATCGGCG CTGAGCACCATCACCGGAACATAAG CTGAGATCACCTGGAACCCGACAG GACGAGATCGCAGTCTGCAACCTG CTGAAGGCTTTGGCGACAACAGGT CTATCCGTTTGAATTTGGCGAGAAC TCTTGTGCCAGCAGCTCTGCTGATA GCCGATGAATCGCGTCCCTTTGTC GAACTCCTCAAGGAAATAGTCCACCG CCTGCTGCTTGACAGCTGCCAGTT GTGACCTCGGGGTCCTTGGTGA GGGTGCCGCTTGTGCGAAGACGAC GTGTTCCGGCTTCATGTCGCCAACAC CATCGGCACTGGGATCATCGATCC AGGTTGATTTCCACTTCCTCGGGAGG TTTCGCCACCTCTTCGCTTTGAG GTTAGCTTCCAGCTTTATCTCCTGC TCTGAGTGTGTACCCGCGCTGCTC TTAAAGTGGTAAGGGAGGTTTCTACT CCTGGGGAACATTAAGTACCTT CTTTCTCCGACTTCGAGATCTGCCCG TGGTCGAGATCGTGGTAGATGATG AACTGGATAGAGCAGACCTTCTAA GCTTGGAGTTGCAAGTTTCCAATCC GAAGATCGGCGCAACGAAGACCGCT TCCACTTCATCAACTGGACCAAGAA TGCTTCTGTGACAGATTAGCTTACAT CTTACCACCTCACCAGAAGAGCT |
| 5618 | db mining | Hs.279114 | AW063635 | 8887572 | DP0774 cDNA, 3' end /clone_end=3' | -1 | |
| 5619 | db mining | Hs.279125 | AW063652 | 8887589 | DP0189 cDNA, 3' end /clone_end=3' | -1 | |
| 5620 | db mining | Hs.279116 | AW063678 | 8887615 | DP0229 cDNA, 3' end /clone_end=3' | -1 | |
| 5621 | db mining | Hs.279117 | AW063709 | 8887646 | DP0336 cDNA, 3' end /clone_end=3' | -1 | |
| 5622 | db mining | Hs.279118 | AW063718 | 8887655 | DP0314 cDNA, 3' end /clone_end=3' | -1 | |
| 5623 | db mining | Hs.279119 | AW063746 | 8887683 | DP0347 cDNA, 3' end /clone_end=3' | -1 | |
| 5624 | db mining | Hs.279120 | AW063778 | 8887715 | DP0954 cDNA, 3' end /clone_end=3' | -1 | |
| 5625 | db mining | Hs.279121 | AW063780 | 8887717 | DP0388 cDNA, 3' end /clone_end=3' | -1 | |
| 5626 | db mining | Hs.279123 | AW063833 | 8887770 | DP0756 cDNA, 3' end /clone_end=3' | -1 | |
| 5627 | db mining | Hs.279138 | AW063909 | 8887846 | SP0953 cDNA, 3' end /clone_end=3' | -1 | |
| 5628 | db mining | Hs.279126 | AW063951 | 8887888 | DP0986 cDNA, 3' end /clone_end=3' | -1 | |
| 5629 | db mining | Hs.279174 | AW063977 | 8887914 | DP1019 cDNA, 3' end /clone_end=3' | -1 | |
| 5630 | db mining | Hs.279128 | AW064020 | 8887957 | DP1073 cDNA, 3' end /clone_end=3' | -1 | |
| 5631 | db mining | Hs.279130 | AW064046 | 8887983 | SP0153 cDNA, 3' end /clone_end=3' | -1 | |
| 5632 | db mining | Hs.279084 | AW064052 | 8887989 | SP0159 cDNA, 3' end /clone_end=3' | -1 | |
| 5633 | db mining | Hs.279825 | AW064053 | 8887990 | SP0992 cDNA, 3' end /clone_end=3' | -1 | |
| 5634 | db mining | Hs.279131 | AW064060 | 8887997 | SP0636 cDNA, 3' end /clone_end=3' | -1 | |
| 5635 | db mining | Hs.279135 | AW064084 | 8888021 | SP0612 cDNA, 3' end /clone_end=3' | -1 | |
| 5636 | db mining | Hs.279136 | AW064098 | 8888035 | SP0575 cDNA, 3' end /clone_end=3' | -1 | |
| 5637 | db mining | Hs.302426 | AW064100 | 8888037 | SP0684 cDNA, 3' end /clone_end=3' | -1 | |
| 5638 | db mining | Hs.279175 | AW064121 | 8888058 | SP0554 cDNA, 3' end /clone_end=3' | -1 | |
| 5639 | db mining | Hs.279139 | AW064129 | 8888066 | SP0696 cDNA, 3' end /clone_end=3' | -1 | |
| 5640 | db mining | Hs.279140 | AW064136 | 8888073 | SP0570 cDNA, 3' end /clone_end=3' | -1 | |
| 5641 | db mining | Hs.279106 | AW064157 | 8888094 | TN1014 cDNA, 3' end /clone_end=3' | -1 | |
| 5642 | db mining | Hs.279141 | AW064160 | 8888097 | SP0594 cDNA, 3' end /clone_end=3' | -1 | |
| 5643 | db mining | Hs.279142 | AW064161 | 8888098 | SP0595 cDNA, 3' end /clone_end=3' | -1 | |
| 5644 | db mining | Hs.279143 | AW064166 | 8888103 | SP0605 cDNA, 3' end /clone_end=3' | -1 | |
| 5645 | db mining | Hs.279144 | AW064175 | 8888112 | SP0615 cDNA, 3' end /clone_end=3' | -1 | |
| 5646 | db mining | Hs.279824 | AW064185 | 8888122 | SP0630 cDNA, 3' end /clone_end=3' | -1 | |
| 5647 | Table 3A | NA | AW064187 | 8888124 | (One single EST, artifact ?) SP0632 KRIBB Human CD4 intrathymic T-cell cDNA library cDNA 3', mRNA sequence | -1 | |
| 5648 | db mining | Hs.279146 | AW064189 | 8888126 | SP0634 cDNA, 3' end /clone_end=3' | -1 | AGCTCAAGAGCTTCCGCGACGTACC CAGCAAAGTAACGCTCGACGAATGC ATCGAAGACGTGATGCTGAACCTTTG GGCGAAGGCCGAGAAGGAAGGCAA |
| 5649 | db mining | Hs.279145 | AW064194 | 8888131 | SP0633 cDNA, 3' end /clone_end=3' | -1 | |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|---|----|---|
| 5650 | db mining | Hs.279147 | AW064201 | 8888138 | SP0650 cDNA, 3' end /clone_end=3' | -1 | CGATACCCCTCACTAGACCTCGGATCG AAATAAATCAGAGCGATCACATCG |
| 5651 | db mining | Hs.279132 | AW064208 | 8888145 | SP0658 cDNA, 3' end /clone_end=3' | -1 | GGGGATACACACCCCAAGCCTTC CTGCGGCTTCATCACGGTTACCACC |
| 5652 | db mining | Hs.279148 | AW064218 | 8888155 | SP0732 cDNA, 3' end /clone_end=3' | -1 | GATCTTGGTGAGAAGCTCGGTCATGT AGAAGACCTCGCCCTGGGACACTA |
| 5653 | db mining | Hs.279826 | AW064223 | 8888160 | SP0676 cDNA, 3' end /clone_end=3' | -1 | ATTTTATCGCCAGCTACGTCGGCATT GGTCAGGACGACCTGAAGGGGAAT |
| 5654 | db mining | Hs.279149 | AW064250 | 8888187 | SP1013 cDNA, 3' end /clone_end=3' | -1 | TGATCGGGAGAGCGAGGTAGATCCC GGCGGAGTTTTCGTCGATGGGAAAG |
| 5655 | db mining | Hs.279150 | AW064255 | 8888192 | SP0105 cDNA, 3' end /clone_end=3' | -1 | GTACACTTCCTGGATCTGATCCACGA GGTAACGAGCGAGAGTGGTGATAC |
| 5656 | db mining | Hs.279134 | AW064258 | 8888195 | SP0717 cDNA, 3' end /clone_end=3' | -1 | GTGACTTCATGCTCGGGGTTGAGCTT GGCGTCCACCACCTTTTCCCACTC |
| 5657 | db mining | Hs.279151 | AW064272 | 8888209 | SP0130 cDNA, 3' end /clone_end=3' | -1 | CCGGTGTCTCTTGATCAGCTTCAGCAG TGGCTTGACGTAGATCGGGTCCGG |
| 5658 | db mining | Hs.302427 | AW064275 | 8888212 | SP1065 cDNA, 3' end /clone_end=3' | -1 | CATCAGTGTCTCTCTGCTGGGACTG TTGCATGTGGTGCATCAGGTTTG |
| 5659 | db mining | Hs.279153 | AW064284 | 8888221 | SP0755 cDNA, 3' end /clone_end=3' | -1 | GCGAGGGCAAACATAGCTTCCATTGT GTCTTTTCTCCTTATGCGTCTTGC |
| 5660 | db mining | Hs.279156 | AW064319 | 8888256 | SP1055 cDNA, 3' end /clone_end=3' | -1 | AATGAGACCCGCGCTCCCTGGAGAT GAAGATGTCGTCGACCTCCGTCAC |
| 5661 | db mining | Hs.279157 | AW064320 | 8888257 | SP1045 cDNA, 3' end /clone_end=3' | -1 | CGGATGTTGCTGTTCCAGAACGAAG GATCGGCCTCTTGGGCTGGATTTC |
| 5662 | db mining | Hs.279164 | AW064343 | 8888280 | SP0916 cDNA, 3' end /clone_end=3' | -1 | GGCAGCGACTTGGGCTGAGAGAGG CGCAGGTCATCAATATAGAATCGGG |
| 5663 | db mining | Hs.279159 | AW064348 | 8888285 | SP1044 cDNA, 3' end /clone_end=3' | -1 | CCATGCTGAACCTGGCCAGGTCCCTTG ACGGCGGTGTTTTCCGACAGCACC |
| 5664 | db mining | Hs.279161 | AW064375 | 8888312 | SP0115 cDNA, 3' end /clone_end=3' | -1 | CGCGATGATCTCGTCTTCGGCATG GCGATGCGCTATTCTTCGACATGG |
| 5665 | db mining | Hs.279162 | AW064377 | 8888314 | SP1066 cDNA, 3' end /clone_end=3' | -1 | GCCCATTGACCGTATCGGTCATCTT GCTGGCATTTCTAAGAAAATACCG |
| 5666 | db mining | Hs.279163 | AW064378 | 8888315 | SP0966 cDNA, 3' end /clone_end=3' | -1 | TGAAACAGGGAAAGCCAGGAAGAT CTCCGGTTCACGTCGAATTTGTAC |
| 5667 | db mining | Hs.279168 | AW064424 | 8888361 | SP1056 cDNA, 3' end /clone_end=3' | -1 | CAAGAAATGACGGAATAATCCGTGAGC ACAAGGCAAAGGCTTCCGCTGTGG |
| 5668 | db mining | Hs.279165 | AW064433 | 8888370 | SP1030 cDNA, 3' end /clone_end=3' | -1 | GACTTGATCAACAACCGATCCGTAAC GACGTATTGGAGCCACTCGAACAA |
| 5669 | db mining | Hs.279166 | AW064445 | 8888382 | SP1042 cDNA, 3' end /clone_end=3' | -1 | CTTCTCGCCGTAACTTTTCCGCCGAG CACGCTACGCACGTAGGTGTTGTG |
| 5670 | db mining | Hs.279823 | AW064450 | 8888387 | SP1048 cDNA, 3' end /clone_end=3' | -1 | TCGACTACGACTTCAACTTCCCAAAA CGGTGGGAGAAGCGAGCTTGAGGC |
| 5671 | db mining | Hs.279167 | AW064452 | 8888389 | SP1069 cDNA, 3' end /clone_end=3' | -1 | AAGTTGATCAGATCACGGGCCACGC CTGCAACCAGAGGCTTGTCTATGTC |
| 5672 | db mining | Hs.279169 | AW064468 | 8888405 | SP1067 cDNA, 3' end /clone_end=3' | -1 | TGATCTGATTGTGAGGAGAGTGGAGA AGGTGGTATAGAAGCTGAAAGGGT |
| 5673 | db mining | Hs.279155 | AW064473 | 8888410 | SP1072 cDNA, 3' end /clone_end=3' | -1 | CTTCATGCTCGAGAAGAAATGCTCC GTGCCTCCGACGACGCCACCATCG |
| 5674 | db mining | Hs.279170 | AW064478 | 8888415 | SP1080 cDNA, 3' end /clone_end=3' | -1 | CAGATGGTCAAGAGACGCTTGTCCG TGATGTCTTCCGTCAGCGTGCAGAG |
| 5675 | db mining | Hs.279171 | AW064479 | 8888416 | SP0147 cDNA, 3' end /clone_end=3' | -1 | TGATGGATTTGGAAGTGTTATTCTG TTTGACTTCTCCCTGCTCTGCTCA |
| 5676 | db mining | Hs.279158 | AW064487 | 8888424 | SP1087 cDNA, 3' end /clone_end=3' | -1 | TTGAACGGGTATAGCCACCAAGGCAT TGGCTGCAAAGTCGGGCAAACTT |
| 5677 | db mining | Hs.330544 | AW064490 | 8888427 | SP1090 cDNA, 3' end /clone_end=3' | -1 | ACTGTGTATTGATGAGTATCTGATGC CTATAACATCTGTAGGAGGCTACA |
| 5678 | db mining | Hs.279160 | AW067725 | 8888472 | SP0110 cDNA, 3' end /clone_end=3' | -1 | GTACGAAGGTGGCGATGATGCGTTC GATCACCTCGGGGATTTCTCGGCG |
| 5679 | db mining | Hs.279129 | AW067742 | 8888489 | SP0150 cDNA, 3' end /clone_end=3' | -1 | CGACCTTCGGCGCTTCCGCTTCGGAA CCCGTGAAGGCGTCTTCACTTTG |
| 5680 | db mining | Hs.279133 | AW067752 | 8888499 | SP0141 cDNA, 3' end /clone_end=3' | -1 | ATTCGCTGGCAACATAATTACCAGAC TCACATCGAAGCAAGCTCGGTTCC |
| 5681 | db mining | Hs.279154 | AW067760 | 8888507 | SP0122 cDNA, 3' end /clone_end=3' | -1 | TGTTGTTGCCATCCTTGTGAGAGAA CATCTCGCTTCCAGTTCGCGCTG |
| 5682 | Table 3A | Hs.89433 | AW071894 | 6026892 | ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant 1, mRNA /cds=(196,4791) | -1 | TTTGGGGGATCCTTTTGTAAATGACTT ACACTGGAATGCGAACATTTGCA |
| 5683 | Table 3A | Hs.299581 | AW073707 | 6028705 | xb01h03.x1 cDNA, 3' end /clone=IMAGE:2575061 /clone_end=3' | -1 | GGACAAGGGGCACCCGGATTATATTT CCCACCAATCCTAATCCTAAACCC |
| 5684 | db mining | Hs.243286 | AW075809 | 6030807 | xa85g05.x1 cDNA, 3' end /clone=IMAGE:2573624 /clone_end=3' | -1 | TGGAGCTTATTTTGGAAGTGTAC CATTTTATCCAGTTGGCAATTTT |
| 5685 | db mining | Hs.277714 | AW075814 | 6030812 | xa85h03.x1 cDNA, 3' end /clone=IMAGE:2573621 /clone_end=3' | -1 | ATTATGGGTAAGGCTTGGGCTTGTTT CCACATGTTAACCAATGGCCTCA |
| 5686 | db mining | Hs.244048 | AW075894 | 6030892 | xa81c04.x1 cDNA, 3' end /clone=IMAGE:2573190 /clone_end=3' | -1 | GGGAGGGCCAAAGAAATCTTTTCCC GTTTCAAATTATGTTCCCAAAAA |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|---|
| 5687 | db mining | Hs.329433 | AW075905 | 6030903 | xa81d05.x1 cDNA, 3' end /clone=IMAGE:2573193 /clone_end=3' | -1 | TTACCCCAATGCTTTTGGCCCGGTGG CCCAGTTTGTAATTGGTTTGATT |
| 5688 | db mining | Hs.329434 | AW075921 | 6030919 | xa81f04.x1 cDNA, 3' end /clone=IMAGE:2573215 /clone_end=3' | -1 | CCCCCCTTGCGCAGGTTAATTGGTGT TAAGGAACCCCTCCAGGGTGGGGGG |
| 5689 | db mining | NA | AW075929 | 6030927 | xa81g05.x1 NCI_CGAP_CML1 cDNA clone IMAGE:2573240 3', mRNA sequence | -1 | CCCCCAGTTTTAATGTTAGGGGGAA GGGATTTAAACCCCTTATTTAAAAAA |
| 5690 | db mining | Hs.265634 | AW075948 | 6030946 | xa82b03.x1 cDNA, 3' end /clone=IMAGE:2573261 /clone_end=3' | -1 | CTATCACCCCTTGATATGAAATCCAG AATTTCTGTGATACCACATGGCC |
| 5691 | db mining | Hs.277716 | AW075986 | 6030984 | xa82f05.x1 cDNA, 3' end /clone=IMAGE:2573313 /clone_end=3' | -1 | ACTCCGGGCCTTAATGGATTGGCCT GTCCTCAAGAATGGTAATTATGAA |
| 5692 | db mining | Hs.241982 | AW076004 | 6031002 | xa82h04.x1 cDNA, 3' end /clone=IMAGE:2573335 /clone_end=3' | -1 | ACGTGGTTTCAGTCCTTAGCACCGTG GTATTGACATGACATCAGTTGCAA |
| 5693 | db mining | Hs.257711 | AW076027 | 6031025 | he31c12.x1 cDNA, 3' end /clone=IMAGE:2920630 /clone_end=3' | -1 | CACAACTTGCTGTTACGCTCTTTGGG GTGTTTTCCATTCTAATAGATGG |
| 5694 | db mining | Hs.277717 | AW076038 | 6031036 | xa83d08.x1 cDNA, 3' end /clone=IMAGE:2573391 /clone_end=3' | -1 | AAACCCGTCCTCCATTATAATTACCTT TCAAAGGGCAAGTCAAAAGTTGT |
| 5695 | db mining | Hs.241983 | AW076068 | 6031066 | xa84a02.x1 cDNA, 3' end /clone=IMAGE:2573450 /clone_end=3' | -1 | AAACAGCACAAACATGAGTGTTCCTA CCACATCAATTTTAATGAAGACAC |
| 5696 | db mining | Hs.277718 | AW076075 | 6031073 | xa84a10.x1 cDNA, 3' end /clone=IMAGE:2573466 /clone_end=3' | -1 | CGGAATCGGGTTTCCATTGGACCCCA AAAATTTCCCTTTGGGCTTCATGA |
| 5697 | db mining | Hs.242605 | AW076083 | 6031081 | xa84b10.x1 cDNA, 3' end /clone=IMAGE:2573467 /clone_end=3' | -1 | TGAGGATAGAAGCAGCCTTTTATATT TTTGTGTGGTAAAGCAAATTGGCA |
| 5698 | db mining | Hs.329436 | AW076127 | 6031125 | xa84g01.x1 cDNA, 3' end /clone=IMAGE:2573520 /clone_end=3' | -1 | GGGGCAAATTTCAAGGGACCTCCCC AAAGGGGGTGTTTTCCCTGGATGGG |
| 5699 | Table 3A | Hs.244816 | AW078847 | 6033999 | xb18g07.x1 cDNA, 3' end /clone=IMAGE:2576700 /clone_end=3' | -1 | AAACAGGAAGGGGGTTTGGGCCCTT TGATCAACTGGAACCTTTGGATCAAG |
| 5700 | Table 3A | Hs.245616 | AW080951 | 6036103 | xc28c10.x1 cDNA, 3' end /clone=IMAGE:2585586 /clone_end=3' | -1 | ACTCTTTGTCTTTTTAAGACCCCTAAT AGCCCTTTGTAACCTTGATGGCTT |
| 5701 | Table 3A | Hs.176498 | AW081098 | 6036250 | xc29a12.x1 cDNA, 3' end /clone=IMAGE:2585662 /clone_end=3' | -1 | CCGGCTGCCTCCATCCAGAAGAGT GCGCAGAGAATTAATCTAGATATT |
| 5702 | Table 3A | NA | AW081232 | 6036384 | xc22e08.x1 NCI_CGAP_Co19 cDNA clone IMAGE:2585030 3' similar to SW:RS1A_HUMAN P39027 40S RIBOSOMAL | -1 | GGGATGTAATACATATTTTTCCAAATA AAATGCCTCATGGGCTTTGGGGC |
| 5703 | Table 3A | Hs.295945 | AW081320 | 6036472 | xc30f12.x1 cDNA, 3' end /clone=IMAGE:2585807 /clone_end=3' | -1 | AGAACCCGTATTCTATAAAATTTAGAC CAAAAAGGAAGGAATCGAACCCCC |
| 5704 | Table 3A | Hs.120219 | AW081455 | 6036607 | xc31c07.x1 cDNA, 3' end /clone=IMAGE:2585868 /clone_end=3' | -1 | AGTTAGTATACAGCCAGAACAGCCAA GCCTCAATTCTGTACCTTGTGTC |
| 5705 | Table 3A | Hs.277738 | AW082714 | 6037866 | xb61f07.x1 cDNA, 3' end /clone=IMAGE:2580805 /clone_end=3' | -1 | CCCTGATCCTCTGTAGGGAACCTTCCT TTTCTCTAATCTAGATCTTTTCA |
| 5706 | db mining | NA | AW088500 | 6044305 | xd10a04.x1 NCI_CGAP_Ov23 cDNA clone IMAGE:2593326 3' similar to SW:BAT3_HUMAN P46379 LARGE PROLINE- | -1 | GAGGCATCAGAGGTTACAGGAGAGTT ACAGGCAGCAGGTGCGGTATAATAT |
| 5707 | Table 3A | Hs.243457 | AW102836 | 6073449 | xd38h12.x1 cDNA, 3' end /clone=IMAGE:2596103 /clone_end=3' | -1 | TTTGTTTCTTTGGGCCTGATTTGTATC TCTGGAAGGCATTAATCTTGAA |
| 5708 | Table 3A | Hs.341908 | AW117189 | 6085773 | xd83f08.x1 cDNA, 3' end /clone=IMAGE:2604231 /clone_end=3' | -1 | GCTTTGCCTCTCGGAGGAGTCAAG GGGCAGTAACTGTATGGGGTGAGAG |
| 5709 | Table 3A | Hs.3642 | AW130007 | 6131612 | RAB1, member RAS oncogene family (RAB1), mRNA /cds=(50,667) | -1 | GCTCCCGAATATTGTAATTTGTTGCC CCCTATGTACCCAACCCCTGAAA |
| 5710 | Table 3A | Hs.248367 | AW131768 | 6133375 | MEGF11 protein (MEGF11), mRNA /cds=(159,3068) | -1 | AGGAAGTATGAGAGTTCTGAAACCCCT TGATAGAACTGGAAGCCTGCCAT |
| 5711 | Table 3A | Hs.203606 | AW131782 | 6133389 | PMO-UT0103-300101-002-f12 cDNA | -1 | GACATAGGGTTGCAGTAGTGAGTGG GCATCTGTTCTCAGAAGGCAGTGCC |
| 5712 | Table 3A | Hs.335449 | AW136717 | 6140850 | UI-H-BI1-adm-a-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2717092 /clone_end=3' | -1 | TTCTGGCCCTTGTTCACCTAGAAACGC TATTTCTGTGTTATGGTTCTGGC |
| 5713 | Table 3A | Hs.8121 | AW137104 | 6141237 | Notch (Drosophila) homolog 2 (NOTCH2), mRNA /cds=(12,7427) | -1 | GCTCTGGGAAAGAGACAGGGAAGTC TGGAATGAAAAGAACACGATGAGA |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|---|
| 5714 | Table 3A | Hs.12035 | AW137149 | 6141282 | 602122419F1 cDNA, 5' end /clone=IMAGE:4279300 /clone_end=5' | -1 | GGGTACATTTGAGTCTCTGTACCTG CTTGAAGAAATAAAAAACGTGT |
| 5715 | Table 3A | Hs.342003 | AW138461 | 6142779 | UI-H-B11-adg-e-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2716882 /clone_end=3' | -1 | CTGGGAATATGAAGCGAACGCCACA CACTAGAACCGCCCTGGGAGCTGG |
| 5716 | Table 3A | Hs.245138 | AW139918 | 6144636 | UI-H-B11-ae-d-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2719136 /clone_end=3' | -1 | GCTGCTTTTGCCCATCCAGTTTCCA CATCCTAATCTTTGCTTTCTTGT |
| 5717 | Table 3A | Hs.276718 | AW148618 | 6196514 | 601473284T1 cDNA, 3' end /clone=IMAGE:3876165 /clone_end=3' | -1 | TGTAAATGTGGTTTGACTATTTCTGTA TGTCCCCATCTATTGATGAGGGT |
| 5718 | Table 3A | Hs.89104 | AW148765 | 6196661 | 602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5' | -1 | TTGTTTTAACAACTCTTCTCAACATTT TGTCCAGTTATTCACTGTAACCA |
| 5719 | Table 3A | Hs.248657 | AW150084 | 6198076 | xg36f03.x1 cDNA, 3' end /clone=IMAGE:2629661 /clone_end=3' | -1 | ACATAAACTGTCCCTTTAGGAAGAAG CCCAATGCCCGATTTCGCCCTTTA |
| 5720 | Table 3A | NA | AW150085 | 6198077 | xg36f04.x1 NCL_CGAP_Ut1 cDNA clone IMAGE:2629663 3' similar to gb:X65018 PULMONARY SURFACTANT-ASSOC | -1 | GGACAAGTGGCATCGGTACTATATTT CCCACCAATCCTAATCCTAATCCC |
| 5721 | Table 3A | Hs.265838 | AW150944 | 6198842 | xg42e09.x1 cDNA, 3' end /clone=IMAGE:2630248 /clone_end=3' | -1 | TATGTCCCTTTTCTCCTCCCTTCCCC ATTCCCTGGCATCATATTGGGAC |
| 5722 | Table 3A | Hs.301104 | AW151854 | 6199839 | 602313002F1 cDNA, 5' end /clone=IMAGE:4422480 /clone_end=5' | -1 | CGCTGTCGCCTTAATCCAAGCCTACG TTTTACACTTCTAGTAAGCCTCT |
| 5723 | Table 3A | Hs.337727 | AW161820 | 6300853 | au70h03.x1 cDNA, 3' end /clone=IMAGE:2781653 /clone_end=3' | -1 | TGTGGGCTTGGTATAAACCCCTACTTT GTGATTTGCTAAAGCACAGGATGT |
| 5724 | Table 3A | Hs.299967 | AW166001 | 6397526 | xf43e11.x1 cDNA, 3' end /clone=IMAGE:2620844 /clone_end=3' | -1 | CCGCCTGAAACGGGCATTTTGAAAT GGGGTTGACTATTTTGTATGTC |
| 5725 | Table 3A | Hs.81248 | AW166442 | 6397967 | CUG triplet repeat, RNA-binding protein 1 (CUGBP1), mRNA /cds=(137,1585) | -1 | ACTGGCAAATGAAGCATACTGGCTTG CAGGGACCTTCTGATTCAAGTACA |
| 5726 | Table 3A | Hs.169738 | AW172306 | 6438254 | xj37a08.x1 cDNA, 3' end /clone=IMAGE:2659382 /clone_end=3' | -1 | GAATTCGATTTGAGATCTGAGGGCAG ACCCGAACCAGGAAAGCAACTCAG |
| 5727 | Table 3A | Hs.8991 | AW172850 | 6438798 | adaptor-related protein complex 1, gamma 2 subunit (AP1G2), mRNA /cds=(45,2402) | -1 | AATGCACCAGGCTGCCACCTGCACC AGTGGTTGCTACATGGGATAAGAAA |
| 5728 | Table 3A | Hs.143525 | AW173163 | 6439111 | xj84b08.x1 cDNA, 3' end /clone=IMAGE:2663895 /clone_end=3' | -1 | TATGATAGGATTCTCCACAGTGGCTT CCGACTCAGGCTCCAATGGACCAA |
| 5729 | Table 3A | Hs.38664 | AW188135 | 6462571 | IL0-MT0152-061100-501-e04 cDNA | -1 | TGCTGTATGGGCAGGTTGTCTTATTA TGTGATCAACAGATGTCCAGGAAC |
| 5730 | Table 3A | NA | AW188398 | 6462834 | xj98c03.x1 NCL_CGAP_Co18 cDNA clone IMAGE:2665252 3', mRNA sequence | -1 | ACCTCCAAGAACATCTGCCTTTGTG AACGTGTTATTACCTGTCCACTC |
| 5731 | Table 3A | Hs.252989 | AW191929 | 6470628 | xl77c10.x1 cDNA, 3' end /clone=IMAGE:2680722 /clone_end=3' | -1 | CCTTTTGCCCTTAGCCCTTGATAA TCCGGCTGGGAATGGGGTGAGGG |
| 5732 | Table 3A | Hs.203755 | AW194379 | 6473179 | xm08h07.x1 cDNA, 3' end /clone=IMAGE:2683645 /clone_end=3' | -1 | CCCAAATAAGCTCTGTACTTCGGTTA CCTATGTACCTGTTACCACTTTCA |
| 5733 | Table 3A | Hs.253151 | AW195119 | 6474139 | xn66b07.x1 cDNA, 3' end /clone=IMAGE:2699413 /clone_end=3' | -1 | GCCACATGTCTCTATTCTCACACAGGT GCTTTAATTCAGCCAGTCTCTA |
| 5734 | db mining | Hs.253154 | AW195169 | 6474211 | xn66h03.x1 cDNA, 3' end /clone=IMAGE:2699477 /clone_end=3' | -1 | CTTGAAGGGGCTTTGTTGGGTTTTTG GGGTTTTGGGTGGGACTCCCAAAG |
| 5735 | db mining | Hs.330019 | AW195270 | 6474330 | xn67c04.x1 cDNA, 3' end /clone=IMAGE:2699526 /clone_end=3' | -1 | GGGGTTTTAAAAATTTCCCGATTTC AAATTAATTTCCGTTGCCCCCGG |
| 5736 | db mining | Hs.253167 | AW195284 | 6474352 | xn67d09.x1 cDNA, 3' end /clone=IMAGE:2699537 /clone_end=3' | -1 | CCCCCTGGGGTTTTTGGGAATGAGG TAAGGCTTTGAATTTGGTTTGATAT |
| 5737 | db mining | Hs.253168 | AW195300 | 6474368 | xn67f12.x1 cDNA, 3' end /clone=IMAGE:2699567 /clone_end=3' | -1 | ACATGCTTAGAGCTGGAGGCTTGAAA CCATAATCCCAATTAAGTGCTGTC |
| 5738 | db mining | Hs.253169 | AW195313 | 6474381 | xn67h05.x1 cDNA, 3' end /clone=IMAGE:2699577 /clone_end=3' | -1 | TGTTTGTCCAGGAAAAGGAAGAGGG GGAAATTAACCTTTCCGGTTAGT |
| 5739 | Table 3A | Hs.253384 | AW204029 | 6503501 | UI-H-B11-aen-d-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2719899 /clone_end=3' | -1 | GCACTGCTCCGTCTAGCTGTATGACC TTTGTTATGTTCTTTCTTCCGT |
| 5740 | Table 3A | Hs.253502 | AW205624 | 6505098 | UI-H-B11-afr-e-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2722657 /clone_end=3' | -1 | CTTCAATCTGGGCTGGGCACTCCAC GCACATAATCGTCACTCTGGAGGA |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|---|----|---|
| 5741 | Table 3A | Hs.330058 | AW206977 | 6506473 | UI-H-BI1-afs-h-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2723180 /clone_end=3' | -1 | GCGGGAAGTGAAAGCGGAGGCTGGG ACAAGGGGAACCTTACTGCTCAAAAA |
| 5742 | Table 3A | Hs.157315 | AW207701 | 6507197 | UI-H-BI2-age-e-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2724172 /clone_end=3' | -1 | AGTGGTGTGGTGGAATAGGAAAAAG AAAAGATCAGGATGAGAAATTGCTT |
| 5743 | db mining | NA | AW236186 | 6568575 | xn70e07.x1 NCI_CGAP_CML1 cDNA clone IMAGE:2699844 3', mRNA sequence | -1 | CCAAGGGCCCTTTTGGGGTTGTTTCCT ATAACTTCAGTATTGTAAATTAGT |
| 5744 | db mining | NA | AW236203 | 6568592 | xn70h07.x1 NCI_CGAP_CML1 cDNA clone IMAGE:2699869 3', mRNA sequence | -1 | CATAAAGGGGCATTGCCCTAGCCGG TCCGGCCTTTTCCAGTCCATCCTG |
| 5745 | db mining | Hs.330063 | AW236208 | 6568597 | xn71a06.x1 cDNA, 3' end /clone=IMAGE:2699890 /clone_end=3' | -1 | AGGTTTAAGAAATTTCCCTAAATCTT GTTTGGTTGGTTGGGATGAAAAGT |
| 5746 | db mining | Hs.253747 | AW236252 | 6568641 | xn71g08.x1 cDNA, 3' end /clone=IMAGE:2699966 /clone_end=3' | -1 | AATTGATCCCATTCTTGCTGAAGTAG ACAGTGCCCTCAAGTGAATTA |
| 5747 | db mining | Hs.253748 | AW236271 | 6568660 | xn72b03.x1 cDNA, 3' end /clone=IMAGE:2699981 /clone_end=3' | -1 | CTCCAATGCTGTTATCCCGCTGGGT CCTCACACTCCCCCAACAATCCCA |
| 5748 | db mining | NA | AW236345 | 6568734 | xn73c12.x1 NCI_CGAP_CML1 cDNA clone IMAGE:2700118 3' similar to contains element MER21 repetitive e | -1 | AGAATGCGCTATTTCCCTCAAAGCCC TGGCTGTAATAAAGAAGCCGATTT |
| 5749 | Table 3A | Hs.253820 | AW237483 | 6569872 | xm72e01.x1 cDNA, 3' end /clone=IMAGE:2689752 /clone_end=3' | -1 | CTGAGGTCAGTGTGGTTTGGTGGAA GGATTATGATATTTACAAGCTGAGT |
| 5750 | Table 3A | Hs.342342 | AW243795 | 6577635 | xo56f02.x1 cDNA, 3' end /clone=IMAGE:2707995 /clone_end=3' | -1 | GGTCAATGTTTTGAAATTTGTGGAGC AAACCCAGTTTTATGCCCTTGGT |
| 5751 | Table 3A | Hs.250591 | AW262077 | 6638893 | xp19e09.x1 cDNA, 3' end /clone=IMAGE:2740840 /clone_end=3' | -1 | AGTTGGAAAAATTTAGAAATGTCCACT GTAGGACGTGGAATATGGCGTCGA |
| 5752 | db mining | Hs.250591 | AW262272 | 6639088 | xp19e09.x1 cDNA, 3' end /clone=IMAGE:2740840 /clone_end=3' | -1 | TTACAGTCCTAAAGTGTGGTAGACGC GCCCGCGAATTTAGTAGTAGTAGG |
| 5753 | Table 3A | Hs.277994 | AW262728 | 6639544 | xq94a12.x1 cDNA, 3' end /clone=IMAGE:2758270 /clone_end=3' | -1 | GGACAAGTGCGATCCGTATTATATTT CCCACCATTCCTATTCTTAATCCC |
| 5754 | db mining | Hs.61345 | AW262891 | 6639707 | mRNA for KIAA1154 protein, partial cds /cds=(0,676) | -1 | GGTCTGCCTCAGTCTTCTACTCATCA GCACCACACTGTCAAATGTTGGA |
| 5755 | Table 3A | Hs.5662 | AW264291 | 6641033 | guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 (GNB2L1), mRNA /cds=(95,1048) | -1 | AGATGAATTGAAGCAAAAAGTTTTC GTACCAGCAGCAAGGCAGACCCCC |
| 5756 | Table 3A | Hs.122655 | AW274156 | 6661186 | hypothetical protein MGC14425 (MGC14425), mRNA /cds=(318,686) | -1 | TCACCTCCACCTCTGAGGGAGCAAC GAATACAAAGGTAGACCCCAAAAG |
| 5757 | Table 3A | Hs.250600 | AW291304 | 6697940 | UI-H-BI2-agk-a-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2724386 /clone_end=3' | -1 | CCCCAGCCAGCACTTCCCTTTTCTGC GAGGGTTTCTGTTCTTTGATTA |
| 5758 | Table 3A | Hs.47325 | AW291458 | 6698021 | UI-H-BI2-agh-c-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2724099 /clone_end=3' | -1 | AGAAAATTTGAACCCCTACGCTTCTCC CATCCCACTTCTTACTCCATCCCG |
| 5759 | Table 3A | Hs.170381 | AW291507 | 6698143 | UI-H-BI2-aga-g-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2723900 /clone_end=3' | -1 | CTGTGGCATCATTACACCACCAGCA GAGTCCCTTCCAAGAGGGGTCTGG |
| 5760 | db mining | Hs.255118 | AW292757 | 6699393 | UI-H-BW0-aij-b-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729423 /clone_end=3' | -1 | CCGTGTTAAACCAAGTTTGGGATT TTTCGGGTATTCTTGGGAAGTCAC |
| 5761 | Table 3A | Hs.255119 | AW292772 | 6699408 | UI-H-BW0-aij-d-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729501 /clone_end=3' | -1 | CGAGAGCCTGGAAGCTTTGCACACTA CTGCCTGGAAGATCTGATTCTTTG |
| 5762 | db mining | Hs.255123 | AW292814 | 6699450 | UI-H-BW0-aij-h-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729691 /clone_end=3' | -1 | TGTTTTAAAGTGGGTTTATTCAACC CCTTCACTCCCGTTGGTGACCG |
| 5763 | db mining | Hs.255129 | AW292855 | 6699491 | UI-H-BW0-aif-d-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729117 /clone_end=3' | -1 | TCTTCTCTCAGTCTTCAAGTAGC TTCTTTCAGAACTGCCTCCTCCCG |
| 5764 | db mining | Hs.255544 | AW292873 | 6699509 | UI-H-BW1-ame-e-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069784 /clone_end=3' | -1 | GTTTTCTGCATCCCAATGTCCTGGG GCATGTGTCCCTTCTTGCTGACC |
| 5765 | db mining | Hs.255134 | AW292900 | 6699536 | UI-H-BW0-aig-a-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729000 /clone_end=3' | -1 | TGTTATGATTCTCTCAATTTATAAAG CTCTTCTGGCAGAGGAGACAGAT |
| 5766 | db mining | Hs.255135 | AW292902 | 6699538 | UI-H-BW0-aig-a-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729004 /clone_end=3' | -1 | AAATGGATTACAATTTCCCTGACATTT GGGCATAAAACATCTGCCATCCT |
| 5767 | db mining | Hs.255139 | AW292928 | 6699564 | UI-H-BW0-aig-d-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729156 /clone_end=3' | -1 | TCCTCCTCCAGAGACCTTTGCTTTA CTGCCATTTTCTGTGGGCTTTT |
| 5768 | db mining | Hs.255140 | AW292941 | 6699577 | UI-H-BW0-aig-f-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729250 /clone_end=3' | -1 | AGGCATAGCAGTAGAATCTGTCAAAA AGGAGGCATGGAATGAATGAACC |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|---|
| 5769 | db mining | Hs.255142 | AW292960 | 6699596 | UI-H-BW0-aih-a-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2728995 /clone_end=3' | -1 | CTGACCCTCTCGCCCTCCACCTGTG CTTCTGCCCTAGGATAACGCTGGG |
| 5770 | db mining | Hs.147728 | AW292989 | 6699625 | RST12623 cDNA | -1 | GACCCAAAGAAAAGATCAAGACCGCA TGAGCAAATGTAGCAAGGAGGCA CTAATTTCCCACTAAAAGGTCAGAA AAATTGATGCCACCTGTAGTTTGG |
| 5771 | db mining | Hs.255152 | AW293001 | 6699637 | UI-H-BW0-aih-d-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729159 /clone_end=3' | -1 | GTAAGATTCCAAGCGAGTGGAAGGTA AATCAGACTGTGGCACC GGAGCC |
| 5772 | db mining | NA | AW293017 | 6699653 | UI-H-BW0-aih-f-06-0-UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2729243 3', mRNA sequence | -1 | GAACTGAATGACCATGGAATGCTGA AATTCCAAAGAAAAACGTCGCGC |
| 5773 | db mining | NA | AW293143 | 6699779 | UI-H-BW0-aih-a-03-0-UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2729356 3', mRNA sequence | -1 | TCTCTCAGGTCGTCTTCAGAGTCCAT TCCCTTTGTCTTGATCTTTCTCT |
| 5774 | db mining | Hs.255172 | AW293158 | 6699794 | UI-H-BW0-aih-b-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729412 /clone_end=3' | -1 | CTCCCATCATTCCTCCCGAAAGCCA TTTTGTTCAAGTTGCTCATCCACGC GCCCTGCCCTTACCCTTGCCCTTTA AATTTTGGGACTGAATAAAGAAAT |
| 5775 | Table 3A | Hs.166975 | AW293159 | 6699795 | splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(218,541) | -1 | TGCAGGATAACTTGCTCATGAAAGGA AATGCCAGATTAAACCCCTTGCCA |
| 5776 | db mining | Hs.255174 | AW293172 | 6699808 | UI-H-BW0-aih-c-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729466 /clone_end=3' | -1 | GCCTTCCCTTCGTTCTTCCAGGCA ATAATGACATCATTAGTGATGCAA CGCCACGGCTCCAATCCCTATATGAG TGAGCAGTAGAATCACATAGGAAT |
| 5777 | Table 3A | Hs.255178 | AW293267 | 6699829 | UI-H-BW0-aih-e-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729562 /clone_end=3' | -1 | CCTAGAATCAGACTTTAAGCACAAAGC AGGGAGGGAAAGCACITGAGCAGT |
| 5778 | Table 3A | Hs.75354 | AW293424 | 6700060 | mRNA for KIAA0219 gene, partial cds /cds=(0,7239) | -1 | GCACATGCAAAAACCTCAGATGTGCAA ATAACTGTTCCCTATTAACACAA |
| 5779 | Table 3A | Hs.255200 | AW293426 | 6700062 | UI-H-BI2-ahm-b-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2727122 /clone_end=3' | -1 | GGTGCTCAAAGTGTATTTCTCCCTC CCTCCCTCCTTCTTCTTCCAGA |
| 5780 | Table 3A | Hs.10041 | AW293461 | 6700097 | 602713308F1 cDNA, 5' end /clone=IMAGE:4853616 /clone_end=5' | -1 | TTCTTCCACGGGATTCTAATTCATTA AATAGGACCTCCACACCAGACCT |
| 5781 | db mining | Hs.291317 | AW293859 | 6700495 | nx40e10.s1 cDNA, 3' end /clone=IMAGE:1258602 /clone_end=3' | -1 | TATCCAGCCTGACTTCTTCATGCTGT ACTAGCCTTCCAATCCTTAACATA |
| 5782 | Table 3A | Hs.255249 | AW293895 | 6700531 | UI-H-BW0-aih-f-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729995 /clone_end=3' | -1 | TGGACATTGGGGGTCAAACCCCTTTTG TTTAAATTTTCCCTTCCAGGGC |
| 5783 | db mining | Hs.255251 | AW293922 | 6700558 | UI-H-BW0-aih-a-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729382 /clone_end=3' | -1 | GCTGTGCCACGGTCAGGTGGCTTCC AATCTGTACTCAATTGTTACTGTAC |
| 5784 | db mining | Hs.255253 | AW293949 | 6700585 | UI-H-BW0-aih-c-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729490 /clone_end=3' | -1 | TCAGAGATGCTGATGTCATATAAGTA GTTTCCCTGTCTGGCCTTGGATGT |
| 5785 | db mining | Hs.255254 | AW293950 | 6700586 | UI-H-BW0-aih-c-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729492 /clone_end=3' | -1 | GTATGACTGATGATGCTGCGAATGA GGAGGAGGGAAGGGAAGGCTGGAG |
| 5786 | Table 3A | Hs.255255 | AW293955 | 6700591 | UI-H-BW0-aih-d-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729528 /clone_end=3' | -1 | CCATTGCCCGGTGTTTTGGTTTAAT TTTCCAGGCTATTTTTAAAGGCC |
| 5787 | Table 3A | Hs.190904 | AW294083 | 6700729 | UI-H-BI2-ahg-b-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2726720 /clone_end=3' | -1 | AGGAAATTAACATGAGCATGACATG ACCCCAACTCTCAAGAAATCCCA |
| 5788 | db mining | Hs.255330 | AW294618 | 6701254 | UI-H-BW0-aih-a-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729385 /clone_end=3' | -1 | ATCAGGTCCCTACAAAATTAGCTAC TTTGGCCTTCTACAAAATTAGC |
| 5789 | db mining | Hs.255333 | AW294644 | 6701280 | UI-H-BW0-aih-c-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729493 /clone_end=3' | -1 | TCATTGTTTGTCTTCTCTGACTGACA GGCAGTAATGACTTCAATAAGCT |
| 5790 | Table 3A | Hs.255687 | AW294654 | 6701290 | UI-H-BW0-aih-d-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729539 /clone_end=3' | -1 | AGGGCCTGCTTCAGAGTTTGTTCCT AAATAAAACATGGCTCTCCCGT |
| 5791 | Table 3A | Hs.255336 | AW294681 | 6701317 | UI-H-BW0-aih-g-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729683 /clone_end=3' | -1 | CCCCCACTTACATGGAAAAGGGATG GTTGCATTCTGTGCATATGCAT |
| 5792 | db mining | Hs.255337 | AW294692 | 6701328 | UI-H-BW0-aih-h-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729733 /clone_end=3' | -1 | GCAGAGGGAAGAGGAAATGCTTTGA AGCCTTGCTAGTTATTTAATTAGTT |
| 5793 | Table 3A | Hs.255339 | AW294695 | 6701331 | UI-H-BW0-aih-a-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729738 /clone_end=3' | -1 | GACATAGTTGCAAAACACAATACTTA ATACTTTTCTGGAGAGGGGGCC |
| 5794 | db mining | Hs.255341 | AW294697 | 6701333 | UI-H-BW0-aih-a-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729742 /clone_end=3' | -1 | |
| 5795 | db mining | Hs.342539 | AW294717 | 6701353 | UI-H-BW0-aih-g-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732333 /clone_end=3' | -1 | |
| 5796 | db mining | Hs.255347 | AW294739 | 6701375 | UI-H-BW0-aih-f-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729988 /clone_end=3' | -1 | |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|---|
| 5797 | db mining | Hs.255354 | AW294769 | 6701405 | UI-H-BW0-ail-g-02-0-UI.s2 cDNA, 3' end /clone=IMAGE:2729667 /clone_end=3' | -1 | ACCCCTTTTCTTAATTTCTCAGGAAAA TGGCAGCTCCTTCTTTGTCTGTC |
| 5798 | db mining | NA | AW294812 | 6701448 | UI-H-BI2-ahi-d-06-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2726842 3', mRNA sequence | -1 | CCTCCGGTGTCTTCGGAAGCACTGAA GGGACATCTGGGGACCTCACCTG |
| 5799 | db mining | Hs.255388 | AW295071 | 6701707 | UI-H-BW0-ait-c-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730245 /clone_end=3' | -1 | ACTCTTTGACCAATAAATCACTGGAA TAGAGGTTCCAGCATATTCTGAGA |
| 5800 | Table 3A | Hs.255389 | AW295088 | 6701724 | UI-H-BW0-ait-d-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730305 /clone_end=3' | -1 | ATGCTTACACCCTGGATGAATAAAGT CTTTATTTACACCTCCACCTCCCC |
| 5801 | db mining | Hs.255157 | AW295376 | 6702012 | UI-H-BI2-ahv-f-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2728085 /clone_end=3' | -1 | CTCTTCACAGGTCATAAGCCCTCTG AGCGGCGACAGTCCTCGCATCCAG |
| 5802 | db mining | Hs.330175 | AW295597 | 6702233 | UI-H-BW0-aip-a-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729779 /clone_end=3' | -1 | CAGCTCGACCTCAGTCCCTTCAGAA ATAAGATGGCGGCTCGCTGACAG |
| 5803 | Table 3A | Hs.255446 | AW295610 | 6702246 | UI-H-BW0-aip-c-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729861 /clone_end=3' | -1 | TTTCAACGTGTACCTTTCCTGGGAAA CCATCTCAATAAACACATTTTGGT |
| 5804 | db mining | Hs.255448 | AW295616 | 6702252 | UI-H-BW0-aip-c-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729873 /clone_end=3' | -1 | GCTGGACACATGGGTTAAGAGGAGG AAAAGTAGGAAAGGAGGAGGGGAAA |
| 5805 | db mining | Hs.255449 | AW295629 | 6702265 | UI-H-BW1-amu-a-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:3071128 /clone_end=3' | -1 | GGCTGGGACCAGGGTTTTTCAAGCC ACCTTTTCTGTCTCAGTTCAGAGA |
| 5806 | Table 3A | Hs.255454 | AW295664 | 6702300 | UI-H-BW0-aip-g-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730071 /clone_end=3' | -1 | CCCACTTTACACATGACTCACACGA CTGAAGGAAAGAAAGGGCATCCTT |
| 5807 | db mining | Hs.255455 | AW295669 | 6702305 | UI-H-BW0-aip-h-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730107 /clone_end=3' | -1 | AAGAAATTAAGGAAGGCAAGAGGGTA GGTGTGGCCCATGGAAGTTTCCC |
| 5808 | db mining | Hs.255457 | AW295688 | 6702324 | UI-H-BW0-aip-b-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730578 /clone_end=3' | -1 | CTGGCAAATATTGCGGAAGATGTACT GAAATGTAATTGAAATGTAGCTGC |
| 5809 | db mining | Hs.255459 | AW295711 | 6702347 | UI-H-BW0-aip-d-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730676 /clone_end=3' | -1 | AGCATAAGAGATACGAAGCTGATGGT AATTAACCTGTACCCCTTGAAGTG |
| 5810 | db mining | Hs.255462 | AW295724 | 6702360 | UI-H-BW0-aip-e-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730734 /clone_end=3' | -1 | AGTGTGACACAATTAGATACTCTTTC CTGTCTTCAGGAGCCCATCTGGAA |
| 5811 | db mining | Hs.255464 | AW295731 | 6702367 | UI-H-BW0-aip-f-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730776 /clone_end=3' | -1 | GAAGTGTAACATGCCAACAGGGTTT ATATTTAGGTTCCAAGAGTTGCCA |
| 5812 | Table 3A | Hs.156814 | AW295965 | 6702531 | KIAA0377 gene product (KIAA0377), mRNA /cds=(126,4346) | -1 | CTTCCCAAATCCATTGTCTCATTCTC ACTGCTTATGTTATTGCTCTTAT |
| 5813 | Table 3A | Hs.255492 | AW296005 | 6702641 | UI-H-BW0-aip-b-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730552 /clone_end=3' | -1 | CCCACACAGCAGAGAAGTATCAGAAA ACATAGAAACATGTGAAATGCGC |
| 5814 | db mining | Hs.255495 | AW296020 | 6702656 | UI-H-BW0-aip-c-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730612 /clone_end=3' | -1 | AGGTTCAATTCATTTCTGAGATGTT TGGTTTATAAGATTGAGGATGGT |
| 5815 | db mining | Hs.255497 | AW296044 | 6702680 | UI-H-BW0-aip-e-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730714 /clone_end=3' | -1 | ATACTTAGATGTGCTTGATCCTGGG TGGGAGGCTTGGTTAGAAGTCACG |
| 5816 | db mining | Hs.255498 | AW296054 | 6702690 | UI-H-BW0-aip-f-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730762 /clone_end=3' | -1 | TGGGTGACGCTGTTCATTTTAAATA GGAATACACTAGCCTTACAACGGA |
| 5817 | db mining | Hs.255499 | AW296058 | 6702694 | UI-H-BW0-aip-g-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730794 /clone_end=3' | -1 | TGTTTCATCTGATGTAATAGAGAAGG AAAGAGAGAGCATCCCTTTTCAGT |
| 5818 | Table 3A | Hs.255501 | AW296063 | 6702699 | UI-H-BW0-aip-g-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730806 /clone_end=3' | -1 | ACCAGTAACACAATGACGGCAAGCAC AGAGAAGGAAAAAGTCAGATCCCC |
| 5819 | db mining | Hs.255502 | AW296066 | 6702702 | UI-H-BW0-aip-g-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730812 /clone_end=3' | -1 | ACTTGGAGCTAGAGAGCCACCCATCA TATGGAGGAGAAGTGGTCACTCTA |
| 5820 | db mining | Hs.34871 | AW296352 | 6702988 | zinc finger homeobox 1B (ZFX1B), mRNA /cds=(444,4088) | -1 | TGCATGTGTGTTGTGTACTTGTCTGT TCTGTAAGATTGTCGGTGTACAC |
| 5821 | db mining | Hs.255543 | AW296373 | 6703009 | UI-H-BW0-aio-c-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729874 /clone_end=3' | -1 | TTCTGGCAGTAAAGAAAAGAAAGAA GATGTGAGTTATGAAGCATTGACT |
| 5822 | db mining | Hs.255546 | AW296398 | 6703034 | UI-H-BW0-aio-f-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730000 /clone_end=3' | -1 | AAATAGGAATATAATCTGTCCACATC AAGAATGGGAAGTCGAAGTGATACA |
| 5823 | db mining | Hs.255549 | AW296404 | 6703040 | UI-H-BW0-aio-f-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730014 /clone_end=3' | -1 | GTTCCAAATGTTTTCCGCTAATAGTTT GTCCTAAAGCCTTTGCCATTCT |
| 5824 | db mining | Hs.255552 | AW296446 | 6703082 | UI-H-BW0-aip-b-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730180 /clone_end=3' | -1 | ACAGAGAAGGCTTATTTACGTTGGGA ATTACATTAAGGAAAAGTGGTGAC |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|---|
| 5825 | Table 3A | Hs.255554 | AW296490 | 6703126 | UI-H-BW0-aiq-f-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730374 /clone_end=3' | -1 | CCTTCCTCCTATATCCTGCCTTGAAT AGGGATGTGATACCTTGAGCCATG |
| 5826 | db mining | Hs.255556 | AW296504 | 6703140 | UI-H-BW0-aiq-g-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730430 /clone_end=3' | -1 | ATATTTGGGTCTCTGTTTAAAGATTTC TTGCCGTGGTAGGGAGAGTTCCA |
| 5827 | db mining | Hs.255558 | AW296511 | 6703147 | UI-H-BW0-aiq-h-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730470 /clone_end=3' | -1 | TGGATGCCATGATGACACCAATAAGC AACCCACAGATTAGGGGAAATACT |
| 5828 | Table 3A | Hs.255559 | AW296532 | 6703168 | UI-H-BW0-aiv-b-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730565 /clone_end=3' | -1 | GGGGCTGGGAGCCACCAAAGGGCC TGCTCTTCGGAGAAATGCTGAATTC |
| 5829 | Table 3A | Hs.255560 | AW296545 | 6703181 | UI-H-BW0-aiv-c-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730621 /clone_end=3' | -1 | AGGCATCTTGAAAGTTCCATAAAGAC AGAAGTAAGGGTCATTCACTCATT |
| 5830 | db mining | Hs.255561 | AW296567 | 6703203 | UI-H-BW0-aiv-f-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730751 /clone_end=3' | -1 | AGCTAAAGCCACGGAACCTCAATGAGA TTTATGCATGGAAGGAAACAGGTT |
| 5831 | db mining | Hs.255569 | AW296695 | 6703331 | UI-H-BW0-aix-c-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730635 /clone_end=3' | -1 | TGTTCTCTCTCGAACTCTGGAGCACA TCAGCTCTCTCTGCATAAAGTGT |
| 5832 | db mining | Hs.255572 | AW296727 | 6703363 | UI-H-BW0-aix-f-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730785 /clone_end=3' | -1 | ATCTGGAGGATGGCAGTTTGAGAAAT AGGACTAAGCCCGTCTCCCCCTTG |
| 5833 | Table 3A | Hs.255573 | AW296730 | 6703366 | UI-H-BW0-aix-g-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730791 /clone_end=3' | -1 | CATTAGCTCTCTAAACATTTGGCCTA AGGGATTCTAGGTGAAGCCTTTA |
| 5834 | db mining | Hs.255575 | AW296758 | 6703394 | UI-H-BW0-ajb-a-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730931 /clone_end=3' | -1 | GGTAGGATTTATCCTTTTCTTCATGTG CAACTGTATAAACTGGCAAAGCA |
| 5835 | db mining | Hs.255577 | AW296773 | 6703409 | UI-H-BW0-ajb-c-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731015 /clone_end=3' | -1 | AGTCTTATGGGACAGAGCAGCTCTCC AGTCTAGGATGGTAGAAGATTCTT |
| 5836 | Table 3A | Hs.255579 | AW296797 | 6703433 | UI-H-BW0-ajb-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731117 /clone_end=3' | -1 | GAGTCTGTACCCCTTTCTAATAAACT GCTCTGGACACAATGAACCCCTGAA |
| 5837 | db mining | Hs.255580 | AW296802 | 6703438 | UI-H-BW0-ajb-f-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731155 /clone_end=3' | -1 | CCATCGGCAAGCCTTGGTGGGTTCAT ATTCACTGGCATTAGGGATTAAGG |
| 5838 | db mining | Hs.255590 | AW296914 | 6703550 | UI-H-BW0-ajc-a-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731294 /clone_end=3' | -1 | CCATTTCCTCTGGATCCTCTCCTAGTT GTCTTTGTGTGGACGCACAAGCG |
| 5839 | db mining | Hs.255591 | AW296947 | 6703583 | UI-H-BW0-ajc-e-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731472 /clone_end=3' | -1 | GATCCTTTGCTGACACTGGTTTCTCT CTTATTTTGCCCCGCCAATAAAAA |
| 5840 | db mining | Hs.255598 | AW297024 | 6703660 | UI-H-BW0-ajf-e-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731495 /clone_end=3' | -1 | TCTGTCTGAAACTTCTTTTCTCTCTGA GAATTAATTTTCCAATGGACCGT |
| 5841 | db mining | Hs.255600 | AW297026 | 6703662 | UI-H-BW0-ajf-e-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731499 /clone_end=3' | -1 | GATCTGTGTTTTCTCCCAAAGAAG ATCATCTTTCCAGAAAAAGAGGAT |
| 5842 | db mining | Hs.255601 | AW297030 | 6703666 | UI-H-BW0-ajf-e-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731507 /clone_end=3' | -1 | TTCCATATGTCACTGTATCTGCCTGG CATTACCCCTTCTTAAACACACA |
| 5843 | db mining | Hs.288403 | AW297036 | 6703672 | AV757131 cDNA, 5' end /clone=BMFAKG04 /clone_end=5' | -1 | GCTCACTACCACTTCTTCAAATCCAG CTAAAGCATCACGGCTCAATGA |
| 5844 | db mining | Hs.255614 | AW297162 | 6703808 | HNC68-1-F10.R cDNA | -1 | GTCTGGTTGTTAGCTTTCCGATCCT CCACACATTGGAAACCTAAGCATA |
| 5845 | db mining | Hs.255615 | AW297175 | 6703811 | UI-H-BW0-ajd-c-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731375 /clone_end=3' | -1 | GGGCAATGGAGCCACAGACTCTCTA ACTTCAAGAGGTGTTTCATAGGTGT |
| 5846 | db mining | Hs.255618 | AW297199 | 6703835 | UI-H-BW0-ajd-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731477 /clone_end=3' | -1 | AGCTGAGGTCAGACAAACCACAACAT ATATGCAGATTTATCAGCAATAAA |
| 5847 | db mining | Hs.255617 | AW297201 | 6703837 | 7k38c02.x1 cDNA, 3' end /clone=IMAGE:3477507 /clone_end=3' | -1 | CCTGCCAGGGTTGTTGGAAGTCGC AGGTCCGAAAATCTCCTCCGCATAC |
| 5848 | db mining | Hs.255621 | AW297220 | 6703856 | UI-H-BW0-ajd-g-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731577 /clone_end=3' | -1 | CTTCTCTGAAATGGTACGCCTATACT TGCATTTCTGAGAAGCCAAACAAA |
| 5849 | db mining | Hs.255622 | AW297233 | 6703869 | UI-H-BW0-aji-a-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731684 /clone_end=3' | -1 | AGTTTTCTGGCTAAGTCACCTCTTAA GGAGATCCCTGTAAATTACCCCT |
| 5850 | db mining | NA | AW297255 | 6703891 | UI-H-BW0-aji-c-04-0-UI.s1 NCL_CGAP_Sub6 cDNA clone IMAGE:2731782 3', mRNA sequence | -1 | CAGATTAAAAACCCCATCCCGGCCCT CACCGAGGTGTTACAACTCTGTCC |
| 5851 | db mining | Hs.48820 | AW297262 | 6703898 | TAFII105 mRNA, partial /cds=(0,2405) | -1 | AGCAAATTACTCTGCCTGGAATAAAA ATTCTGTCACTTCAAGCATCTCCT |
| 5852 | db mining | Hs.255626 | AW297265 | 6703901 | UI-H-BW0-aji-d-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731826 /clone_end=3' | -1 | TCCAGGCATGTATAGGTGGCAGG ACACAATGATAGGCAAGTAGTACA |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|---|
| 5853 | db mining | Hs.255630 | AW297294 | 6703930 | UI-H-BW0-aji-f-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731936 /clone_end=3' | -1 | ACAGACCCAAACCTCACAGAGTGAAA GGGGACTTTCTCACAGAGTGAAA |
| 5854 | db mining | Hs.255632 | AW297313 | 6703949 | 7k46h07.x1 cDNA, 3' end /clone=IMAGE:3478525 /clone_end=3' | -1 | TTGCTTCAGACTTTTAAACAATCCT AGAAGCCAGAAAACAATGAAGAAA |
| 5855 | db mining | Hs.255633 | AW297317 | 6703953 | UI-H-BW0-aji-h-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732038 /clone_end=3' | -1 | TTCTGTCCAGGGCTTCAAAAGAGACTT CCATAGTTTTGGGAATGGAGTCA |
| 5856 | db mining | Hs.255634 | AW297318 | 6703954 | UI-H-BW0-air-a-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730121 /clone_end=3' | -1 | GATATATTGAAGGTCAGAGGCAGAGC TAAACAGGTGATGCCACTGGGTCT |
| 5857 | db mining | Hs.255635 | AW297328 | 6703964 | UI-H-BW0-air-a-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730141 /clone_end=3' | -1 | AGGCTCTTGTGAGTATTCCTTTGATT CCTGCTTCTGTCTTTTAAATCA |
| 5858 | Table 3A | Hs.255637 | AW297339 | 6703975 | UI-H-BW0-air-c-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730221 /clone_end=3' | -1 | ACACACCAAAAGAAATAGAAGAGTCT TTTTCTGCCCTTGGGGAATCTGCA |
| 5859 | db mining | NA | AW297356 | 6703992 | UI-H-BW0-air-d-08-0-UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2730279 3', mRNA sequence | -1 | ACACCCAGCACCACAGGGAAGAAA TAATTCACAGAGCTAAGTATTCCA |
| 5860 | db mining | Hs.330185 | AW297367 | 6704003 | UI-H-BW0-air-f-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730361 /clone_end=3' | -1 | TGTGCCTGTGTGCTCCAGCCTCTTCC TATGTGTGAACCTCAATAAAACC |
| 5861 | db mining | Hs.255644 | AW297374 | 6704010 | UI-H-BW0-air-f-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730375 /clone_end=3' | -1 | ACCGAGTGTTACCGCAAGAGGTGTAA AAATCCAGGTTTCATGTTTGCACAC |
| 5862 | db mining | Hs.255645 | AW297384 | 6704020 | UI-H-BW0-air-g-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730423 /clone_end=3' | -1 | TCCTGATTCTCAAAGTACCCCTTCC CTACAACCTAACATGCTTTGTCT |
| 5863 | db mining | Hs.255646 | AW297390 | 6704026 | UI-H-BW0-air-h-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730465 /clone_end=3' | -1 | CCATGATTTTTCCAATGGACAAGCAC TATTAACATGGGACTGTATTTCT |
| 5864 | Table 3A | Hs.255647 | AW297400 | 6704036 | UI-H-BW0-ais-a-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730152 /clone_end=3' | -1 | AATAGAAGTATAGCCCATGATGATT GGCTGGCAGGGTTAAGGAAGTGGG |
| 5865 | db mining | Hs.255648 | AW297401 | 6704037 | UI-H-BW0-ais-a-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730154 /clone_end=3' | -1 | TCCCAGGAGAGTACATTCTTTTTC ACTAAATAAGGAGGGGAAGAAAAA |
| 5866 | db mining | Hs.255649 | AW297407 | 6704043 | UI-H-BW0-ais-b-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730194 /clone_end=3' | -1 | GGGTTACCTCACTTTCTAGGTTCCCA AGATTCCCAAGTTAAGGAAGCTTT |
| 5867 | db mining | Hs.255650 | AW297411 | 6704047 | UI-H-BW0-ais-b-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730204 /clone_end=3' | -1 | AAAGCGTCCAGTCCCCCTAACTCAAA CACAGAAACATAACAATTTTACAA |
| 5868 | db mining | Hs.255653 | AW297426 | 6704062 | UI-H-BW0-ais-c-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730262 /clone_end=3' | -1 | CCCAGGGCTCCTCCACCTGAAAGAAT TGTCAGGGTTTCAGATCAGCTAAA |
| 5869 | db mining | Hs.255657 | AW297443 | 6704079 | UI-H-BW0-ais-e-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730352 /clone_end=3' | -1 | TGGCCTCCACCCATTAACTGTCTTT GCCTAAGACAATAATCCCAGGA |
| 5870 | Table 3A | Hs.255661 | AW297522 | 6704158 | UI-H-BW0-aja-e-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731106 /clone_end=3' | -1 | TGTAATCCTGATGCCTGAAAATCGTT AAGTGAAGACTTATCACATTACCG |
| 5871 | db mining | Hs.255665 | AW297581 | 6704217 | UI-H-BW0-ajg-b-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731718 /clone_end=3' | -1 | ATCCTTCAGATTGAGCTGGGTGTGAG CATTCAATTCACAAGGGTACCTG |
| 5872 | db mining | Hs.255666 | AW297590 | 6704226 | RST6539 cDNA | -1 | TGGATAAGCAATATGTTGGACTAGTA TGAAATGGCATTCCAGCAGTGA |
| 5873 | db mining | Hs.255672 | AW297626 | 6704262 | UI-H-BW0-ajg-f-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731918 /clone_end=3' | -1 | TCCTAGCAGAAATATAGTGGGCATGA CCAGTATCCTAGTAGAGCTGACCC |
| 5874 | db mining | Hs.255673 | AW297636 | 6704272 | UI-H-BW0-ajg-h-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731996 /clone_end=3' | -1 | AGTTTCTTTCTTACAATGGGGTCTG AAATCCAGGGTTCCACACCAGGG |
| 5875 | db mining | Hs.255674 | AW297649 | 6704285 | UI-H-BW0-ajh-a-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731665 /clone_end=3' | -1 | CCAAATACCTAGTGAGTTGACTTGT CTTGGGTTGCACTGTAAGGCAGAG |
| 5876 | db mining | Hs.255675 | AW297651 | 6704287 | UI-H-BW0-ajh-a-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731669 /clone_end=3' | -1 | CAAGAGTTTCCATGCGTCCAGTGATG ACCGGAATTAATCATGTATGGTGT |
| 5877 | db mining | Hs.255677 | AW297664 | 6704300 | UI-H-BW0-ajh-b-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731725 /clone_end=3' | -1 | GTTTCTAACCCATAAGTGCCCTCATAC ATACATTGCTAGTCTAAAGACTTT |
| 5878 | db mining | Hs.255679 | AW297692 | 6704328 | UI-H-BW0-ajh-e-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731857 /clone_end=3' | -1 | ACCGGCTAATTTTGTAACTGGCTTGT TTGTAATAATAATCCTTCTGTGT |
| 5879 | db mining | Hs.255681 | AW297694 | 6704330 | UI-H-BW0-ajh-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731861 /clone_end=3' | -1 | TGGTGGGACTATGTGTTATTCTTGTA TACTTGCAGTGGGTAGATGTCACT |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|--|
| 5880 | db mining | Hs.255682 | AW297698 | 6704334 | UI-H-BW0-ajh-e-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731869 /clone_end=3' | -1 | ACTTCCCTACCTCACAGGTTAGGATT CAAAGTGTGATTCCCCATTGTG |
| 5881 | db mining | Hs.255686 | AW297728 | 6704364 | UI-H-BW0-aiy-a-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730888 /clone_end=3' | -1 | GGGTGCTTTACAGGATTCTTGAAAT GTGTAGTGGATGCTGGCTCTAGGG |
| 5882 | db mining | Hs.255688 | AW297749 | 6704385 | UI-H-BW0-aiy-c-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730988 /clone_end=3' | -1 | ACAGAAGCAGGGGGTCAAAAAGTTT CATAAAGGAGGTGCTTGGAAACAAA |
| 5883 | db mining | Hs.342530 | AW297756 | 6704392 | UI-H-BW0-aiy-d-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731032 /clone_end=3' | -1 | CTATTGTGTGGGTTGCCTTGTCTTAC TCAACTTCAAATATTCACCACCCC |
| 5884 | db mining | Hs.255691 | AW297780 | 6704416 | UI-H-BW0-aiy-e-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731100 /clone_end=3' | -1 | CAGGTGTGCTTACTGGCAGGAACCG AGGGAATAAATAAGATCACTGGAA |
| 5885 | db mining | Hs.255692 | AW297781 | 6704417 | UI-H-BW0-aiy-e-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731102 /clone_end=3' | -1 | ACCAGCCTTATGTGTGTGGGTATTCA ATACTCTGCACATTATATACTGTA |
| 5886 | db mining | Hs.255693 | AW297785 | 6704421 | UI-H-BW0-aiy-f-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731134 /clone_end=3' | -1 | GGGCATTGTACCCCTCCTCACCA CCATCCCCATTAAAGGCTTCGGGG |
| 5887 | Table 3A | Hs.255695 | AW297813 | 6704438 | UI-H-BW0-aiy-g-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731192 /clone_end=3' | -1 | CTGTATCTACAACCTCTGACTTCAGA TTTTTGTCTTCTCAAACAGCCT |
| 5888 | Table 3A | Hs.255697 | AW297827 | 6704452 | UI-H-BW0-aiy-h-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731244 /clone_end=3' | -1 | AGCAAGACTTAACCACTAATTACTATT ATCTGACCCAGGAAACTCCGCC |
| 5889 | db mining | Hs.255698 | AW297843 | 6704468 | UI-H-BW1-aoa-c-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:3083913 /clone_end=3' | -1 | TGGATAGTTGCTCAATGTAGCAGTGA TGTTCTTGGAAATGCCAGCAGAGC |
| 5890 | db mining | Hs.328317 | AW297929 | 6704565 | yg18e06.s1 cDNA, 3' end /clone=IMAGE:32551 /clone_end=3' | -1 | CCAACAGATTGCTGCTTACCCTGAGG TGAAGCCTCGTTTGAGAACCAAT |
| 5891 | db mining | Hs.255705 | AW297949 | 6704585 | UI-H-BW0-ajn-d-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732229 /clone_end=3' | -1 | CAACCTTCTTGTGAATTGATTTACTA CTCATCAGGGTCATGCACAAGCA |
| 5892 | db mining | Hs.255706 | AW297951 | 6704587 | UI-H-BW0-ajn-e-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732257 /clone_end=3' | -1 | ACATTCAAACGCCAGAATATGACTG TAAACAGCGAAGTGTCTCTTGC |
| 5893 | db mining | Hs.255708 | AW297970 | 6704606 | UI-H-BW0-ajn-f-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732323 /clone_end=3' | -1 | TCTTCCTGGGAATGTGATGTGTTTTT CACTGGTTCTAATTCTGTCTTCT |
| 5894 | db mining | Hs.255710 | AW297974 | 6704610 | UI-H-BW0-ajn-g-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732355 /clone_end=3' | -1 | ACTTATTAATTCTCACCTCAGCCTCA GGGATGTATGTAGGGAAGGAGCAT |
| 5895 | db mining | Hs.255713 | AW297994 | 6704630 | UI-H-BW0-ajn-h-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732421 /clone_end=3' | -1 | ACATTCCTGTCTATTAGTGAATAAGAA GCTGAGGTGTGACTAAGAAGACAA |
| 5896 | db mining | Hs.255717 | AW298042 | 6704678 | UI-H-BW0-ajp-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732629 /clone_end=3' | -1 | CCTCCTTGATAAAATCAAGAACAGGT TAGATTAAAGCAGTAAATCCTAGACT |
| 5897 | db mining | Hs.330189 | AW298048 | 6704684 | UI-H-BW0-ajp-f-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732665 /clone_end=3' | -1 | TCCTGGCCTTTGTGGGTTTTTAATTC CCTTTACCTTTTCCCTTTTGGAT |
| 5898 | db mining | Hs.255721 | AW298073 | 6704709 | UI-H-BW0-ajp-h-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732769 /clone_end=3' | -1 | ACTGTGCAACTACAATTCTCAGATA GTCCCATTTGTTAAATCACGCAT |
| 5899 | db mining | Hs.342533 | AW298095 | 6704731 | UI-H-BW0-ajs-b-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732878 /clone_end=3' | -1 | CCTTCCCTCTGCCTGTAGGTTCTGT GGCTATAAACAAATCATAACTTTT |
| 5900 | db mining | Hs.255725 | AW298106 | 6704742 | UI-H-BW0-ajs-c-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732916 /clone_end=3' | -1 | TTAAATGCTTCCCTGGCTCTCCCTGG GTTTCAGTTTCTATCCATGCCCTG |
| 5901 | db mining | Hs.255726 | AW298110 | 6704746 | UI-H-BW0-ajs-c-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732924 /clone_end=3' | -1 | TTGTTCTCCTCCCAAGTCTCTGGTTC TATTTGGCTTTTTCAGCTCTGTGC |
| 5902 | db mining | Hs.255727 | AW298123 | 6704759 | UI-H-BW0-ajs-e-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733000 /clone_end=3' | -1 | GCATTTCAGGGACACAAATGGTCCAT GGCAGAGACCAGTAATGCCAGATA |
| 5903 | db mining | Hs.255736 | AW298201 | 6704837 | UI-H-BW0-ajt-d-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732967 /clone_end=3' | -1 | TTTTATCCCCGCTTTAACTTTGTTTGC TTGGTACTTTTCTGTGGTTACA |
| 5904 | db mining | NA | AW298208 | 6704844 | UI-H-BW0-ajt-e-05-0-UI.s1 NCL_CGAP_Sub6 cDNA clone IMAGE:2733009 3', mRNA sequence | -1 | CACGCACCCAACTCCCCACTGCTCCT CTCCATCCAGATGTTGCTCCAGAG |
| 5905 | db mining | Hs.255740 | AW298234 | 6704870 | UI-H-BW0-ajt-g-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733113 /clone_end=3' | -1 | TTTGAGGGCAATTTAATGGTTAAGTG TAGGAAAATCCACTCTTACAGTGT |
| 5906 | db mining | Hs.330191 | AW298238 | 6704874 | UI-H-BW0-ajt-h-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733151 /clone_end=3' | -1 | GGCCTTTTGATTTTCCATTGGGGTCC CCCGCTTCCCATTTTGGTTTTT |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|---|
| 5907 | db mining | Hs.255743 | AW298239 | 6704875 | UI-H-BW0-ajt-h-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:273153 /clone_end=3' | -1 | GACAGTTTGGGGAAGGGATTGAAGG TCTGCGTCAAAGAGAACAGAAAACC |
| 5908 | db mining | NA | AW298271 | 6704994 | UI-H-BW0-ajk-d-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732184 /clone_end=3' | -1 | AGGGGCGCTTTTACC GGTTTGTTCCT CTTAAATTTTAAAGGAATTGAATT |
| 5909 | db mining | Hs.183669 | AW298312 | 6705035 | mRNA for KIAA1271 protein, partial cds /cds=(72,1700) | -1 | TCCTCTTTCTTGCTACTGTGAAGCGA TGAATAAACCTGGGTGTAGATCCA |
| 5910 | db mining | Hs.302681 | AW298348 | 6704908 | 7j80e10.x1 cDNA, 3' end /clone=IMAGE:3392778 /clone_end=3' | -1 | CCTAGAAATTATTATACAGGGATAAAT GAGGCACTGAAGGTGGGAGAACC |
| 5911 | db mining | Hs.255746 | AW298349 | 6704909 | UI-H-BW0-ajj-c-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731795 /clone_end=3' | -1 | ACGACAACTGCACAGTAAATATCAC AAACACGGAAATACCACAGTGTCT |
| 5912 | db mining | Hs.255747 | AW298355 | 6704915 | UI-H-BW0-ajj-d-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731835 /clone_end=3' | -1 | ACCATGACTTGGCAAAGAGTTTCAAG AGAGGCATAATCAAAGTAACCA |
| 5913 | db mining | Hs.255749 | AW298388 | 6704948 | UI-H-BW0-ajj-g-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731983 /clone_end=3' | -1 | GATTAATCAAGGGAAGAGCTTCAAGC AGAGCTCCTTAGGTTTTTCAAAA |
| 5914 | Table 3A | Hs.313413 | AW298430 | 6705066 | 602721745F1 cDNA, 5' end /clone=IMAGE:4838506 /clone_end=5' | -1 | GCTCAGGGGACAGCTATTCTTTTCA AAGCGTTTACCGACTGGATCACCT |
| 5915 | db mining | Hs.255762 | AW298437 | 6705073 | UI-H-BW0-ajl-d-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732199 /clone_end=3' | -1 | TGAGAGCTTTCCTCCTACGATC CAACCATGTCAAACATTTCTACA |
| 5916 | db mining | Hs.255763 | AW298445 | 6705081 | UI-H-BW0-ajl-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732245 /clone_end=3' | -1 | TGTGCCAACGCATGATTTCTTTGAGT AAATTTCTAAACGTACAGAAAGTT |
| 5917 | db mining | Hs.255764 | AW298447 | 6705083 | UI-H-BW0-ajl-e-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732249 /clone_end=3' | -1 | AGTCAACATGGAGCAAGTGAGCTAAG GAAGTAATGGAACTGTTTGAGAG |
| 5918 | db mining | Hs.255766 | AW298482 | 6705118 | UI-H-BW0-ajl-h-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732397 /clone_end=3' | -1 | AGCTCAGGTCTTCCCTCATCTGTTAG TTTCTGGAGTCTGTTCTCATACT |
| 5919 | db mining | Hs.255767 | AW298489 | 6705125 | UI-H-BW0-ajm-a-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732078 /clone_end=3' | -1 | AAACATACTCCTCTTACCAGCACTC AGACATTTGTATCCAGAGAAAGCT |
| 5920 | db mining | Hs.255768 | AW298490 | 6705126 | UI-H-BW0-ajm-a-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732080 /clone_end=3' | -1 | AGTCTGTCAATTGTTAAGCCTGTGA TCTTTCTTTCCAGTTAAGAGTT |
| 5921 | db mining | Hs.255769 | AW298494 | 6705130 | UI-H-BW0-ajm-b-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732112 /clone_end=3' | -1 | TGTCCTCTCAACCCTACTTGTGGTTT TACACTGTTAATTACACTATTTC |
| 5922 | db mining | Hs.132781 | AW298502 | 6705138 | class I cytokine receptor (WSX-1), mRNA /cds=(138,2048) | -1 | GTGTGTGTATGGTTGTTGGGCGTAG GACAGGTTTCGGGGATGCGCGGTAC |
| 5923 | db mining | Hs.255770 | AW298503 | 6705139 | UI-H-BW0-ajm-b-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732134 /clone_end=3' | -1 | CTGTGCTTGACTATTGAAAACCTTAGA ATTGGGATGCCAAAGTTACTTCCT |
| 5924 | db mining | Hs.255772 | AW298510 | 6705146 | UI-H-BW0-ajm-c-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732180 /clone_end=3' | -1 | GGTTGTATCAAAAGAACTCCACATCC ATATTGAATAAATCCCACTAGCC |
| 5925 | db mining | Hs.255777 | AW298559 | 6705195 | UI-H-BW0-ajm-h-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732406 /clone_end=3' | -1 | GGCTGCCAGATCTCGTGGGAAGAA GACCACAGGAGGACTCGGCTCAATG |
| 5926 | db mining | Hs.255779 | AW298607 | 6705243 | UI-H-BW0-ajr-d-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732615 /clone_end=3' | -1 | TGGAAAAATGATAGCAGCCAACCTGA CAGAAGAACCAGCATACACATTC |
| 5927 | db mining | Hs.255782 | AW298616 | 6705252 | UI-H-BW0-ajr-e-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732659 /clone_end=3' | -1 | TTGGTTTTGGGGATTGGGAAGTCTTA AGCCAAATGTCCCCGGTCTCCCC |
| 5928 | db mining | Hs.255783 | AW298627 | 6705263 | UI-H-BW0-ajr-f-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732707 /clone_end=3' | -1 | GCCCTATATCTAGTGAGCAGGTTGTG GCAATCAGGAAGGGATTGATATTT |
| 5929 | db mining | Hs.255784 | AW298632 | 6705268 | UI-H-BW0-ajr-g-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732743 /clone_end=3' | -1 | TGCACGCAATGCTTGAAGTGTCCCA GGTATTTAGTTTCAGTAAATTTT |
| 5930 | db mining | Hs.255785 | AW298647 | 6705283 | UI-H-BW0-ajr-h-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732801 /clone_end=3' | -1 | CTGTAGGTATGAGCTGCCAGGATCCA GGTGTGACTCGGGTATTCTAGGG |
| 5931 | db mining | Hs.255788 | AW298675 | 6705311 | UI-H-BW0-ajo-c-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732524 /clone_end=3' | -1 | TCCCATTTGGGGGGTGGGCTGTTTAA ATTTTGACTCCCTGTTTTAAACCC |
| 5932 | db mining | Hs.255794 | AW298720 | 6705356 | UI-H-BW0-ajo-g-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732724 /clone_end=3' | -1 | CCACTTGCATCTCTTCTGGGGGTTCT TTCTTTCTTCTCTGTTCTAAGGC |
| 5933 | db mining | Hs.255797 | AW298752 | 6705388 | UI-H-BW0-ajq-b-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732506 /clone_end=3' | -1 | TGGGTAATCAACACTCAACCATCAAC AAACACTCTCTATTCCAGGCACTG |
| 5934 | db mining | Hs.255799 | AW298806 | 6705442 | RC4-MT0235-061200-011-e11 cDNA | -1 | AGGAGAAATAATTAGAGTGGCACACT AGCATGATGGTAAACATTCTGTCA |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|--|----|---|
| 5935 | Table 3A | Hs.157396 | AW300500 | 6710177 | xs66c06.x1 cDNA, 3' end /clone=IMAGE:2774602 /clone_end=3' | -1 | AGGAGTTCAAGAAGCAGAGATTTCCTCA GGTCCATGCACCAAGCTCATGTG |
| 5936 | Table 3A | Hs.262789 | AW300868 | 6710545 | xk07d09.x1 cDNA, 3' end /clone=IMAGE:2666033 /clone_end=3' | -1 | CTTGCTCTCTCTGATCCAGGGCTCC AGTGCCCATGTCCAGTGCCTTGGT |
| 5937 | db mining | Hs.255880 | AW337887 | 6834513 | he12d07.x1 cDNA, 3' end /clone=IMAGE:2918797 /clone_end=3' | -1 | GCATCTCCCGCTGTACAGCTCAGC CCTCTCTACCAAAATCTCTTTCGA |
| 5938 | Table 3A | Hs.328348 | AW338115 | 6834741 | tp39g05.x1 cDNA, 3' end /clone=IMAGE:2190200 /clone_end=3' | -1 | GGCGTTTCCCATTGACCAGTTTGACC CTGGTTTGAATAAAGAGAAGTGGC |
| 5939 | db mining | Hs.255920 | AW339530 | 6836156 | he13d09.x1 cDNA, 3' end /clone=IMAGE:2918897 /clone_end=3' | -1 | AGCCCATGAAAACCTTGGCAAAATG TCAGACCTTAAGACTTTCCTACTAT |
| 5940 | Table 3A | Hs.255927 | AW339651 | 6836277 | he15g04.x1 cDNA, 3' end /clone=IMAGE:2919126 /clone_end=3' | -1 | TCAGAGACAACGGAAGCTGAAAAATA AGAGCTGAGAAAGGAAGAACTTTT |
| 5941 | Table 3A | Hs.207995 | AW340421 | 6837047 | hc96h02.x1 cDNA, 3' end /clone=IMAGE:2907891 /clone_end=3' | -1 | ATATACATACAAATCTAAGCTCCAAG AAGCCTAAGAAAACCCCTTAGGGG |
| 5942 | Table 3A | Hs.256031 | AW341086 | 6837631 | xz92h04.x1 cDNA, 3' end /clone=IMAGE:2871703 /clone_end=3' | -1 | GGGCAATTTACATCGGGACTCGTTTC ATCTCTAGACCTTCACTTACCTGA |
| 5943 | Table 3A | Hs.283667 | AW341449 | 6838075 | arginyl aminopeptidase (aminopeptidase B) (RNPEP), mRNA /cds=(9,1982) | -1 | AGCTCTGGAGTGGCCCTCCCTCCAAA TAAAGTATTTTAAGCGAACACTGA |
| 5944 | Table 3A | Hs.337986 | AW440517 | 6975823 | Homo sapiens, clone MGC:17431 IMAGE:2984883, mRNA, complete cds /cds=(1336,1494) | -1 | GCCAGTCTCTATGTGTCTTAATCCCT TGTCTTTCATTAAAGCAAAACTA |
| 5945 | db mining | Hs.256956 | AW440813 | 6976044 | he03b05.x1 cDNA, 3' end /clone=IMAGE:2917905 /clone_end=3' | -1 | CCCTCAGGCATAGAAATTGAATCTGA AATGGCTGATGAATAAGCAAAGGC |
| 5946 | db mining | Hs.313573 | AW440817 | 6976048 | he03c02.x1 cDNA, 3' end /clone=IMAGE:2917922 /clone_end=3' | -1 | CAGCCCTGCCTGAGTTTTTGACACCT GCATCCCTCCCTGCCTCACCTCAC |
| 5947 | Table 3A | Hs.256961 | AW440866 | 6976172 | he05f02.x1 cDNA, 3' end /clone=IMAGE:2918139 /clone_end=3' | -1 | AGAGCAGGAGAAATCCTACTGCATTA TTAATCTGAAAGCACAAGGACAGC |
| 5948 | Table 3A | Hs.173730 | AW440869 | 6976175 | Mediterranean fever (MEFV), mRNA /cds=(41,2386) | -1 | CTGTCTTGGTTTGTATGGGAAATCT GCGGGTTGTGGAATATTAGGTTCT |
| 5949 | Table 3A | Hs.118446 | AW440965 | 6976271 | HNC35-1-D12.R cDNA | -1 | TGGGATTATAGGGGAGACAGGAGT TGTGGAATTACAGGAGAGGTTCACT |
| 5950 | db mining | Hs.118446 | AW440965 | 6976271 | HNC35-1-D12.R cDNA | -1 | TGGGATTATAGGGGAGACAGGAGT TGTGGAATTACAGGAGAGGTTCACT |
| 5951 | Table 3A | Hs.256971 | AW440974 | 6976280 | he06e12.x1 cDNA, 3' end /clone=IMAGE:2918254 /clone_end=3' | -1 | CTGAGAAAAGGAGTGTCTCTCTCTG CTCCAACTTCCAGTAGCTTCCA |
| 5952 | Table 3A | Hs.342632 | AW444482 | 6986244 | UI-H-BI3-akb-e-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733777 /clone_end=3' | -1 | TCGAGGTTCTTCCCAAGAAAAGCCCA ATCTTATAAACTGTTACTTCCCT |
| 5953 | Table 3A | Hs.250 | AW444632 | 6986394 | xanthene dehydrogenase (XDH), mRNA /cds=(81,4082) | -1 | TGCAATGAGGCAGTGGGGTAAGGTT AAATCCTCTAACCGTTCTTGAATCA |
| 5954 | Table 3A | Hs.335815 | AW444812 | 6986574 | UI-H-BI3-ajy-d-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733380 /clone_end=3' | -1 | TGGCAACTTCAACTCCTTGATGGCGA TAATCTCTGGTATGAATATGAGCC |
| 5955 | Table 3A | Hs.99665 | AW444899 | 6986661 | UI-H-BI3-ajz-d-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733373 /clone_end=3' | -1 | TTGTGCTCCTGATACGACGTTGCCAC AGTTAATCCGTTCTGATCTCTGCT |
| 5956 | Table 3A | Hs.257283 | AW450350 | 6991126 | UI-H-BI3-akn-c-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2734825 /clone_end=3' | -1 | CAAGCCTAATTTCCAACACTCCCGC GACGCAACCCCTTCCCTTTTCCTC |
| 5957 | Table 3A | Hs.313715 | AW450835 | 6991611 | UI-H-BI3-alf-f-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2736539 /clone_end=3' | -1 | CACGGTTAGAGTCACCAACCTGTAT TTCAGGGGACATCTTCCAGCTCC |
| 5958 | Table 3A | Hs.199014 | AW450874 | 6991650 | 601499703F1 cDNA, 5' end /clone=IMAGE:3901440 /clone_end=5' | -1 | CCAAAGGCTCACTACCCCTGTGCGTT GTCCAGCACACAGACTATGTGC |
| 5959 | Table 3A | Hs.342873 | AW451293 | 6992069 | RC3-HT0230-130100-014-g06 cDNA | -1 | TGCTTGGGAAATTTGGTTTGTAACC TAAATAGCCCTTATTTCTGGGGA |
| 5960 | Table 3A | Hs.101370 | AW452023 | 6992799 | AL583391 cDNA /clone=CS0DL012YA12-(3-prime) | -1 | CATCTGCTGAGCAGTGTGCTGTGTCA ACCTCCTCCTAGGTCTCCTCTATG |
| 5961 | Table 3A | Hs.342735 | AW452096 | 6992953 | UI-H-BI3-alo-d-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3068186 /clone_end=3' | -1 | CTTTCTGCCTGAAGCTGCCCCCATGA CTCCCTTCTTTGTGCAAAAGCATG |
| 5962 | Table 3A | NA | AW452467 | 6993243 | UI-H-BI3-als-e-09-0-UI.s1 NCI_CGAP_Sub5 cDNA clone IMAGE:3068632 3', mRNA sequence | -1 | GAAATGAGTTGGTGTCTTCACAGAAT GAGGATCCCCAGAGCCATCTTGCC |
| 5963 | Table 3A | Hs.257579 | AW452513 | 6993289 | UI-H-BW1-ame-b-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069628 /clone_end=3' | -1 | GTCTCCCTCCCACTCTCTGCCTTACC TGGTATCTATGACTCGACTGAAAT |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|---|----|---|
| 5964 | db mining | Hs.257581 | AW452528 | 6993304 | UI-H-BW1-ame-c-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069684 /clone_end=3' | -1 | TGCGAGAGGAAGCAGAGACCACCTT GAAACTCGGGTGCATTAAGTCCTTG |
| 5965 | db mining | Hs.257582 | AW452545 | 6993321 | UI-H-BW1-ame-d-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069742 /clone_end=3' | -1 | TTAGCCACTGCTATTCTAGGTTCCCTT GATGGAGCCCCACTCCCACGCCTA |
| 5966 | db mining | Hs.257630 | AW452932 | 6993708 | UI-H-BW1-amd-c-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069325 /clone_end=3' | -1 | ACCACCCAGAGGTTGCTGGCTTCCTT AATAAAGCTAACTTTCTTTTCACC |
| 5967 | db mining | Hs.257632 | AW452953 | 6993729 | UI-H-BW1-amd-e-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069415 /clone_end=3' | -1 | AGGGGAGCCAGTGGTTTTTGGTCAT GGGAAGTGTCTCATAAAATTCATT |
| 5968 | db mining | Hs.257633 | AW452960 | 6993736 | UI-H-BW1-amd-e-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069429 /clone_end=3' | -1 | GCACCAGACTTCTGAACAGGCTGGG AGAGTGAGGCATAAACACATGAAAT |
| 5969 | db mining | Hs.257636 | AW452985 | 6993761 | UI-H-BW1-amd-g-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069527 /clone_end=3' | -1 | ACACAGTACTTTGTGAGATGTTGGC TTCTTGGTTATGGCATGAATTCT |
| 5970 | Table 3A | Hs.257640 | AW453021 | 6993797 | UI-H-BW1-ama-c-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069290 /clone_end=3' | -1 | ACTTATCTTTTGCCACCCATGTTCCCT GGATGCCTTGCCTTCTCTTTCAT |
| 5971 | db mining | Hs.257644 | AW453034 | 6993810 | UI-H-BW1-ama-d-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069340 /clone_end=3' | -1 | AAACAGGAAGCCTCTCATGAATTTGA CCAAGGAGCTACATTCGTCTCTA |
| 5972 | db mining | Hs.257645 | AW453039 | 6993815 | UI-H-BW1-ama-d-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069350 /clone_end=3' | -1 | TGAGGAAGAGGAGATTTATTAAGCCC CTTCTTTTAGGCTAGGAGGTTTCC |
| 5973 | Table 3A | Hs.257646 | AW453044 | 6993820 | UI-H-BW1-ama-e-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069384 /clone_end=3' | -1 | GGACACTGGCTTTTGTGCAGCTCTTC ATCACAGAGTCTGTTGAGCTACAA |
| 5974 | db mining | Hs.257647 | AW453055 | 6993831 | UI-H-BW1-ama-e-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069406 /clone_end=3' | -1 | ACAGTGATTTTCAACCAAGGGGCTTT TTCAAACATACATTCCTTAGCTCCC |
| 5975 | Table 3A | Hs.257667 | AW467193 | 7037299 | he07a04.x1 cDNA, 3' end /clone=IMAGE:2918286 /clone_end=3' | -1 | GGTGGTGGCTACAAGGGTGATTGCC TTATGATAATTGACCGTGTCAAT |
| 5976 | db mining | Hs.257668 | AW467208 | 7037314 | he07c09.x1 cDNA, 3' end /clone=IMAGE:2918320 /clone_end=3' | -1 | AGCTGGGAGGCCATTACTTTTTGTCT GAGTCTTCTGGAGTCTAGCAAAA |
| 5977 | db mining | Hs.255877 | AW467312 | 7037418 | he09b01.x1 cDNA, 3' end /clone=IMAGE:2918473 /clone_end=3' | -1 | AGTTGCATTAAACTGAGCTTAGATGT GTAAGTTTGCTAACGGATGGGTTT |
| 5978 | db mining | Hs.257677 | AW467338 | 7037444 | he09e07.x1 cDNA, 3' end /clone=IMAGE:2918532 /clone_end=3' | -1 | CCTCTAAGGCATTATTTACTGACAA CATAAAATCTTGAACCCAGGTCA |
| 5979 | db mining | Hs.257679 | AW467385 | 7037491 | he10d12.x1 cDNA, 3' end /clone=IMAGE:2918615 /clone_end=3' | -1 | TCACCTCCATCAACTTACTAGCACAT AAAGGGTGGGATTTTCATGTGTTGA |
| 5980 | Table 3A | Hs.257680 | AW467400 | 7037506 | he10f11.x1 cDNA, 3' end /clone=IMAGE:2918637 /clone_end=3' | -1 | CTGGCAAAGGCATGGGTACAACCTG CTCTGTGATCTACCTTCTGAACCAC |
| 5981 | db mining | NA | AW467421 | 7037527 | he17b02.x1 NCI_CGAP_CML1 cDNA clone IMAGE:2919243 3' similar to contains Alu repetitive element;con | -1 | ACACCTGTGGTATATTTGTATCATTCA GTCTGGTTTCTCACCCCTTCTAA |
| 5982 | Table 3A | NA | AW467437 | 7037543 | he17d05.x1 NCI_CGAP_CML1 cDNA clone IMAGE:2919273 3', mRNA sequence | -1 | AACCCCTCGTAAGGTTTCATCTTCCTT GATTGCAAAATGAGTTTGTGTGAA |
| 5983 | db mining | NA | AW467445 | 7037551 | he17e08.x1 NCI_CGAP_CML1 cDNA clone IMAGE:2919302 3' similar to contains element MSR1 repetitive el | -1 | CCCGCTTACCTTCCCTAAATAACTC GTTTGCAGGCTAATTCATCAAAAT |
| 5984 | db mining | NA | AW467448 | 7037554 | he17f02.x1 NCI_CGAP_CML1 cDNA clone IMAGE:2919291 3' similar to contains Alu repetitive element;con | -1 | ATTTTGCTCATTACCTGTCAGGAGAA AACCCCTCTTCCCCAGTCTCCACT |
| 5985 | Table 3A | Hs.257687 | AW467501 | 7037607 | he19e06.x1 cDNA, 3' end /clone=IMAGE:2919490 /clone_end=3' | -1 | ACCTACTGAATCTCCAGATTGCCAAG TGAAACACAATGGTTGCCTCTTCA |
| 5986 | db mining | Hs.257688 | AW467571 | 7037677 | he21f02.x1 cDNA, 3' end /clone=IMAGE:2919675 /clone_end=3' | -1 | TGCGAAAGCTAATTCCTAGTATGAA TAACTTCAGACCTTGCTCTCCTT |
| 5987 | db mining | Hs.257690 | AW467582 | 7037688 | 602497524F1 cDNA, 5' end /clone=IMAGE:4611316 /clone_end=5' | -1 | AGCCTGAGGTGGGTGAAGAAATAC CTGCTTTATACTGTTCTGGAAACTC |
| 5988 | db mining | Hs.266387 | AW467607 | 7037713 | he22c05.x1 cDNA, 3' end /clone=IMAGE:2919752 /clone_end=3' | -1 | CTTTTCCCCTTCATGGTAGTTGCTGC TTAAGTTTCTCTAACATGCCTGCA |
| 5989 | Table 3A | Hs.257695 | AW467746 | 7037776 | he23d05.x1 cDNA, 3' end /clone=IMAGE:2919849 /clone_end=3' | -1 | TGAATGTGCAGATGCAGAACCCATTG ATATGGAGGGCTGAGTGTCTGAAA |
| 5990 | Table 3A | Hs.257705 | AW467863 | 7037969 | he27c04.x1 cDNA, 3' end /clone=IMAGE:2920230 /clone_end=3' | -1 | TGTACTACTTATTTATGTGTAACCAT ACACAGGGCTAGAAAGGAAGGGAT |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|---|----|---|
| 5991 | Table 3A | Hs.257706 | AW467864 | 7037970 | he27c05.x1 cDNA, 3' end /clone=IMAGE:2920232 /clone_end=3' | -1 | TGTAGAATTGCGGAGTAGAAAGACCC TTGAAAGATCATTTGTCTGTGGT |
| 5992 | Table 3A | Hs.257709 | AW467992 | 7038098 | he30b01.x1 cDNA, 3' end /clone=IMAGE:2920489 /clone_end=3' | -1 | GCTCAAGTTCCCAGCACCTGGGGAA TTCTAAGCCTGAGGAAGACAAGGTG |
| 5993 | db mining | Hs.257713 | AW468139 | 7038245 | he32g11.x1 cDNA, 3' end /clone=IMAGE:2920772 /clone_end=3' | -1 | TGTTTTTATGCTCTGAGCAAGCAAATT GCTGCAATTTAAATCACCAATTT |
| 5994 | Table 3A | Hs.257716 | AW468207 | 7038313 | he34a12.x1 cDNA, 3' end /clone=IMAGE:2920894 /clone_end=3' | -1 | AGGCCTGATATTGAAAGCTTTTGATA CTGAGATCCTATTAATCTCAGATGA |
| 5995 | db mining | Hs.257719 | AW468316 | 7038422 | he36a05.x1 cDNA, 3' end /clone=IMAGE:2921072 /clone_end=3' | -1 | TGTTAGTTTGCTTTTGAAATTCCTTTGG AGGGTACTCTTCAGGGCTTCACA |
| 5996 | db mining | Hs.278060 | AW468430 | 7038536 | he37h10.x1 cDNA, 3' end /clone=IMAGE:2921251 /clone_end=3' | -1 | TAGTGATTATCTCCAGGAATCAAGTA CAAACCTTTGAAAAAGACTGGAGGT |
| 5997 | Table 3A | Hs.257727 | AW468431 | 7038537 | he37h11.x1 cDNA, 3' end /clone=IMAGE:2921253 /clone_end=3' | -1 | TTTGTCCCAAGGGCTCAGACTGAAAG AATGCAATGTGAGAGGTATGCCAC |
| 5998 | db mining | Hs.330268 | AW468459 | 7038565 | he38d05.x1 cDNA, 3' end /clone=IMAGE:2921289 /clone_end=3' | -1 | TCTGTGAAAACTTTCTGCAATGTCT TTGCTTGCTTGACTCAGCTTTT |
| 5999 | db mining | Hs.257738 | AW468559 | 7038665 | he41a07.x1 cDNA, 3' end /clone=IMAGE:2921556 /clone_end=3' | -1 | TGCTTTTAACGCACAGATGTTACTTC AGCACCACAAGGACTGTTGATGGA |
| 6000 | Table 3A | Hs.257743 | AW468621 | 7038727 | he42e03.x1 cDNA, 3' end /clone=IMAGE:2921692 /clone_end=3' | -1 | CAGTCAGATGTTGGAATTGGGGGTA GAGGGATTATAGAGTTGTGTGTGCT |
| 6001 | Table 3A | Hs.122116 | AW469546 | 7039652 | hd19e09.x1 cDNA, 3' end /clone=IMAGE:2909992 /clone_end=3' | -1 | AAAGGAGGGACTATGGCATCAAACA GCCTCTTCAGCACAGTGACACCATG |
| 6002 | Table 3A | Hs.80618 | AW510795 | 7148873 | hypothetical protein (FLJ20015), mRNA /cds=(31,522) | -1 | ACCCAGTTTGTGCATAGTTCATGATC CTCTATAAAACAGCTTTTGTGGA |
| 6003 | Table 3A | Hs.193669 | AW512498 | 7150576 | hypothetical protein DKFZp586J1119 (DKFZp586J1119), mRNA /cds=(27,2153) | -1 | CTGTCCGGCTCTGAAAGCAGCTGGT TTAGTTGTAGAAGATGCTCTGTTTG |
| 6004 | Table 3A | Hs.42915 | AW572538 | 7237271 | ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA /cds=(74,1258) | -1 | TGGAATGGACTCTTAAACAATGAAA GAGCATTTATCGTTTGCCCTTGA |
| 6005 | Table 3A | Hs.342858 | AW572930 | 7237663 | hf17f07.x1 cDNA, 3' end /clone=IMAGE:2932165 /clone_end=3' | -1 | TCACTACCTTCAATTGTTTACAAGGT GGATATGGGCAGGCAACAGATACT |
| 6006 | Table 3A | Hs.325991 | AW573211 | 7237944 | 602679187F1 cDNA, 5' end /clone=IMAGE:4812093 /clone_end=5' | -1 | CTAGGCCGGATGGGCCAGAGAAGGA GAACCATGGCAGGAGCCGAAGCAG |
| 6007 | db mining | Hs.258933 | AW589231 | 7276337 | he27g09.x1 cDNA, 3' end /clone=IMAGE:2920288 /clone_end=3' | -1 | AAATGTTGAGCAACTGTTCAATAACA GCACTAATTGTGTGTTCAATGGCT |
| 6008 | Table 3A | Hs.304925 | AW592876 | 7280068 | hg04d05.x1 cDNA, 3' end /clone=IMAGE:2944617 /clone_end=3' | -1 | CTGGCACATCCAGGTTTTAGAGCAGG CAGCCTGAGATTTCAAAATGAGG |
| 6009 | Table 3A | Hs.298654 | AW614181 | 7319367 | hg77d03.x1 cDNA, 3' end /clone=IMAGE:2951621 /clone_end=3' | -1 | GGAGCGGAATACAGTAAAGCACTG GACTGACCTAAGAGTTTGTCTTCTGC |
| 6010 | Table 3A | Hs.259842 | AW614193 | 7319379 | cDNA FLJ11025 fis, clone PLACE1003968, moderately similar to 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT /cds=(159,1145) | -1 | ACACCATTTCAGCGTTGGATCACAGA CAGCTCTTCTTTATATCCCAGCA |
| 6011 | Table 3A | Hs.342967 | AW629176 | 7375966 | 602619939F1 cDNA, 5' end /clone=IMAGE:4745649 /clone_end=5' | -1 | CCACCTTGCTGCCTTTTGAAACACTC AGGAAATATAGTTGGCTAAAACCTG |
| 6012 | Table 3A | Hs.140720 | AW629485 | 7376275 | FRAT2 mRNA, complete cds /cds=(129,830) | -1 | CACCTCGCAACGGAGTGTGTTGAAATT GTGGTGGTCTGATTATAGGATT |
| 6013 | db mining | Hs.175437 | AW771958 | 7704007 | hn66h09.x1 cDNA, 3' end /clone=IMAGE:3032897 /clone_end=3' | -1 | GCTTTGGCAGATGGATTAACTTGTT CTTTTGGAGCCAGATCAATATCTA |
| 6014 | Table 3A | Hs.151393 | AW778854 | 7793457 | glutamate-cysteine ligase, catalytic subunit (GCLC), mRNA /cds=(92,2005) | -1 | AGAATGCCTGGTTTTCGTTTGCAATT TGCTTGTTGAAATCAGGTTGTAA |
| 6015 | Table 3A | Hs.109441 | AW780057 | 7794660 | cDNA FLJ14235 fis, clone NT2RP4000167 /cds=(82,2172) | -1 | TTCTGAACATTTTAGTCAAGCTACAAC AGGTTTGGAAAACCTCTGTGGGG |
| 6016 | Table 3A | Hs.343475 | AW873028 | 8007081 | 601556208T1 cDNA, 3' end /clone=IMAGE:3826392 /clone_end=3' | -1 | TGCAAGTGGATGGTTTGGTATCACTG TAAATAAAAAGAGGGCCTGGGAAA |
| 6017 | Table 3A | Hs.166338 | AW873324 | 8007377 | h192a07.x1 cDNA, 3' end /clone=IMAGE:3009396 /clone_end=3' | -1 | GTGGCTTTTCTGTTGACGCCAAAGGT TACTCCCTCTGCCTACCATAAAA |

Table 8

| | | | | | | | |
|------|-----------|-----------|----------|---------|---|----|---|
| 6018 | Table 3A | Hs.90960 | AW873326 | 8007379 | 602563938F1 cDNA, 5' end /clone=IMAGE:4688769 /clone_end=5' | -1 | ACCTCCTACGCTCTGTTTTCTGGCTGT GGTGACTTGGGATTTTTAACCTTA |
| 6019 | Table 3A | Hs.120243 | BE044364 | 8361417 | gamma-parvin (PARVG), mRNA /cds=(0,995) | -1 | ATCGTTGGATTATCTTTGAACCCCTT TGTGTGGATCATTTTGAGCCGCCT |
| 6020 | db mining | Hs.157489 | BE047166 | 8364219 | 602462536F1 cDNA, 5' end /clone=IMAGE:4575393 /clone_end=5' | -1 | AGCTCCAAAGTGGTTTGATGACCACA GGCTAAAATTCATAGTCTTAAAAAT |
| 6021 | Table 3A | Hs.82316 | BE049439 | 8366494 | interferon-induced, hepatitis C- associated microtubular aggregate protein (44kD) (MTAP44), mRNA /cds=(0,1334) | -1 | TCAGAAAGGAGAAAACACAGACCAAA GAGAAGTATCTAAGACCAAGGGA |
| 6022 | Table 3A | Hs.121587 | BE217848 | 8905166 | 602637362F1 cDNA, 5' end /clone=IMAGE:4765191 /clone_end=5' | -1 | GCATCACGATTTGTCTACATAAGTCC AGTTCATCTCGCGTTTGTITTTGGC |
| 6023 | Table 3A | Hs.5734 | BE218938 | 8906256 | meningioma expressed antigen 5 (hyaluronidase) (MGEA5), mRNA /cds=(395,3145) | -1 | ATACAGGGTTCCATCCAGAAAGCATT CAGTCAGAGCAAGTTAAAGTCAGT |
| 6024 | Table 3A | Hs.203772 | BE220869 | 8908187 | F5HD region gene 1 (FRG1), mRNA /cds=(191,967) | -1 | AAGTGCCAGATTTTGATAATCACCAG CCTCTCATTTCACTCCTATGTTGC |
| 6025 | Table 3A | Hs.73931 | BE220959 | 8908277 | major histocompatibility complex, class II, DQ beta 1 (HLA-DQB1), mRNA /cds=(57,842) | -1 | ACCCTTGGTCACTGGTGTTTCAAACA TTCTGGCAAGTCACATCAATCAAG |
| 6026 | Table 3A | Hs.128675 | BE222032 | 8909271 | hr61g11.x1 cDNA, 3' end /clone=IMAGE:3133028 /clone_end=3' | -1 | AGCTCTGGAGCCTTTGCTTCCTCAAA TACGAGCGGGAAGTGGCTTGAGCG |
| 6027 | Table 3A | Hs.167988 | BE222301 | 8909619 | neural cell adhesion molecule 1 (NCAM1), mRNA /cds=(201,2747) | -1 | AAGTTGCTCTGTGCTAAAGCAAGCGT GGGATGATCCTACCTACCTCTAGG |
| 6028 | Table 3A | Hs.79914 | BE222392 | 8909710 | lumican (LUM), mRNA /cds=(84,1100) | -1 | ATTTGGACAGATGCAGAAGGAAGTGT TAGTGAGTCAAGACAAACACATCT |
| 6029 | Table 3A | Hs.99237 | BE326857 | 9200633 | hr65h06.x1 cDNA, 3' end /clone=IMAGE:3133403 /clone_end=3' | -1 | CCCCTACCCCTGGAAAGTAATATACT GAAGTCTCATCATACTGTTTGGG |
| 6030 | Table 3A | Hs.83623 | BE328818 | 9202594 | nuclear receptor subfamily 1, group I, member 3 (NR1I3), mRNA /cds=(272,1318) | -1 | TGTTTCGTAATAATTAAGGTCTGGC CCAGAAGACCCACTCAATTGCCCTT |
| 6031 | Table 3A | Hs.27774 | BE348809 | 9260662 | 602386841F1 cDNA, 5' end /clone=IMAGE:4515730 /clone_end=5' | -1 | AGCTAGTGATGTTTTGTCCAAAGGAA GATTCTGACAACAGCTTCAGCAGA |
| 6032 | Table 3A | NA | BE348955 | 9260808 | hs91h01.x1 NCI_CGAP_Kid13 cDNA clone IMAGE:3144625 3', mRNA sequence | -1 | ACACAGACATATTGACCGCACACAAC ACTGAAATGGACTGACTTGAGAAA |
| 6033 | Table 3A | Hs.56156 | BE349148 | 9261087 | 601463367F1 cDNA, 5' end /clone=IMAGE:3866512 /clone_end=5' | -1 | TGGTTCTCTGATTGTGAATGAGCACC TGGATATGTCAATTAATGATGCCCA |
| 6034 | Table 3A | Hs.315050 | BE351010 | 9262791 | ht22g04.x1 cDNA, 3' end /clone=IMAGE:3147510 /clone_end=3' | -1 | GGTCCATGTACCCGTGAGTACACCC CTATGATTGGTTTGTGTCAAGAAG |
| 6035 | Table 3A | Hs.5027 | BE379724 | 9325089 | 601159415T1 cDNA, 3' end /clone=IMAGE:3511107 /clone_end=3' | -1 | TGCTAGTTCAGGTCCTCCAGGCATTG ATTTGTACAGTTAAACTCCGAGTG |
| 6036 | Table 3A | Hs.86437 | BE464239 | 9510014 | 602411368F1 cDNA, 5' end /clone=IMAGE:4540096 /clone_end=5' | -1 | ACAAGCATTTAGATCATAACATGGTA AAGCCTATTACCAGCCAATGTTGT |
| 6037 | Table 3A | Hs.127428 | BE466500 | 9512198 | Homo sapiens, Similar to homeo box A9, clone MGC:19648 IMAGE:2987818, mRNA, complete cds /cds=(62,880) | -1 | GGCCTACTGACCAAATTGTTGTGTTG AGATGATATTTAACTTTTGCCTAA |
| 6038 | Table 3A | Hs.21812 | BE467470 | 9513245 | AL562895 cDNA /clone=CS0DC021YO20-(3-prime) | -1 | AAGTTTGTGAGCAGCATTCTGAGTG TACGATATTGACCTGTAGCCGAGC |
| 6039 | Table 3A | Hs.122575 | BE502246 | 9704654 | endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4 (EDG4), mRNA /cds=(6,1061) | -1 | CGATAGAATTGAAGCAGTCCACGGG GAGGGGATGATACAAGGAGTAAACC |
| 6040 | Table 3A | Hs.279522 | BE502919 | 9705327 | hz81b08.x1 cDNA, 3' end /clone=IMAGE:3214359 /clone_end=3' | -1 | ATAGACTCCAAAGAGGCGTTAAGCAC CTGGTTTTCCTTTGGCTCAGAAAA |
| 6041 | Table 3A | Hs.197766 | BE502992 | 9705400 | clone 23932 mRNA sequence /cds=UNKNOWN | -1 | CTCAAACGAAATTGGGCAGGCCATTT GCGTGGTTTCTCTGGATAAGTTCC |
| 6042 | Table 3A | Hs.61426 | BE550944 | 9792636 | 602329933F1 cDNA, 5' end /clone=IMAGE:4431248 /clone_end=5' | -1 | GCACATGACAGTAAGCGAGGTTTTGG GTAATATAGATGAGGATGCCTAT |
| 6043 | Table 3A | Hs.201792 | BE551203 | 9792895 | 7b55h12.x1 cDNA, 3' end /clone=IMAGE:3232199 /clone_end=3' | -1 | TCCCAGAGTAAGTACAGTATCAAAT AGCAAGAGAGTTAGGATGAGGACT |
| 6044 | Table 3A | Hs.122655 | BE551867 | 9793559 | hypothetical protein MGC14425 (MGC14425), mRNA /cds=(318,686) | -1 | ACACAGGAACCGCTTACCCACCAGCT CTGCCCGCGTCTCTACCCGCATAG |
| 6045 | Table 3A | Hs.282091 | BE552131 | 9793823 | hw29b05.x1 cDNA, 3' end /clone=IMAGE:3184305 /clone_end=3' | -1 | TTCTTCCAAGAGAAATAACCCATTATAA GGCTAAAATGGAAGCTCCAGT |